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US-09-46

US-09-616-289-46

US-09-616-289-46

US-09-616-289-46

Sequence 46, Application US/09616289

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCIEROSIS

TITLE OF INVENTION: ATHEROSCIEROSIS

TITLE OF INVENTION: ATHEROSCIEROSIS

TITLE OF INVENTION: ATHEROSCIEROSIS

FILE REFERENCE: 10797-004401

CURRENT APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 46

LEWALTH: LABBER OF SEQ ID NOS: 53

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Sequence 119, App
Sequence 548, App
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US-09-029-938-11
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                            TYPE: DNA
ORGANISM: Homo
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NAME/KEY: CDS
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-Q=/Cogn21/USTSFTO spool/USIOS3523/runat_08062004_063749_29963/app_query.fasta_1.1422
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-LOOPEXT=0 -UNITS=Fits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Sequence 17,
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12. /Ggn2_6/ptodata2/lina/5B_COMB.seq:*
31. /Ggn2_6/ptodata/2/lina/6A_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-979-608A-17
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Arjona, Anibal A.
OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
TREATING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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GluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGlu
                                                                 GluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeuValAspAlaLys
                                                                                               GAGCATATCGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGGATGCCAAG
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                               901 GAGAACATGGAGCTGAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
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Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
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ZIP: 02110-2804
COMPUTER READABLE FORM:
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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                    543 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAG
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GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
                                                                                          AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
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                                                                                                                                                                                                                                                                                                             NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version;
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UUN-1997
APPLICATION NUMBER: US 60/031,930
PILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Coding Sequence
COGATION: 3..1592
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-979-608A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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Pred. No.:
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   123 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGGGC 182
                                                                                                                                                                                     117 ValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln
                                                                                                              GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr
                                                                                                                                  GAGGATGGGGTGAGCCGGCTGAACCCGAAGATGCAGAAGAAGTCCCGGACCTAT
                                                                                                                                                                                                               LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis
                                                                                                                                                                                                                                                                                                                                                                 423 CGAAGGCCACAGGAGAAAAAAAGCCAAGGGTTTGGGGAAGAGAGATCACGTTGCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                             177 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
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                                                                         183 ceccaactecaacatacteaecacatacteteteteseaeaataaccaeeeeeceeee
                                                                                                                                                                                                                                                                                                    363 AAGGGGGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCAT
                                                                                                                                                                                                                                                                                                                                        ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMet
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                                       ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
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                                                                                                                                                                                               Law, Simon w.
Arjona, Anjola A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1563 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/517,849 FILING DATE: 02-Mar-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 3...1592
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                        Sequence 17, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4697 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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2693.00
99.81%
99.81%
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STATE: MA
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Best Local Similarity:
Query Match:
DB:
                                                                         US-09-517-849-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-517-849-17
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                                                         RESULT
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37 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 56 	57 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 76	77 ArgGinLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGinGiyGiyProGiy 96	97 GluaspGlyalaGlnGlyGluProalaGluProGluaspAlaGluLysSerArgThrTyr 116 [117 ValalaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer 136	137 LysglyaspProasnThrGluGluIleargGlnSerAspGluValGlyaspArgAspHis 156	157 ArgargFroGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMet 176	177 GlnThrLeuAsnThrLeuSerThrProGluGluLySLeuAlaAlaLeuCySLySLySTyr 196	197 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 216	217 GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 236	237 AlaargSerLysLeuGluSerLeuCysArgGluLeuGlnargHisAsnargSerLeuLys 256	257 GluGluGlyValGlnargAlaArgGluGluGluGluLysArgLysGluValThrSerHis 276	277 PheclinvalThrLeuasnaspileGlnLeuGlnWetGluGlnHisasnGluArgasnSer 296	297 LysLeuargGlnGluasmWetGluLeualaGluargLeuLysLysLeuIleGluGlnTyr 316 	317 GluLeuargGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu 336 	337 ValAspAlaLysLeuGInGInAlaGInGluMetLeuLysGluAlaGluGluArgHisGIn 356	357 ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 376	7 LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu	FF 3
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Qy 437 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 456 Db 1263 GAGAGCACCAACAAGGCCCTGCTTGAGATGCCTCAGGAAAAAAAA	gAlaLeuGlnThr 476	Company Comp		ro H		ď	; Patent No. 6632923 ; GENERAL INFORMATION: ; APPLICANT: Lees, Ann M.	. 1969, ADDEL 3. . Arjona, Anibal A. INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TANDANTON: DEOTTER AND THEFT HER IN DIAMOGRAM	; TITLE OF INVENTION: ATHEROSCLEROSIS; TITLE OF INVENTION AND INDICATOR ; FILE REFERENCE: 10797-004001 ; CURRENT APPLICATION UNMERS: 105/09/616,289 ; CURRENT FILING DATE: 2000-07-14	FRIOR APPLICATION NUMBER: US 09/517,849 PRIOR FILING DATE: 2000-03-02 PRIOR FILING DATE: 1000-03-05 PRIOR FILING DATE: 1977-11-26	FRIOR APPLICATION NUMBER: US 60/031,930 FRIOR FILING DATE: 1996-11-27 FRIOR FILING DATE: 1996-11-27 FRIOR FILING DATE: 1997-6-03	EXAL H	; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KRY: CDS	; LOCATION: (3)(1592) US-09-616-289-17 Alignment Scores.		96.70% Intellige: 4 Gaps: 66.70% Tre_no_616_200_17 (1_0607)	LysserSerProGlyGlnProGludalglyProGluGlyAlaGlnGluArg	Db 3 AAAGCAGCCCAGGACAACCGGAAGCAGGACCCGAGGAGCCCAGGAGCGAGCCAAG 62

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1443 ActigAcAgragic circa GAGGAGGCCAGAGGGGCCTGGGGCTCAAGCACCCAGCTCCCCC 1502
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                                                 417 LysMetThrLysLysLysLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp
                                                                      1203 - AAGATGACTAAGAAGATCCAAGGTCCGGTCCCGGTCCCGGTCCCGGTCC
                                                                                                                437 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu
                                                                                                                                                                                LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SASTEM: DOS
SOFTWARE: FASTESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 GlyProGlnGluProThrSerAlaArgAla 546
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lees, Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-979-608A-14
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61 ATGAAGAATCAAGAAGAAAAGGGGGCTGCCAAAACAGCCCAAAAAGCAGCACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AAAACTGCTCAGCCTGGGGGGCTCTGTGATGTCTCTGAGGAGCTGAGCCGCCAGTTGGAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 GACATACTCAGTACATACTGTGTGGACAACAACCAGGGGGCCCCGGGTGAGGATGGGGTC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 CAGGGTGAGCCCCCTGAACCTGAAGATGCAGAGAAGTCTCGCGGCCTATGTGGCAAGGAAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GlnGluLysLysLysAlalysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeu 179
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Mismatches:
                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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                                                                                                                                               NAME/KEY: Coding Sequence
LOCATION: 61...1731
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
LENGTH: 4722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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2552.50
93.19%
91.04%
91.65%
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Best Local Similarity:
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Richardson P.C.
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4722 base pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.41e-206
2552.50
93.19%
91.04%
91.65%
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       ADDRESSEE: Fish
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Best Local Similarity:
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Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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                                                                                       ACGCTCAACGACATTCAGCTGCAGATGGAGCAGCACAACGAGCGCAACTCCAAGCTGCGC
                                                                                                                                                         958 CAGGAGAACATGGAGCTGGCCGAGCGGCTCAAGAAGCTGATTGAGCAGTACGAGCTGCGA
                                                                                                                                                                                                     320 GluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAla
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                                                                                                                              300 GinGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArg
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                                                      ThrieuAsnAspileGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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US-09-517-849-14
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81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100
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508
12
25
13
                                                                                                                                                                                      2.0
COUNTY: USA

COUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette.

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

CORRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/517,849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION NUMBER: US/09/517,849

FILING DATE: 26-MAR-2000

FILING DATE: 26-MOV-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-523-44 (1-546) x US-09-517-849-14 (1-4722)
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SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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i c	m	GGTCCTGAGCGGAGGCCAGCCCGCCACCACCTCCAAGGAGCA
: <i>ኢ</i>	GlnGluLysLysLysAlaLysGlyLeuGly	Oy GlyAlaGliAlaProSerSerProArgValIntGluAlaProCyS
ą	538 CAGGAAAAAAAAAAGCCAAAGGATCTGGGAAAGGAAGTCACGCTGCTGATGCAGACACTG 597	Qy 529 SerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSer
à 6	180 ASSITELEUSETTHFFOGLUGLULYSLEUNIAALALEUCYSLYSLYSTYTALAGLULEU 199 598 AACAGGGGGCACCCGAGAGAGAGAGAGAAGAAGAAGAGAGAGAGAGAGAGAGAG	
:	200 LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln 219	RESULT 7 US-09-616-289-14 ; Sequence 14, Application US/09616289 ; Patent No. 632923
g & :	LeuvalGinGluLysAspHisLeuargGlyGluHisSerLysAlaValLeuAlaArgSer 	GENERAL INFORMATION: ; APPLICANT: Lees, Ann M. ; APPLICANT: Lees, Robert S. ; APPLICANT: Lees, Robert S.
a k	LysleugluserLeucysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGly	APPLICANT: Arjona, Anibal A. TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDIN TITLE OF INVENTION: PROFESINS AND THEIR USE IN DIAGNOSIN
අ :	778 PAGCTCGAGAGCCTGTGCCGGGAGCTGCAGCGCGCCACCAACCGCTCAAGAAGAAGAAGA	; TILE REFERENCE: 10797-004001; CURRENT APPLICATION NUMBER: US/09/616,289
a a	GIBCAGCGAGCCCGAGAGGAGGAGGAGGAGGAGGAGGGAGGG	; CURRENT FILING DATE: 2000-07-14 ; PRIOR APPLICATION NUMBER: US 09/517,849 ; PRIOR FILING DATE: 2000-03-02
જે ક	280 ThrLeuAsnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArg 299	PRIOR APPLICATION NUMBER: US 08/979,608 PRIOR FILING DATE: 1997-11-26 PRIOR APPLICATION NUMBER: US 60/031,930
3 8	GlidesnMetGlubeudlaGlubrgbeulySteelleGluGlubrglubeuarg	; PRIOR FILING DATE: 1996-11-27 ; PRIOR APPLICATION NUMBER: US 60/048,547 ; PRIOR FILING DATE: 1997-06-03
qq	958 CAGGAGAACATGGCCTGGCCGGCTCAAGAAGCTGATTGAGCAGTACGAGCTGCGA 1017	NUMBER OF SEQ ID NOS: 53 SOFTWARE: FastSEQ for Windows Version 4.0
Oy Ob	320 GluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeuValAspAla 339 	; SEQ ID NO 14 ; LENGTH: 4722 ; TYPE: DNA
Qy Db	340 LysLeuGinGinalaGinGiuMetLeuLysGiuAlaGiuGiuArgHisGinArgGiuLys 359 	PEATURE: NAME/KEY: CDS LOCATION: (61)(1731
\dagger \dagge	360 AspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGln 379	Length:
3 8 8	GluthrhisLeulysGlnGlncellomatownstallisters (GluthrhisLeulysGlnGlnClncellomann 39	2552.50 milarity: 93.19% Similarity: 91.04% h:
ì ò	ThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThr	Gaps: 116-289-14 (1-4722)
음 & 음	1258 ACTCTTTCCAAAAGCAGGAGGTGTTCACCATTCAAACAGGAAATGGAAAAGAGGATGAAA 131/ 420 LysLysIleLysLeuGlubysGluThrThrHYFTYAATGSerArgTrpGluSerSer 439	Oy . 1 MetLysAsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsi
QQ	1318 AAGAAGATCAAGAAGCTGGAGAAAGAAGACCACCATGTACCGTTCCCGGTGGGAGAGCGC 1377	21
<u>ک</u> د	440 AsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGly 459 1378 alabaGGGCCGAGAGAGAGAGAGAAAAGAGGGGGAAAGAGGGGGAAAGAG	121
à	LeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsn	Qy 41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysPro
Dp.	ω (Oy 61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeu
상 음 장	480 ABDLeuABNLYSKTQALGINABDLeuBSTRALBGLYVIYGINGLYSSTLEULINSDEUL *9.9 1498 GACCTGAACTAGAGGGTGCAGGACCTGAGTGCCGGTGGCCAGGGCCCGTCTCCGACAGG T557	238
		Qy 81 Aspliedeuserinilyicysvalaspasiasidalyddyr.

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Db 1378 AACAAGGCCCTGCTTGAGATGGCTGAGGAGAAAA Qy	RESULT 8 PCT-US94-01101-1/c SEQUENCE 1, Application PC/TUS9401101 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: FACTOR: INTERLEUKIN-14 NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE COUTY: MAGGING	COUNTRY: USA COUNTRY: USA COMPUTER READLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM FC Compactible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version CURRENT APPLICATION DATA: PRIOR APPLICATION NUMBER: PCT/US94/01101 PRIOR APPLICATION NUMBER: US 08/005,156 FILING DATE: 15-JAN-1993 ATTORNEY/AGRAT INPORMATION: NAME: GATES, EDWARD R. REGISTRATION NUMBER: 31,616	REPERENCE/DOCKET NUMBER: BCB19//000WO TELECOWGUNICATION INFORMATION: TELEPHONE: 617/720-3500 TELEPHONE: 617/720-341 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LINGTHH: 1854 Dase pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: nucleic acid STRANDEDNESS: single HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORIGINAL SOURCE: ORIGINAL SOURCE: ORIGINAL SOURCE: CELL TYPE: LYMPHOMA
	LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln		GACTTTCTCTGAAGGAGG GACTTTCTCTCTGAAGGAGG GAGACCCACTGAAGGAGCACTACL ThrLeuSerLysSerSerGl ThrLeuSerLysSerSerGl ThrLeuSerLysSerGaAGCAGGA ACTTTCCAAAAGCAGGGA LysLysIleLysLysLeuGl Thrlill
8 4 8 4 8 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8		8 8 8 8 8 8 8	8 8 8 8 8 8 8 8

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CysargalaLeuGlnThrGluargasn 479
                                            GalyglyglnglySerLeuThrAspSer 499
                                                                                     GlualaProCysTyrProGlyAlaPro 528
ACACTCCGGGACAAAGAGCTGGAAGGC 1437
                                                                            IGIUProThrSerAlaArgAla 546
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899 CACTGGGGCATCAAGCACCCAGCTCCCCCAGGGTCACAGAAGCGCCTTGCTACCCAGGAG 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 aProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys--
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE READABLE FORM:

MEDIUM TYPE Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT PAPLICATION DATE:

APPLICATION NUMBER: US/08/968,751

FILING DATE:

CLASSIFICATION NUMBER: 32,028

REPRESENCE/DOCKET NUMBER: ONYX1024 GG

REPRESENCE/DOCKET NUMBER: ONYX1024 GG

REPRESENCE/DOCKET NUMBER: ONYX1024 GG

TELEPHONE: (510) 222-9758

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1191 base pairs

TYPE: NUCLEIC ACID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1191 base pairs

TYPE: NUCLEIC ACID NO: 5:

STRANDEDNESS: double
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                                                                                                                                                                                                           APPLICANT: Rubinfeld, Bonnee
APPLICANT: Polakis, Paul G.
APPLICANT: Polakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Vuong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, In
                                                                                                                                                    Sequence 5, Application US/08968751
Patent No. 5948643
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
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Best Local Similarity:
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US-08-968-751-5
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Best Local Similarity:
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110 16 SerProGlyGlnProGluAlaGlyProGlu-GlyAlaGlnGluArgProSerGlnAlaAl 56 uGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSe

RESULT 10 US-09-616-289-51 Sequence 51, Application US/0961 Patent No. 6632923 GENERAL INFORMATION: APPLICANT: Lees, Ann M. APPLICANT: Lees, Robert S. APPLICANT: Lees, Robert S. APPLICANT: Law, Simon W. APPLICANT: Arjona, Anibal A. TITLE OF INVENTION: PROTEINS F. TITLE OF INVENTION: ANIBAL A. TITLE OF INVENTION: ANIBAL ANIBE S.	REFERENCE: 10797 WIT APPLICATION NUT APPLICATION NUT FILLING DATE: 20 APPLICATION NUT FILLING DATE: 19 FILLING DATE: 19	; SOFTWARE: FastSEQ for Windows 1; SQ ID NO 51; EAGTH: 22255; TYPE: DNA; ORGANISM: Homo sapiens US-09-616-289-51 Alignment Scores: 1.01e-51 Score: Pred. No.: 740.50 Percent Similarity: 40.56 Best Local Similarity: 39.06\$	ery Match: -10-023-5231200	Oy 21 GlyGlnProGluhlaGlyPr 	Qy 56
76 rargGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl 96	136 rLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHi 156	196		296 rivsLeuArgGlnGluAshMetGluLeuAlaGluArgLeuLysIvsLeulieGluGlnTy 316	
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GlySerSerGlaAlaProArgLysProGlu------- 56 UysanGlyalaalauysGlnSeranProLysSerSerPro 20 ProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40 CAGGGGGAGCTGTGGGGTCGGCCTCGCTTCTGGACTTAC 2339 CCGGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGC 2399 CTGGCGAGTTGGCGGAGCTGCCCCTCTAAGCACAGAACAG 2459 TTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGT 2579 CGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGT 2519 DENSITY LIPOPROTEIN BINDING AND THEIR USE IN DIAGNOSING AND TREATING LEROSIS 22255 182 7 23 255 Length:
Matches:
Conservative:
Mismatches:
Indels: -616-289-51 (1-22255) JS/09/616,289 7-14 09/517,849 Version 4.0 08/979,608 60/031,930 60/048,547 616289

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        PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SEQ ID NO 1333
LENGTH: 614
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Patent No. 5616500
GENERAL INPRMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
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LOCATION: (1)...(614)
OTHER INFORMATION: n =
                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
CURRENT FILING DATE:
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Pred. No.:
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US-08-056-200-93
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Patent No. 6672186
EAPLICANT: ROBISON, Keith E.
TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
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                                                 85 ThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGly-GluPr 104
                                                                                                                                                                                                                                                                                                                                                                                               pProAsnThrGluGluIleArg-----GlnSerAspGluValGlyAspArgAspHisAr 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaLysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGlyProGluGly 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGln 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSer 84
APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichchyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using, Same
CORRESPONDENCE: 117
                                                                                                                                                                                                                                                                                          COUNTRY:

ZIP: 92660

ZIP: 92660

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/056,200

TTLING DATE: 30-APR-1993

TTLING DATE: 30-APR-1993
                                                                                                              STREE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach STATE: CA STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMONICATION INFORMATION:
TELERPIONE: (714) 760-0404
TELERAX: (714) 760-0502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY:: linear
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283.00
41.43%
24.48%
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1507..1644
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2512..8070
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1645..2511
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Best Local Similarity:
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NAME/KEY:
LOCATION:
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LOCATION:
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US-08-056-200-93
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MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: NAME/KEY: CDS LOCATION: 15071644 FEATURE: intron LOCATION: 16452511 FEATURE: COSTION: 25128070 B-800-644-93 mment Scores:	Pred. No.: 1.39e-13 Length: Score: 283.00 Matches: Percent Similarity: 41.43% Conserval Best Local Similarity: 24.48% Mismatch Query Match: 10.16% Indels: DB: 2 Gaps: US-10-023-523-44 (1-546) x US-08-800-644-93 (1-	Oy 10 AlaAlaLysGlnSerAsnProLysSerSerPro	Qy 30 AlaGlnGluArgProSerGlnAlaAlaProAla' ::: Db 3096 AGAAGAAAGAAGAGAGGGGGGGGGGGGGGGGGGGGGG	Qy 45 GlyProGlySerSerGlnAlaProArglysPro(Cy 65 SerGlyAlaLeuArgAspValSerGluGluLeu	Cy 85 ThrTyrCysValAspAsnAsnGlnGlyGlyPro	Qy 104 oalaGlubroGluAspAl. ::::: bb 3336 GCGCGAGCAGCAGGAGAGGGCGCGAGCAGGA	Qy 119 gAsnGlyGluProGluProThrProValValAs:	Oy 139 pProAsnThrGluGluIleArgGlnSe :::::::	Oy 157 gargProGlnGluLysLysLysAlaLysGlyLe	Qy 177 nThrLeuAsnThrLeuSerThrProGluGluLy	Oy 197 aGluLeuLeu-GluGluHisArgAsnSerGlnL	Qy 217 InSerGinLeuValdinGluLysAspHisLeuA ::::::::::::::::::::::::::::::::::::	Oy 237 laArgSerLysLeuGluSerLeuCysArgGluL
Qy 408 heThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysG 428 Db 4289 TGAAGGGGGGAGGAGAGAGGGGCCACGAGGCTGCTGAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	488 euseralaglyglyglnglyserLeuThraspserGlybrogluargargProgluglyProgluargargProgluglyPlint	528 528 4570	RESULT 13 US-08-800-644-93 ; Sequence 93, Application US/08800644	INFO	; APPLICANT: KIM, In-CyU ; APPLICANT: Chung, SOG-II ; APPLICANT: Park, Sang-Chul ; TITLE OF INVENTION: Trichchyalin and Transglutaminase-3 and : TITLE OF INVENTION: Mehode of Insing Same	Martens, Olson & Bear	, ve	ORM: ppy disk compatible	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/800,644	; FILING DATE: 14-FBB-1997 ; CLASSIFICATION: 424 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/056,200	1993 ION: el F. 36,799	; REFERENCE/DOCKET NUMBER: NIH054.001A ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (714) 760-0464 ; TELEPEAX: (714) 760-9502	; INFORMATION FOR SEQ ID NO: 93: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 9551 base pairs ; TYPE: nucleic acid	STRANDEDNESS: single TOPOLOGY: linear

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ogluglyalaglnalaargfhralagln 64
                                                                                                                                                                                                                                                                                                                                    codlygluhspglyaladlngly-GluPr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCGCGAGCAGCAG-----CTGA 3706
                                                                                                                                      ;
rgctccggaaggaagaagaagtrgca 3155
                                                                                                                                                                                                                                                                                                         AGGAAGAGCAGCAGCAAAGGCTGAG 3275
                                                                                                                                                                                                                                                                                                                                                                                                             | | | ::: | | | 3395
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BAGGAGGAGGCGCGAGCAGCTGAG 3506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 snGlyGluLysGluProSerLysGlyAs 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euGlyLysGluIleThrLeuLeuMetGl 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysLeuAlaAlaLeuCysLysLysTyrAl 197
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                                                                                                       oGlyGlnProGluAlaGlyProGluGly 29
                                                                                                                                                            aVal------GluAlaGlu 44
                                                                                                                                                                                                                                                                             uSerArgGlnLeuGluAspIleLeuSer 84
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582 GCTCCAGGACACCCAGGAGTTGCTTCAAGAAAACCCCGGCAGAAGCTCAA---CGTGTC 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 54
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            APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
                                                                                                                                                                                                                                                                                                              COMPULEN. .....

MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANDES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
FREREANCE/DOCKET NUMBER: 2115-00869COB
TELECOMMUTICATION INFORMATION:
TELEPHONE: (810) 641-0200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
TISSUE TYPE: subtype (inv16)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-023-523-44 (1-546) x US-08-533-306A-5 (1-2680)
                                                                                                                                                             ADDRESSEE; Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
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  APPLICANT: Collins, Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SerProGlyGlnPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA to mRNA
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279.50
38.90%
22.99%
10.04%
                                                                                                                  NUMBER OF SEQUENCES: 14
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POSITION IN GENOME:
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HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                     48303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                              3761 AGCAGCGGCTGAAGCGCGGAGCAGGAGGAGGCGCGATTGGCTGAAGCGCGAGGAGGAGAAA 3820
                                                                                                                                                                                                                                                                                                         3881 GGCGCGAACGTTGGCTGAAGCTCGAGGAGGAGGAGGCGCGCGAGCAGCAGGAGAGGCGCG 3940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4178 AGGAGAGGCGCCAGCAGCGGCTGAAGCGCGAGCAGGAAGAAGAGGCTCGAGCAGCGACTGA 4237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1238 AG-----CGCGAGGAGGTGGAGACTCGAGCAGGAG---GAGAGCGCGCGAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1289 TGAAGCGCGGAGGAGCCGGAGGAAGAGAGGCGCCACGAGGCTGCTGAAGAGCGAGGAGCAGG 4348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1349 AG------GAGAGGCGCCACGAGCAACTGAGGGGCGCGAGCAGCAGCAGGAAAGGCGCG 4396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1510 CGGGAGCGGATTAAGAGCCGCATCCCGAAGTGGCAGTGGCAGCTAGAAAGCGAAGCCGAC 4569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 isGinArg--------GluLysAspPheLeuLeuLysGluAlaValG 368
                                                                                                                                                                274 hrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluA 294
                                                                                                                                                                                                                                                              294 rgAsnSerLysLeu------ArgGlnGluAsnMetGluLeuAlaGluArgLeuL 310
                                                                                                                                                                                                                                                                                                                                                          310 ysLysLeulle-----GluGlnTyrGluLeuArgGluGluHislleAspLysValPheL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 ----ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 luSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 laLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 heThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysG 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 roGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaP 528
                                                                  257 luGluGlyValGlnArgAlaArgGluGluGluGlu------LysArgLysGluValT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 ysHisLysAspleuGlnGlnGlnLeu------
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684 CCAGCTGCACGAGGAGATGCAGGCCAAGCAGAACCTGGAGCGCCACATCTCCACTCTCAA 743

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Sequence 5, Application US/08533306A Patent No. 2837457 GENERAL INFORMATION: APPLICANT: Liu, Pu

74 GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly 93

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CAAGAACGICCAIGAGCIGGAGAAGICCAAGCGGGCCTTGGAGACCCAGAIGGAGAI 1265
                                                                                                                                                                                                                                                                                                                                          GAAGACGAGCTGGAAGAGCTGGAGGACGAGGA-----CTGCAAGCCTCGAAGACGCCAA 1319
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                                                                          plleGinLeuGlnMetGluGinHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMe
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|aagaagctggaaggggacctgaaagacctggagcttcaggccgactctgccatcaagg
                                                                                                                                      sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr
                                                                                                                                                                                                                         gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe
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                                                sLeuAlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy
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804 GGAAGAGGGAAGAAGAGGTICCAGAAGGAGATCGAGAACTTCACCCAGCAGTACGAGGA
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101
225
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia,
TISSUE TYPE: subtype (inv16)
POSITION IN GENOME:
CHEOMOSOME/SEGMENT: 16 [inv (16) (p13q22)]
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Matches:
    2115-00869DVC
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639 TACGAAGCTGCGCCAGCT----
REFERENCE/DOCKET NUMBER: 2115
TELECOMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEPAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2680 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                         CDNA to mRNA
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279.50
38.90%
22.99%
10.04%
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                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNI HYPOTHETICAL: NO
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Best Local Similarity:
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US-08-742-923A-5
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DB:
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Align Pred. Score Perce	Best Query DB:	08-10 Oy	9 & B	g &	g S	Š í	8 8	3	ò	, q ₀	ò	og Og	ò	qq	03	qu	6	qq	ò	QQ	ò	qq	ŏ	QC C	ò	q	à	qq	δλ	qq
Oy 471CysargalaLeuGlnThrGluargasnaspLeuAsnLysargValG1 486	Cy 486 nAspLeuSeralaGlyGlyGlyGlySerLeuThrAspSerGl 500 ::::::	Oy 500 yProGluargArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 520- Db 2249 CAGAGAAAGGCAATGCCAGGGTCAAGCGTCAAGAGGCAGCTGGAGGAGGAGGAGGAGGAGGCAGAGGGAGG	Qy 520 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 534	RESULT 16 US-08-533-306A-3 . Seminne 3 Innlication 118/08533306A	5 m 2	u s, Francis S.	no, Michael J , David , Markons for	VENTION: Mainers for Defection of Wilders 1 VENTION: Rearrangements	SS.	.O. Box 828 omfield Hills	; STATE: MI ; COUNTRY: USA	; ZIP: 48303 ; COMPUTER READABLE FORM:	lop PC		CURRENT APPLICATION NUMBER: 10/08/533,306A	; Filing Date: September 25, 1995 ; CLASSIFICATION: 435	; ATTORNEY/AGENT INFORMATION: ; NAME: Smith, Deann F.	; REGISTRATION NUMBER: 36683 ; REFERENCE/DOCKET NUMBER: 2115-00869COB	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (810) 641-1600	; TELEFAX: (810) 641-0270 ; INFORMATION FOR SEQ ID NO: 3:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 2887 base pairs	띦	Ξ) ORIGINAL SOURCE:) ORGANISM: Homo sapiens	; INDIVIDUAL ISOLATE: Sample 1 ; TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo	orype : m.		i NAME/KEX: CUS LOCATION: 12658	US-08-533-306A-3

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1244
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951 CATCCAGCTCTCCGACTCGAAGAAGAAGCTGCAGGACTTTGCCAGCACCGTGGAAGCTCT 1010
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|1011 GGAAGAGGGAAGAAGAGGTTCCAGAAGGAGATCGAGAACCTCACCCAGCAGTACGAGA 1070
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           Length:
Matches:
Conservative:
Mismatches:
Indels:
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789 GCTCCAGGACACCCAGGAGTTGCTTCAAGAAGAAACCCGGCAGAAGCTCAA---CGTGTC 845
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           TITE OF INVENTION: Markers for Detection of Chromosome ITILE OF INVENTION: Rearrangements NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 828
CITY: Bloomfield Hills
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101
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                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,923A
FILING DATE: NO. 5869611ember 1, 1996
CLASSIPICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                         CLASSITIONING
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
REPERENCE/DOCKET NUMBER: 2115-00869DVC
TELECOMOUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
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INDIVIDUAL ISOLATE: Sample 1
TISSUE TYPE: Acute myelomono
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David
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POSITION IN GENOME:
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Query Match:
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                                                                                                                                           USA
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STATE: M
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                     LeuAlaGluArgLeuLy 310
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                                                                                                                                                319 -ArgGluGluHisileAspLysValPheLys-
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APPLICANT: Liu, Pu, APPLICANT: Collins, Francis S. APPLICANT: Siciliano, Michael J.
                                                                                    sLysLeuIleGlu
                          tGlu--
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Qy 36	00	rgMetCysGluLeuM	etLysGlnGlnGluTh	Z-	388
199,	00	CGGGAAGGAACGCAĊ	TCCAGGACGAGAAGCC	TAGCCTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCCTGGAGGCCCGGATCGC 2	2057
Qy 38	œ	aLeuTyrThrGluLysPheGluG	uGluPheGlnAsnThrLeuSerLysSerS	ValPh	408
Db 205	œ	AGGAGGAGCTGGAGG	AGGAGCAGGCAACAT	CCAGCTGGAGGAGCTGGAGGAGGAGGCCAACATGGAGGCCATGAGGGAC 2:	2112
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7		AGGAGCTCCGGAGCA		 GGGGCCGTCAAGTCCAAGTT 2	0 (
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Db 2337		sagagaaacagggagg	caccaagtcgctdaa	CAAGAAGCTGA	396
Qy 486		nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp	ySerLeuThrAsp		200
Db 2397		III I-GCTGCAGGTGGAGC			455
Qy 500		rgArgProGluGlyPr	roGlyAlaGlnAlaPr	yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 52	20
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Alignment Sco Pred. No.: Score: Percent Simil	t scores: .: Similarity:	3.35e-13 278.00 41.87%	Length: Matches: Conservative:	8948 146 114 ,	

Oy 284 eGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGl 304	304 uLeuAlaGluArgLeuLy 	520 -GINGINHISIIQASDLYS	527 ELYSHIBLYBASDICUGINGINGINGINGINGINGINGINGINGINGINGINGING	347 tledulyseluaideluarghiselaintyesspriededulgedulyseluarara 	367 1GluserGinArgMetCysGlubeuMetLysGl ::: 5729 GGATCAAAGAATCAGTGTTACTCAGGTGGTACAGGA	386 nLeuAlaLeuryYrInrGluys	OY 401 USETLYSSETSETGIUVALFREIDENBEIRELYSGINGLUNGLUNGSGUTTELYSTY 12.1	TrpGluSerSerAs 44	440 niysalaLeuLeuGluMetAlaGluGluLysThrValArgAspLys	456 -GluLeuGluGlyLeuGlnVallysll :-: 6023 TGAGATCGAAAGACTCCAAGCAGAGT	473	483 SAFQVAIGHASPHEUSSETAIGLYGINGIYSELLEGIIIMSEPSETGIYFFOCIAN. 6143 GGAGATTGATAAACTCAGACA	BAGTG 62	E 6203 T	NEOUL 12 US-09-480-884A-119 Sequence 119, Application US/09480884A Patent No. 648259597	APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Hosken, Mancy A. APPLICANT: Hosken, Mancy A.	NATION: GALY R. NVENTION: COMPOUN NVENTION: AND DI	
arity: 23.51% Mismat 9.98% Indels 4 Gaps:	US-10-023-523-44 (1-546) x US-09-643-597-119 (1-8948) QY 9 GlyAlaAlaLysGlnSerAsnProLys	Oy 18SerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgPro 34	Oy 35 SerGlnAlaAlaProAlaValGluAlaGluGly-ProGlySerSerGlnAlaProArgLy 54	Oy 54 SPro		Oy 76 rargGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl 96		SGITCA	131 131 4925		Oy 171 ulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAl 191	191	Oy 211 sLeu	Oy 218 rGlnLeuValGinGluLysAspHisleuArgGlyGluHi 231 :::	Oy 231 SSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGl 249 :::::	Oy 249 nArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaAr 264 :::	Oy 264 gGluGluGluGluLsArgLysGluValThrSerHisPheGlnValThrLeuAsnAsp11 284	

FILE REPERENCE: 210121.455C6 CURRENT APPLICATION NUMBER: US/09/48C,884A CURRENT FILING DAFE: 2001-08-27	oy O	218 rGlnLeuValGlnGluLysAsp
	Sy Gy	SSerLysAlaValLeuAlaAr
7. ONCANASH: NOME SAPIEM US-09-480-884A-119	A A	249 MAIGHISASMAIGSEILEULYSGIU :::
Alignment Scores: 9.35e-13 Length: 8948 Score: 278.00 Matches: 146 Percent Similarity: 41.87% Conservative: 114	og Op	264 gGluGluGluGluLysArgLysGluValT) ::::: ::: 5399 AGAAGATAAAAGCAGA
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Qy 54 SPro 65 Db 4664 ACAGCAGCTGAAGTTGAGCTGAACACACACACACAACAACAAAAAAAA	3 40	3-5
66	\dot{\dot{\dot{\dot{\dot{\dot{\dot{	367 1GluSerGlnArgMetCysGluLeuMe :::::::
Db 4724 ATATAAGCAATCTCTTGATGATGCTGCCAAAACCATCCAGGATAAAAAGAAGAGATAGA 4783 Qy 76 FALGGInLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGInGlyGlyProGl 96	λō	386 nLeuAlaLeuTyrThrGluLys
4784 AAGGT	g .	
96 yGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThr	à a	401 userbyssersergiuvaikneinrinikr ::: 5849 AAAATCAACTCTAGAGGCAGAAACCAGGGT
DD 4824AAATGCCIGGAGGTGAAAACGCGAGATTACAAAGGGTCCA 4864 Qy 116 -TyrValAlaArgAsnGlyGluProGluProThrProValValAsnGl 131	8 8	
4	g ò	9909 AAIICAGAAIGACIGAAICAGIGGAAGACACAGAGACACAGAGACACAGAGACACAG
Oy 131 yGlubysGlubroSerLysGlyAspProAsnThrGluGlulleArgGlnSerAspGluVa 151	ପ୍ର	
151 1GlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGlyLysGl	\$ a	456 -GluLeuGluGlyLeuGlnValLysIleGl :::
Db 4985 GAAGGACCAGGATATCACGCGGTTCCAGAACTCTCTGAAAGAGCTGCAGCTGCAGAAGGA 5044 Ov 171 vtlambet antiquimaeClambet anabaantatangaagan colambet angaambet	ò	473Al
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aLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLy	ර් සි	483 sArgValGlnAspLeuSerAlaGlyGlyGl : :: 6143 GGAGATTGATAAACTC
CAAGAGGAAGAAGCTGGAAGGAAGGCTGGAAGGCATGAGGAGGTCGCTGAAGGAGCAAGG	ò	503 gArgProGluGlyProGlyAlaGlnAlaPr
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	218	LeuValGlnGluLysAspHisLeuArgGlyG
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	5279	crcriciaagarcaaggcccr
	24	GluGlyValGlnArgAlaAr 264
	5339	CACTTGAGGAATGAGCA
	264	
	5399	
	284	eGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGl 304
	5429	CAAAATAGAAATTGAGAGGCTGCAGTCTCTCACAGAGAACCTGACCAAGGAGCACTTGAT 5488
	304	uLeuAlaGluArgLeuLysLysLeu1leGluGlnTyrGluLeuArg 319
	5489	Griagaadaagaacidegaaccidaggcigdagiacgaigaccidaddagagagacgaag 5548
	320	-GluGluHisIleAspLysValPh 327
	5549	
	327	eLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMe 347
	5609	CAACAACCGGACCCTGGAACTGCAGGGGCTGATTAATGATTTACAGAGAGAG
	347	tLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaVa 367
	5669	SAGACAGGAAA
	367	GluSerGlnArgMetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGl 386
	5729	rcracr
	386	nLeuAlaLeuTyrThrGluIvsPheGluGluPheGluAsnThrLe 401
	5789	akagcaaggcracagaggcragaggargagcraak
	401	rSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLys
	5849	AAAATCAACTCTAGAGGCAGAAACCAGGGGGGGGGGGGG
	421	GuGluLysGluThrThrMetTyr
	5909	acctgaatcagtggaagactcaatattcccgcaaggaggaggct
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•	5969	GAAGATAGAATCGGAAAGAGAAAAGAGTGAGAGAGAAGAAGAACAGTCTTAGGAG 6022
	456	-GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArg 472
	6023	TGAGATCGAAAGACTCCAAGCAGAGATCAAGAGAATTGAAGAGAGGGGGGGG
	473	
	6083	ACAGT
	483	uSerAlaGlyGlnGlySerLeuThrAspSerGlyPro
	6143	GGAGATTGATAAACTCAGACA 6163
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lGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGl
                                                                                                                            171 ulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAl
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APPLICANT: HOSKEL, NAMOY A.
TITLE OF INVENTION: COMPOUNDS AND METHODS ITILES OF INVENTION: AND DIAGNOSIS OF LUNG FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
KUNBER OF SEQ ID NOS: 350
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                                                                                                                                  US-09-542-615A-119
; Sequence 119, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy A.
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US-09-542-615A-119
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Best Local Similarity:
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Pred. No.:
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APPLICANT:
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Qy 35 SerGlnAlaAlaProAlaValGluAlaGluGly-ProGlySerSerGlnAlaProArgLy 54	4625 ACA	Db 4664 ACAGCAGCTGGAGGTTGAGCTGAGACACACAGAGGAACAGAGAGAG	Oy 66	Qy 76 rArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl 96	Oy 96 yGluAspGlyAlaGlnGlyGluEroAlaGluEroGluAspAlaGluLySSerArgThr 115	OY 116 -TYFValAlaArgAsnGlyGluProGluProThrProValValAsnGl 131	Oy 131 yGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluVa 151	Oy 151 IGlyAspArgAspHisArgArgProGInGluLySLySLySLySlyLeuGlyLySG1 171	Qy 171 ulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGlubysLeuAlaAl 191 :::::::::::::::::::::::::::::::::::	Oy 191 aLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLy 211	Qy 211 SLeu	Qy 218 rGlnLeuValGlnGluLysAsp	OY 231 SSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGl 249 ::::::	Oy 249 nArgHisAsnArgSerLeuLysGluGluGlyvalGlnArgAlaAr 264 	264 gGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIl ::::::::::::::::::::::::::::::::::	Oy 284 eGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGl 304	304 uLeualaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArg	5489 GITAGAAGAAGAACTIGGGAACCTGAGGCTGGAGTACGATGACCTGAGGAGAGGA	Db 5549 CGAAGCGGACAGTGATAAAAATGCAACCATCTTGGAACTAAGGAGCCAGCTGCAGATGAG 5608
Db 5729 GGAATCAAAGAATCAGTGTACTCAGGTGGTACAGGAAAGAGAGAG	5789 CAAAGTCCTGGAGGAAGACAAGGCTGCAGAGGCTGGAGGAGGAGGAGGATGAGTGGGG	Oy 401 uSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLy 421	421 silelyslysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAs	5909 AAITCAGAATGACCTGAATCAGTGGAAGACTCAAIATTCCCGCAAGGAGGAGGCIATTAG 440 nLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys	9959 GANG-TALMGAALUGGAAAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGA	ON 473AGORANGARICAAGARICAAGARAATITGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	483 sArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluAr	6143 GGAGATTGATAAACTCAGACA 503 GAGATTGATAAACTC 303 GAGATTGATAAACTC 304 GACA 505 GAGATA 505 GAGACA 505 GAGATA 505 GAGACA 505 GAGATA 505 G	6164 GCGCCCATATGGG	Db 6203 T 6203 RESULT 22 US-09-221-107-119	pplication US/09221107 338 TION: g, Tongtong	; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER; FILE REFERENCE: 210121.455C2; CURRENT APPLICATION NUMBER: US/09/221,107; CURRENT FILING DATE: 1998-12-22	; NUMBER OF SEQ ID NOS: 161 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 119 ; LENGTH: 8948	; TYPE: DNA ; ORGANISM: Human US-09-221-107-119	Alignment Scores: 3.35e-13 Length: 8948 Score: 278.00 Matches: 146 Percent Similarity: 41.87% Conservative: 114	est Local Similarity: 23.51% Mismatches: uery Match: 9.98% Indels: B: Gaps:	-10-023-523-44 (1-546) x US-09-221-107-119 (1-8948)	OY GIVALANIALUNGSITASHIRIDINGSI	Oy 18SerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgPro 34

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                                          theulysGluAlaGluGluArgHisGluArgGluLysAspPheLeuLeuLysGluAlaVa
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DET
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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APPLICATION NUMBER: US/09/023,655
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 31.72.
CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AAATACGNACAAATGAAACAGCAAGCAGTACAACTAAAACAGCAGCTTTCTCTTTATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAsp
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                         PA-0001
            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.51e-14
273.00
59.15%
44.51%
                                                                                                                                                                                                                                                                       TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
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HEREWITH
                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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LIBRARY: PANCNOT01
CLONE: 224798
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3854
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--GCTAGAGGCGGAGCGCACAGC 3230
                                                                                                                                                             3282 GATCAGTGAGAGGCTAGAGGCGAAGCCGGTGGGGCCACATCTGTGCAGATAGAGATGAACAA 3341
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                                                                                                                       156
                                                                                                                                                                                                       156 sArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 uleuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSe 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3735 ACTGATTTGGCAGCTGACCCGGGGCAAGCTCTCCTATACCCAGCAGATGGAGGACCTCAA
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                                                                                                                         --- AspArgAspHi
                                                                                                                                                                                                                                                                                       176 tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTy
                                                                                                                                                                                                                                                                                                                                                                     196 r-----AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLe
                                                                             3231 CCGGGC-----CAAGGTGGAGAAGCTGCGCTCAGACCTGACCCGGGAGCTGGAGGA
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                                           ProThrProValValAsnGlyGluLysGluProSerLysGlyAspProAsnThr-GluGl
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                                                                                                                           144 ulleArgGlnSer---AspGluValGly----
  3183 GGCACGCATCGAGGAGCTGGAGGAGGA----
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                     GENERAL INFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Leinwand, Karen L.
APPLICANT: Vikstrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/938,105 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2946 rerggaggarecerggaggaggaggaggr----
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                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3595-4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01e-13
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36.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                          Denver
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                                                                                                                                                                                                                              COUNTRY: U
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US-08-938-105-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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No.:
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SEQ ID	LENG	, ORGAN US-08-87	Aliqument	Pred. No.	Percent S		US-10-023	à	QD (χ. Έ	3 8	da da	ìò	qq	ò	qq	λ٥	Ор	ð í	go o	Š i	ad .	à i	8 &	අය	ò	qa	ò	q q	ؠڽ	qq	ά	đđ	δ
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	383 uLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLy 403	4260 GAAGGAGGCGCCCCCTGAGCACAGAGCTCTTCAAGCTCAAGAATGCCTATGAGGA 4316	403 sSerSerGluValPheThrThrPhelysGlnGluMetGluLysMetThrLysLysIle 422	4317 Gréficresadecercesagaéctresadesegadaacaagaacerceagagadatere 4376	422 422	4377 AGACCTGACTGAACAGCTGGGAGAAAGGGGGTAAAAATGTGCACGAGCTGGAGAAGATCCG 4436	423 -LyslysleuGlulysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl 442	LeuGlnVa		462 lLys1leGlnArgLeuGluLysLeuCysArg	4551 CAAGGCAGAGATCGAAAGGTGGCAGAGAAGGACGAGAGAAGAAGGAGCAGCCAAGCG 4610	473Gluar 478	4611 CAACCACCTGCGGGTGGTGGACTCCTTACAGACCTCCCTGGATGCCGAGACACGCAGCGG 4670		4671 CAACGAGGCCCTGCGGGTGAAGAAGAAGATGGAGGGGGGACCTCAATGAGATGGAGATCCA 4730	487 pleuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyFroGluArgArgProGluGl 507		CCCAAGCCCACTTGAAGGACACCCAGCTGCAGGTGAAGGATGACGCAGTCCGTG	523 sTyrProGlyAlaProSerThrGluAlaSerGl 534		534 yGlnThrGly 537	4895 CGGAGCTGGA 4904	RESULT 25	-08-8/5-43-58-5 Sequence 5, Application US/08875435B Patent No. 6593304	APPLICANT: Hasegawa, Kazuhide	APPLICANT: ATAKAWA, EMI APPLICANT: Oda, Shoji APPLICANT: WARMA, Vinner		AFFLICANT: Suganara, Michiniro AFFLICANT: Ishivama, Haruo	OF INVENTION:	OF INVENTION:	FERENCE: 07898-013001	CURRENT APPLICATION NUMBER: US/08/875, 435B CURRENT FILING DATE: 1997-07-25 DBIOD ADDITIONATION NUMBER: DCM/TRG/AA13	FRIOR AFFILTATION NOMBER: FCI/UF90/UUI54 PRIOR FILING DATE: 1996-01-25 NUMBER OF SEO ID NOS: 5	RE: FastSEQ for
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3549 GAAGACGGAGCTGGAGGACACGCTGGGCCCACCCAGCGAGGAGGTCCGGGGCCAA 3608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3771 ------CAAGCAGACGCTGGAGAAGAAGAACGCAGACCTGGCCGGCGAGCTGCG 3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3879 GCAGGAGCTGCAGTCCAAGTGCAGCGATGGGGAGCGGGCCCGGGCGGAGCTCAACGACAA 3938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3669 gecccadáriccádak---gargagdcágaaacacacacaggdgragaggagcrec--- 3722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GluProGluAspAlaGluLysSer----ArgThrTyrValAlaArgAsnGlyGluPro 123
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4116 GCTGGAGGACGAGGAACAGCCTGCAGGAGCAGCTGGACGAGGAGATGGAGGCCAAGCA 4175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4296 AATTGAGAGCCTCACCCAGCAGTAC-------GAAGAGAAAGCAGCTGC 4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4236 GCAGGACTTTGCCAGCACCGTGGAGTCCTTGGAGGAAGGCAAGAAGAGGGTTCCAGAAGGA 4295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 Glu------ProThrProValValAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LysLysLysAla 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAl 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LeuCysLysLysTyrAlaGluLeuLeuGl 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 ProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGlu 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 AlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIle
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4176 GAACCTGGAGCGCCACATCTCCACCTCTCCGACTCTCAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                           4 GlnAspLysLysAsnGly---AlaAlaLysGlnSerAsnProLysSerSerProGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 LeuSerThrTyrCysValAspAsnAsnGlnGly---------
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178
104
213
295
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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D NO 5
3TH: 6644
E: DNA
ANISM: Oryctolagus cuniculus
75-4358-5
                                                                                                                                                            1.38e-12
268.50
35.74%
22.56%
                                                                                                                                                                                                          Similarity:
scal Similarity:
fatch:
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us-10-023-523-44.rni

1597	Qy .359 ysAspPn Db 1657 AG	Qy 377 ysglngl	Db 1708 TGGAGCA	Oy 397 heGlnAs 	417	Db 1807 CCCGGGC	436	Db 1867 AGGACCT	1927	465	Db 1987 AGCAGGA	2047	Qy 491 G1yG1	Db 2106 CTGGGGG	Oy 505ProGl	2166	07 323 CYSIY 	Qy 536 hrGlyPr	2286	RESULT 27 US-09-976-594-268	, Sequence 268, Appli , Patent No. 6673549	; GENERAL INFORMATION ; APPLICANT: Furness ; APPLICANT: Furnest	TITLE OF INVENTION : FILE REFERENCE: PA	CURRENT APPLICATION CURRENT FILING DAT	; PRIOR APPLICATION ; PRIOR FILING DATE:	, NUMBER OF SEQ ID No ; SOFTWARE: PERL Pro	; LENGTH: 6617 : TYPE: DNA	GRGANISM: Homo sal	; NAME/KEY: MISC IS ; OTHER INFORMATION US-09-976-594-268
		GAAGCAGGCCTGTGAAAAGATGATCCAGGCGCTGGAACTGGACCCCAACCTCTACCGCGT	57 GlyAlaGlnAlaArgThrAla-GlnSerGlyAlaLeuArgAspValSerGluG'uLeuSe 76	rArgGlnLeuGluAsp1leLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl	CCTGAAGGTCACCGACATCATCGTCTCCTTCCAGGCAGCTGC-CCGGG	96 yGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTy 116	rValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSe	938CCTGAG	136 rLysglyAspProAsnThrGlugluIleArgGlnSe 148	rdspGluValGlyAsp-ArgAspHisArgArgProGlnGlubysLysL	:-: 1021 CACTGCTGCAGGTGACGCGGCAGGATGAGGTGCTGCAGGGCCCCAGGAGCTGCAGA 1080	ysAlaLysGlyLeuGlyLysGluIleThrLeuMetGlnThrLeuAsnThrLeuSerT		184 hrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuCluGluGluHisA 204	recorrections in the second control of the s		GluHisSe	1210 CCGAGGAGACGCGGGGGAGGCTGGCAGCCCGCAAGCAGGAGCTGGAGCTGG	244 euCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGlyValGlnArgAlaA 264 :: ::	rqGluGluGluGluLysArqLysGl		284 leGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetG 304	1357 TAGAGGCCCACCTTGAGGCTGAGGAGGTGCGCGCAGAAGCTGCAGCTGGAAGGTGA 1416	304 luLeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeuArgGluGluHisIleA 324	1417 CGACAGAGGCAAAAATGAAGAAATTTGAAGAGGACCTGCTGCTCCTGGAAGACCAGAATT 1476	324 spLysValPheLysHisLysAspLeuGlnGlnGlnGlnLeuValAspAlaLysLeuGlnG 343	1 mA] mG] u		347
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binder, Jenny
ON: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
PA-0041 US
ION NUMBER: US/09/976,594
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-----CTGAAGCGGAGGCTGGATGGGAGGAGCTCAGAGCTGCAGGAGATGG 1707
                                                                                                                                                 cccagcracraaanccraccaaagcraaacaacccraccaaga 1866
                                                                                                                                                                                                                                        ----GAGGGTGGGG 1806
                                                                                                                                                                                                                                                                                                                                                                                       TGGAGTCTGAGCCTGTGGCCAGGACCAAGGCGGAGAAGCAGCGCCGGGACCTGG 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGACATGGAGGACCGCCTACGGAAGGAGGAGAAGGGTCGCCAGGAGCTGGAGA 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crescarceaceaceacadrecadadecreas-ecadeceaceaceaceacea 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGCCCTGGAGGCCGAGGTGCCGAGCTGCGGGCAGCAGCTGAGCTGCAG 2225
                                      heLeuLeuLysGluAlaVal----GluSerGlnArgMetCysGluLeuMetL 377
                                                                                                                    InGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluP 397
                                                                                                                                                                                                  snThrieuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluL 417
                                                                                                                                                                                                                                                                            hrLysLysIleLysLysLeu---GluLysGluThrThrMetTyrArgSerArgT 436
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DN: Incyte ID No. 6673549 994387.65
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                                                                                                                                                                                                                               CTGCCCTGGCCAGGGCAGAAGAC---
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NN NUMBER: 60/240,409
FE: 2000-10-12
NOS: 1143
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TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:	q À	1764 TGCAGAGAGGAGAGGCCTCCTTAAGGCAGCAGCAGCTCTCAAGCAGCTGGAGGC 1823
& THIBEAULT	g :	1824 ACTGGAGAAGAGAAGACTGCCAAGCTGGAGATTCTGCAGCAGCAACTTCAGGTGGCTAA 1883
,	4 4	TRANSCRIPTION OF THE TRANSCRIP
	& ଶ	110 aGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValAs 130
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	λō	
US/08/466,390	qu	1983 AGCCCGCCAGGAACAGCATGAGGCCCAGGCCCAGGTTGCAGAGCTAGAGTTGCAGCTGCG 2042
	& A	146 gGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysAlaLy 166 :::
29 MTP-013 N:	8 8	
	8 &	
	qq	2154 TGAAGAGAGAAGCGCAGGGCTGCAGATGCCCTGGAAGAGCAGCAGCGTTGTATCTCTGA 2213
	λό qq	191 aLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMet 210
	& 65	211
	λō	GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLy
PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR PROTEIN THAT DEFINES A NOVEL PATHWAY FOR SRORFGATTON OF DPOTETINS AT MITCHES	d y	2334 TCAGGCTGAGACTGAAGTCCTGCGGGGAGCTGGCAGAGGCCATGGCTGCCCAGCACCAC 2393 240 stendinsertencysaradinien
	³ 원	
	8 8	249GlnArgHisAsnArgSerLe 255
ive:	3 & A	uLyscludluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGlu caaGGAGAATGTGAGAAGGCCCCCCAGGAGCTGCAGGAGGCAAAGGAAGG
M.smatches: 254 Indels: 198 Gaps: 27	& B	273ValThrSerHisPheGlnValThrLeuAsnAspIleGln 285 ::: ::::: : ::::
US-10-023-523-44 (1-546) x US-08-466-390-3 (1-6306) Qy 6 LysLysAsnGlyAlaAlaLysGlnSerAsnProLysGerSerProGlyGlnProGluAla 25	ð í	286LeuGlnMetGluGlnHisAsnGluArgAsnSerLy 297
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26 GlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAla 43 1447 CCGCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	qa	
Thral	è 8	308 -ArgLeuLysLysLeuIle 313 :: :: :: 2751 CCGCTTGGAGCAGGAAGGCAGGAACAGCAGCAGGAAACAGCCTCCCGGGAGGT 2810
GGTAGCGGAGAGCAGGAACTAGGCAGGACCATGCCCAGCAACTGGCCACTGC 1763 GInSerGlyAlaLeuArgAsp	්දු පි	314

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1587 AGAGAAGCAGGCCCAGCTAGCACAGACCTCCAACAGGAAAAACAGGCCTCCCAGGGCCT 1646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GlyProGluGly-----AlaGlnGluArgProSerGlnAlaAlaProAlaValGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GluGlyProGlySerSer-GlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 -ValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GCCCGGGACAGTGCCCAGACCTCAGTGACACAG-
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155
108
254
198
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                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 a-----GlnSerGlyAlaLeuArgAsp-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PITTERE ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELEPRONGHUTCATION INFORMATION:
TELEPRONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6305 base pairs
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEVELAND, DON W
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36.83%
21.71%
9.19%
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LOCATION: 1..6306
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1395-1408
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Best Local Similarity:
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AUTHORS:
AUTHORS:
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JOURNAL:
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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plysvalphelysHisLysAspLeuGlnGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAl 344
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APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAIAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
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                                                                                       344 aGlnGluMetLeu----
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125 HIGH STREET
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ADDRESSEE: TESTA, HU
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COUNTRY: USA
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130 031/yGlu/yGGllproSert/yGJlyAspProAsmThtGllGlu	1982 Qy 370 146	2042 Db 3051	2097 Oy 410	2153 Db 3141 CCTGC	191 Up 3		2273 Qy 442		240 Db 3381	AC 2393 Oy 482 nLysArgValGlnAspLeuSe 248 248 248	2453 Cy 498	2513 Db 3500		285 Db 3617 AAGATGAAGGCCCAGGTGGCCCGGGGCC	2630 RE		307 APPLICANT: TOUKATLY, GARY APPLICANT: LIDGARY GRAHAM 7-FO TITLE OF INVENTION MOVEL MAILGUANT	313	CORRESPONDENCE ADDRESS 2810 ; ADDRESSEE: TESTA, H	324 ; STREET: 125 HIGH 5 CITY: BOSTON 7 STATE: MA	2870 ; COUNTRY: USA ; ZIP: 02110	2930 COMPUTER KEALABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	352 ; CURRENT APPLICATION INTERER. APPLICATION INTERER. APPLICATION NUMBER.	; FILING DATE: 06-JUN-1995
		gGlnSeraspGluValGlyAspArgAspHisArgArgProGlnGluLy			184 rProGluGlubys	191 aleuCysLysLysTyrAlaGluLeuLeuGluGlüHisArgAsnSerGlnLysGlnMet	GCTGAAGGCAGAGACCCG	AGAAGAGGGCTGGGCGC	223GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLy	2334 TCAGGCTGAGACTGAGACTCCTGCGGCGGGGGTGGCAGGGCCATGGCTGCCCAGCACACACA	::: CAGCTCGTCAAAGAAGTAGCT	GGATAGCCAGCAAGAGGAGGCACAGTATGGCGCCATGTTC	255 uLysGluGluGlyValGlnArgAlaArgGluGluGluGluGluLysArgLysGlu	2514.dataGataGata1G1CatGataGGCCCGCCAGGAtGCTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2571 AGGCATAGAATCCCACAGCGAGCTCCAGATAAGCCGGCAGCAGCAGAACTAGCTGAGCT 286ArgAsnSerLy	2631 CCATGCCAACCTGGCCAGAGCACTCCAGCAGGTCCAAGAAGGAAG						324 piysvalPhelysHisLysaspLeuGinGinLeuvalAspAlaLysLeuGinGinAl :::		

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                       CGGCTGACCCAGGAGCGGGCCGTGCCCA 3050
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|CTCAACGAGCGTGTGGAGTTCGCTAC 3140
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             gGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLy 166
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                                                 sGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeu----SerTh
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                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1.6306
PUBLICATION: 1.06306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUANE A
AUTHORS: CLEVELAND, DON W
AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SEGREGATION OF PROTEINS AT MITOSIS
JOURNAL: J. Cell Biol.
VOLUME: 116
PAGES: 1195-1408
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ. EDWUND R
REGISTRATION NUMBER: 27,629
REFERENCE/DOCKET NUMBER: MTP-0
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 248-7000
TELEPAX: (617) 248-7000
TELEPAX: (617) 248-7100:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
TYPE: Nucleic acid
TYPE: Nucleic acid
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36.83%
21.71%
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC LENGTH: 6306 base par TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: CDN FRATURE: NAME/KEY: CDS LOCATION: 16306 PUBLICATION INFORMATION AUTHORS: SILLAK, ILL: STRUCTION INFORMATION AUTHORS: CLEVELAND, TITLE: PROPENT ITALE: SEGREGATION OUTHORS: CLEVELAND, TITLE: SEGREGATION OF COUTHORS.	y VOLUME: 116; j PAGES: 1395 j DATE: MAR-1 US-08-195-487-3 Alignment Scores: Fred. No.: Score: Forcent Similarity: Best Local Similarity: Best Local Similarity: DB: US-10-023-523-44 (1		Oy 26 Db 1647 Oy 44 Db 1707	Oy 63 Db 1764 Oy 71 Db 1824	Oy 90 Db 1884 Oy 110	н н	Oy 146 gGlnSerAspGluValGlyAspArgAspHisA Db 2043 GTCTGAGCAGCAAAAGCAACTGAGAAAGAAA Oy 166 sGlyLeuGlyLysGlulleThrLeuLeuMetG
	3381 AGAGGTGAGCAGCTGGA 482 nLysArgValGln 3441 ACGAGCCTCGAGGCTGA 498 pSerGlyProGluArgAr 498 pSerGlyProGluArgAr 515 rProArgValThrGluAl	9	487	TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA HURMITZ & THIBEAULT STREET: 53 STATE STREET CITY: BOSTON CITY: BOSTON		#1. 195,	AT TE

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                                   GluMetGluLysMetThrLysLysIl 422
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APPLICANT: TOUGATLY, GARY
APPLICANT: TOUGATLY, GARAM
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBBAULT
STREET: 125 HIGH STREET
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/483,924
ELLING DATE: 07-UTN-1995
CLASSIFICATION: 435
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION UNDRER: 27,829
REFERENCE/DOCKET NUMBER: MTP-C
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: CDS
LOCATION:
LOCATION:
LOCATION:
NUNFORMATION:
AUTHORS: COMPITON, DIABA
AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF WOVEL PATHWAY FOR
TITLE: SEGREGATION OF PROTEINS A NOVEL PATHWAY FOR
TITLE: SEGREGATION OF PROTEINS A MITOSIS
JOURNAL: J. Cell Biol.
VOLUME: 116
PAGES: 11395-1408
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Matches:
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Mismatches:
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2334	23
240	augluserLeuCysArggluLeu
2394	CAAAGAAGTAGCTGCCTGGCGTGACGGGTATGA 245
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255	ulyscludludlyvalGlnargAlaArgGluGluGluGludluLysaxgLysclu 272
27	ValThrSerHisPheGlnValThrLeuAsnAspIleGln 285
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3201	CAAGCTTCGTGGTCTGGAGGCAGCCCAGATAAAAGAGCTGGAGGAACTTCGGCAAACCGT 32
422	elystysteugluLysgluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl 442 :: :: :: :: :: :: :
3261	GAAGCAACTGAAGGAACAGCTGGCTAAGAAAAGGAAGGAA

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1764 TGCAGAGGAGGAGGCCTCCTTAAGGGAGCGGGATGCGGCTCTCAAGCAGCTGGAGGC 1823
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Matches:
Conservative:
Mismatches:
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36.83%
21.71%
9.19%
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Best Local Similarity:
                                                       MAR-1992
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                                                  3321 ccaarcreadecrecrecagacagacageccaacageccccaagcredaagaacacreggec 3380
                                                                                                                                                                                                                                                  3441 ACGCAGCCTCGAGGCTGAGCGGGCCTCCCGGGCTGA-GCGGGACAGTGCTCTGGAGACTC 3499
                                                                                                                                                                                                                                                                                                                                                 3500 TGCAGGGCCAGTT---AGAGGAGAGGCCCAGGAGCTAGGGCACAGTCAGAGTGCCTTAG 3556
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442 aLeuleuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnVa 462
                                                                                                                                                                                                   482 nLysArgValGln------AspLeuSerAlaGlyGlyGlnGlySerLeuThrAs 498
                                                                                                                                                                                                                                                                                                                                                                                                      515 rProArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly-- 534
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                                                                                                    462 liysileGlnArgieuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF OF NUMA, AN INTRANUCLEAR
TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SECREGARION OF PROTEINS AT MITOSIS
JOURNAL: JOURNAL OF CELL BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1617 AAGATGAGTGGAAGGCCCAGGTGGCCCGGGGGCCGGCAAGA 3656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 -----GlnThrGlyProGlnGluProThrSerAlaArg 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06160
FLING DATE: 19930621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9306160 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO. 3: SEQUENCE CHARACTERISTICS:
LENGTH: 6306 Dasse pairs
TYPE: mucleic acid
STRANDEDNESS: single
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PUBLICATION INFORMATION:
AUTHORS: COMPTON: JULYA
AUTHORS: CLEVELAND, DON W
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QY 498 pSerGlyProGluArgArgProGlyAlaGlnAlaProSerSe 515	US-09-023-655-1463 Sequence 1463, Application US/09023655 Sequence 1463, Application US/09023655 Sequence 1463, Application US/09023655 GENERAL INFORMATION: APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508	CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTY: USA ZIP: 94304 MEDIUM TYPE: FLORMY: MEDIUM TYPE: FLORMY: COMPUTER READABLE FORM: MEDIUM TYPE: FLORMY: COMPUTER: ISM PC compatible	S HOLFAN	FILING DATE: CLASSIFICATION: ATTONEY/AGENT INFORMATION: NAME: Zeller, Karen J. REGISTRATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0001 US TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: AFFLEDENCHE. (66,0) 855-0555	FOR FOR CHAR 75 DUC1 DNES SOU	Y: GENBANK 9641957 -1463 res: 3.42e-11 Length: 253.00 Matches:	ry: 38.28% Conservarity: 22.99% Mismatc arity: 22.99% Mismatc 4.00% Gaps:	US-10-023-523-44 (1-546) x US-09-023-655-1463 (1-7596) Qy 12 LysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGly 26
2394 AGCTGAGGAGTGGAGCAGCTCGTCAAAGAAGTAGCTGCCTGC	286	2751 CCCTTGGAGACCTTGGAGGGGGGGGGGGGAGGAGGGGGAGGTT 2810 314	344 aGlnGluMetLeu	370 nargMetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTy 390	TTGGC Lysil S:	422 eLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl 442	ILYSI EGINArgieuGluLysieuCysargalaieuGlnThrGluArgasnAspleuAs	482 nLysArgValGlnAspLeuSerAlaGlyGlyGlyGlyGerLeuThrAs 498 ::: :::::::::::::::::::::::::::::::::

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Db 5032 GGCTCAGATGAAGGATTACCAAGGTGAATTAGAAGGCTCGTGCATCAGAGATGAGAT 5091		Oy 343 naladingluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAs 360	Qy 360 pPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlnGl 380	Oy 380 uThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnTh 400 : :::::	Oy theuserlyssersergluvalPheThrThrPheLysGlnGluMetGluLysMetThrLy 420	Oy 420 siysilelyslysleudlulysdluThrThrMetTyrArgserArgTrpGluSerSerAs 440	Cy 440 nLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLe 457 :: ::	Qy 457 uGluGly	Qy 465 nArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsn 482	Qy 483LysargValGlnAspLeuSeralaGlyGlyGlnGlySerLeuThrAs 498	Qy 498 pSerGlyProGluArgArgProGluGlyProGlyAlaGln 511	Oy 512AlaProSerSerProArgValThrGluAla	Qy 522 0CysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGl 537	537 yProGlnGluProThrSerAla	DD 5847 CCCTGAAGAACCGGCTGAGGCG 5868	US-09-688-188B-20; Application US/09688188B; Patent No. 6656716	; GENERAL INFORMATION: ; APPLICANT: PLOWING, REGGRY ; APPLICANT: MARTINEZ, RICARDO ; APPLICANT: MHYTE, DAVID	; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES ; FILE REFERENCE: 0.38602/03.28 ; CURRENT APPLICATION NUMBER: US/09/688,188B ; CURRENT FILING DATE: 2000-10-16	MBER: 09/29 999-04-14 MBER: 60/08	and the second s
	4081 GAGCAGTCGGATCCGGCAGCTGGAAGAGAAGAACAGTCTTCAGGAGCAGCAGGAGGA 4140 27 ProGluGlyAlaGlnGluArgProSerClnAlaAlaProAlaValGluAlaGlu 44	GlyProGlySerSerGlnAlaProArgLySProGluGlyAlaGlnAlaArgThrAlaGln 64	SerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSer 84	ThrTyrCysValAspAsnAsnGlnGlyGlyproGlyGluAspGlyAla		ValAlaArgAsnGlyGluProGluProThrPro-ValValAsnGlyGluLysGluPr	oSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAs [PHISALGARGE CONSTRUCTION OF THE PHISALGARGE CONTROL OF THE PHISALGARGE CONT	uMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLy 1	STYRAlaGlubeuLeuGluGluHisArgAsmSerGlnLysGlnMetLysbeuLeuGlnLy 2	stysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGl		uCyskrgGluLeuGln	4/32 GGARGACGARCICCAGGCCACGGAGGTGCCAAGCTTCGTCTGGAGGTCAACATGCAGGC 4791. 250ArghisAsnArgSerLeuly 256	4792 CATGAAGGGGCAGTTCGAGAGAGCCTGCAAACCAGGGATGAGCAGAATGAAGAGAAGAAGAAAAA 4851	256 sGluGluGlyValGlnArgalaArgGluGluGluGluLysArgLy 271	271 sGluValThrSer	286 uGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGluAsnMetGluLeuAl 306		The state of the s

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1049 CAGCTTAAAGAGGAGCTAAATGAAAACCAGAGTACCCCCAAAAAAAA	290 1229 301 1289	7 7 6 7	Oy 361 PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGluGlnGlu 380 1454 CTAAGACGAAGAGGTGTATGGAAGATTCGACAACAGGCTAAGATTTAAAGAA 1513 Oy 381 ThrHisLeuLysGluGlnLeuAlaLeuTyThrGluLysPheGluGlu 396 1514 CTCCAAATAAAAAGCAGTTTCAGAAAATCCGAAAATCCAAACCAGACAGA	397 1574 417	1619 437 1673	1733 GCACAGGAAGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAACTGGAGCTGTTG	459 GIYLDUSTRAINFELTE	
ILING DATE: 1998-04-14 DF SEQ ID NOS: 155 E: Patentin Ver. 2.1 D.20 : 3824 DNA SNH HOMO SapienS	Artylment Soles. Pred, No. 1.69e-11 Length: 3824 Score: 251.50 Matches: 139 Percent Similarity: 39.91% Conservative: 118 Best Local Similarity: 21.58% Mismatches: 196 Query Match: 9.03% Indels: 191 DB: 4.0S-09-688-188B-20 (1-3824)	OALAVAIGIUALAGIU		503 AIGATGGAGGAGACCACACAGTGATGTCTAACAGTTCTGTTATCCATTTAAAACCAGAG 97 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArg	OY 115 ThrTyrValAlaArgAsnGlYGluProfluProThrProValValanGlYGluLysGlu 134	Oy 155 ASPHisArgArgProGlnGluLySLySAlaLySGlyLeuGlyLySGlulleThr 173 Db 698ACGAGGCAAATGCAAGAACATGAGCAGGACTCTGAGCTTAGAGAACAAATGTCTGGC 754 Oy 174LeuLeuMetGlnThrLeuSenThrLeuSerThrProGluGluLySLeuAla 190 Db 755 TATAAGCGAATGAGGCGAAACATCAAAAGCAACAAGATGACTAGAAAACAAGCTAAAG 814	Oy 191 AlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsn 205	222 935 235 4 25 25 4 25 25 4 25

Qy 191 AlaLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsn 205	815	Qy 206SerGlnLysGlnMetLysEuleuGlnLysElnSerGlnLeuValGlnGlu 223	Qy 224	Cy 234 AlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg 253	4 SerLeulysGluGluGlyValGlnArgAlaArgGluGluGluGluGluGluGluGluGluGluGluGluGluG	Qy 269LysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIle 284	Qy 285 GlnLeuGlnMetGlu289 ::: :: Db 1169 CGACGTCAAAGACAATACCTAGAGCTGGAATGCCGTCGCTTCAAGAGAAGAATGTTACTT 1228	Oy 290GINHISASHGIUARGASHSGELLYSLEUARGGIN 300 :::	Oy 301 GluasnMetGluteualaGluargLeuLysLysLeuIleGluGlnTyrGluLeuargGlu 320	Qy 321 GluHisileAspLysValPheLysHisLysAspLeuGlnGlnClnLeuValAspAlalys 340	Oy 341 LeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAsp 360	Oy 361 PhebeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlnGlu 380 1454 CTAAGACGAAAGCATGTCATGGAAGTTCGACAACACCCTAAGAGTTTGAAGTTTTGAAGTTTTGAAGAA 1513	Oy 381 ThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 396 ::: ::: ::: :::	Oy 397 PhedlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 416	Oy 417 LybMetThrLysLysLesLysLeuGluiysGluThrThrMetTyrArgSerArgTrp 436 ::: :::::	Qy 437 GluSerSerAsnLysAlaLeuLeuGluWetAlaGluGluLysThrValArg 453 	Qy 453 453 Db 1733 GCACAGGAAGCAGAGTGCCAGGTTTTGAAGATGCAGCAGCAGGAACTGGAAGCTGTTG 1792	Oy 454	
Oy 535 GlnThrGlyPro 538	2105 GGTCCAGGACCT	RESULT 36 US-09-291-417D-20 . Semiance 30 Explication Ins/Depositation	; Patent No. 6680170; GENERAL INFORMATION: ; APPLICANT; PROFINAL INFORMATION: ; APPLICANT; PLOWMAN, GREGORY	MAYTE, DAVID NVENTION: STE20-RELATED PROJ SNCE: 038602/0329	CURRENT APPLICATION NUMBER: US/09/291,417D; CURRENT FILING DATE: 1999-04-13; PRIOR APPLICATION NUMBER: 60/081,784; PRIOR FILING DATE: 1998-04-14;	; NUMBER OF SEQ 1D NOS: 155 ; SOFTWARE PatentIn Ver. 2.1 ; SEQ 1D NO 20 ; LENCHT: 3824	; TYPE: DNA ; COCANISM: Homo sapiens US-09-291-417D-20	1.69e-11 251.50 39.91%	: 21.50% Intellations: 9.03% Indels: 4 Gaps: 46) x US-08-291-4170-20 (1-3824)	OAlavalGluAlaGlu 	3lnAla :::	ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 	81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly ::	97 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArg 	ThrTyrValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGlu	135 ProSerLysGlyAspProAsnThrGluGlulleArgGlnSerAspGluValGlyAspArg 647 CACTATGGAATGGAAACACTTTGCTACTATAGGACACGATAACGATA	155 AspHisArgArgProGlnGluLysLysAlaLysGlyLeuGlyLysGluIleThr	ACGAGGCAAATGCAAGAAGAAGAAGAACATCTGAGCTTAGAGAACAAATGTCTGGC	DD 755 TATAAGCGAATGAGGCGACAACATCAAAAGCAACTGATGACTCTGGAAAACAAGCTAAAG 814

Best Local Similarity: 21.91% Mismatches: 211 Query Match: 8.98% Indels: 176 DB: 3 Gaps: 30	46) x US-09-060-410-1 (1-3312)	Oy 39 ProAlaValGluAlaGlu	Qy 45GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla 60	61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu	1210		pAlaGluLysSerArgThrTyr 11		Oy 117 ValalaargasnGlyGluProGluProThrProValValasnGlyGluLysGluProSer 136	137 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis	Db 1417 CGTAATAGAGAACACTTTGCAACTATACGAACAGCATCACTGGTTACA 1464	Qy 157 ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIteThr 173		Oy 174LeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeu 192 :::	193	Db 1585 ATGGACGAACATCAGATTAGACAAAGATCTTGAAACTCAGCGCAACAATTTCGCT 1644	207 GlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu	1645	Oy 224				1819 AAGGAGGAGGTGAATGAAAACCAGAGCACACACAAAAAAGAAAAAGAAAAAAAA	Db 1879 AGCAGAAGGGAGAATATTCAAGGCAGAAGAAGAAGAAGCTAATCTTCTCGACGT 1938	287		Db 1999 CATAACTTGGAACAGGACCTTGTCAGGGAGGAGTTAAACAAAAGGCAGACTCAGAAGGAC 2058
Db 1853 GAGCTTGAACAGAGGTCTCCCTCCGGAGGGCACTCTTAGAACAAAAGATTGAAGAAGAG 1912		Leu	GAGATTGAAGCTTTTGACTCTGAAAGCATGAGACTAGGTTTTAGTAATATGG ASDSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerS	2033 TCTAATCTCCCCTGAG	Oy 517 ArgvalThrGluAlaProCysTyrProG17AlaProSerinrGluAlaG17y 334	535 GlnTh		RESULT 37 US.09-060-410-1	Apr ORA	, APPLICANT: Cobb, Melanie , APPLICANT: Hutchinson, Michele : APPLICANT: Chen. Zhu	; APPLICANT: Berman, Kevin ; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE	; TITLE OF INVENTION: THEREFOR ; NUMBER OF SEQUENCES: 26 ; ADDRESS: 26	BERRY LLP	; STREET: 6300 Columbia Center, 701 Fitth Avenue ; CITY: Seattle ; STATE: Washington) COUNTRY USA ; ZIP: 98104 ; COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MA-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	; CURKENI AFFLICATION DAIA: ; APPLICATION NUMBER: US/09/060,410 PILING DATE: 14-APR-1998	SHI	ROTESTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 860098.421	(20 (20	; TELEFAX: (206) 682-6031 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 3312 base pairs ; TYPE: nucleic acid	; STRANDEDNESS: single ; TOPOLOGY: linear ;	; NAME/KEY: CDS ; NOAME/KEY: ; LOCATION: 1213123 US-09-060-410-1	res: 1.84e-11 Length:	250.00 Similarity: 40.28%

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; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/EUS; ; LOCATION: (1)(4362) US-09-620-312D-248	Alignment Scores: Pred. No.: 8e-11 Length: 7453 Score: 248.50 Matches: 147 Percent Similarity: 38.54% Conservative: 102 Best Local Similarity: 22.76% Mismarches: 235 District Matches: 235	DB: 27 US-10-023-523-44 (1-546) x US-09-620-312D-248 (1-7453) QY	Db 4002 GAGCAGTCGGTAGCTGGAAGAGAGAGAGAGAGAGTCTTCAGGAGCAGGAGGA 4061 Qy 27 ProGluGlyalaGlnGluArgProSerGltAlaAlaProAlaValGluAlaGlu 44 Db 4062 GGAGGAGGAGGAGAAAAACTGCTAGAGAGTGCTGGAGTCCCAGTTC 4118	E 4	Qy 65 SerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSer 84	Qy 85 ThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100 :::	Qy 101GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 116	OY 117 ValalaArgAsnGlyGluProGluProThrProValValAsnGlyGluLyGGluProSer 136		Oy 157 ArgArgProGlnGluLysLysLysLysDlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 176	LeuCysLysLysTyr 	197 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 4478 GAGGAAGCCCTGCAGGGCCAAGGAGGAGGAGGAGGAGCAGCAGCAGCAGCA	GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHis	. 4 . 2 . 4 . 6 . 6 . 6	246 ArgGlubeuchanners	Db 4658 GACGAACTCCAGGCACGGAAGATGCCAAGCTTCGTCTGGAGGTCAACATGCAGGCCATG 4717

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----GAAGGACGCGGAGGCCCTGAGCCAGCGCCTGGAGAGGAAAGGCACT 4286
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                                                                    ------GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr
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URRENT FILING DATE: 2000-07-19
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FRIOR APPLICATION NUMBER: 09/552,317
FRIOR FILING DATE: 2000-04-25
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 249
LENGTH: 7501
                                                                                                                                                                                              Sequence 249, Application US/09620312D
Patent No. 6569662
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5773 GAAGAACCGGCTGAGGCG 5790
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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Jian-Rui
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tang, Y.
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ThrThrPheLysGlnGluMetGluLysMetThrLy	5306 GAGCTGCTCAACGACCGCTTC	422 IleLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsf:::	442 AlaLeuLeuGluMetalaGluGluLysThrValargAspLysGluLeuGlu 	459 GIV	467 LeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsn	483LysArgValGlnAspLeuSerAlaGlyGlnGlySerLeuThrAspSer	500 GlyProGluArgArgProGluGlyProGlyAlaGln	512 AlaProSerSerProArgValThrGluAla	523CysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyPro	539 GlnGluProThrSerala 544 ::: 5821 GAAGAGCGCTGAGGCG 5838	SULT 41 -09-220-132-79 Sequence 79, Application US/09220132	OMPOSITONS FOR THE 1	TILLE OF INVENTION: OF PROSTAIL CANCER THERAFIES AND THE DIAGNOSIS FILE REFERENCE: 07334-0740HER US/09/220,132 CURRENT APPLICATION NUMBER: US/09/220,132 CURRENT FILING DATE: 1998-12-23	PRICR APPLICATION NUMBER: US 60/079,303 PRICR FILING DATE: 1998-03-25 PRICR APPLICATION NUMBER: US 60/068,821 PRICR FILING DATE: 1997-12-24	NUMBER OF SEQ ID NOS: 191 SEQ TWARE: FastSEQ for Windows Version 4.0 LENGTH: 5857	TYPE: DNA ORGANISM: Homo sapiens -09-220-132-79		N. O.

2890 GAGCATCGAGCTGATCTCGACCAGCCCGAGCCACACACAC	
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402 SeriysSerSerGluValPheTrPheLysGlnGluMetGluLysMetThrLysLys 422 IlelysLysLeuGluLysGluThrThrPheLysGlnGluMetGluLysMetThrCochada 421 IlelysLysLeuGluLysGluThrThr	19 SerProdyGlarProdLudladlyProdludlyAladlnGluArgProSerGlnAla 37 3121 GCGCCTGAAGAGCATCAAGCTGGCGGGCTTCAAGTCCTTCGTCGACCAC 3068 38 AlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLySProGluGly 57 3067 GGTGAACTTCCCCAGCAACATGCGGCAGTGGGGCCGAAGGCTGCGGCAAGTC 3011 58 AlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArg 77 50 GGTGAACTTCCCCAGCACATGGCGGCAGTGGTAGGCCGCAAGGCTGCGGCAAGTC 3011 69 3010 GAACATCATCGCGGGGGGGGTGGTGGTGGTGGCGGAAGACTGCGCGGG 2951 78 GlnLeuGluAsplleLeuSerThrTyrCySValAspAsnAsnGlnGlyGlyProGly 96 5950 CGAGTCGATGACCATCTTCAACGGCTCGAATACCCGCAAGCCGCAGGC 2891 60 97 GluAspGlyAlaGln-GlyGluProAlaGlu

us-10-023-523-44.rni

ია კგ გევნობევსტემესგევნებები განისტიმესგება გამ გამ გამ გამ გამ გამ გამ გამ გამ გა	174 GGTGAACTTCCCCAGCAACATGGCGGCAGTGGTAGGGCCGAACGCCTGCGGCAAGTC	ις 60	231	78		Qy 97 GluAspGlyAlaGln-GlyGluProAlaGluProGluAs 109	Db 351 GAGCATCGACTGATCTTCGACAACGCCGAGACCACACTGGTGGGCGAATACGCCCAGTA 410	109 pAlaGluLysSerArghhTyrValAlaArgAsnGlyGluProGluProThrProVa	411 CGCCGAGATATCCATTCGCCGGCGGGTCTCGCGGGATGGGCAGAACACCTATTT	Qy 128 lVallanGlyGluLysGluProSerLySGLY	Qy. 139 -AspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgAr 158	Db 525 GGGGCCGCGCACTACTCGATCATCGAGGCATGATCTCCAAGCTGATCGAGGCGC 584	Oy 158 gProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlulleThrLe 174	174 nlenMetGlnThrLeuAsnThrLeuSerThrProGluGluLvsLeuAlaAlaLeuCvs	645 CCGCCGCGAAACCGAAAGCCGCTCGGACCCAGGAAACCTGGCACGCCTCACCGA	194	705 CCTGCGGGAAGAGCTGGGGCGGCAACTGGAACGCCTGCACCGGCAG	Oy 198 uLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLys	765 AAAATACCAGGAGCACAAGGCCGAGGAGCGCCAGCTCAAAGCCCAGCTGGGCGCCGTGCG	Qy 213 uGlnLysLysGlnSerGlnLevValGlnGluLysAspHisLeuArgGlyGluHisBerLy 233 .:::::::::::::::: ::::::: :::::::::	233	882		TCCGAACG	Qy 269 sarglysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGl 287 ::: :::	287 nMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGl	1032	Oy 307 uargleulysLysLeulleGluGluGluTyr	Db 1092 ACGGACCGCCAGGAAACCGAATGGCACCTCGGGCATGACCGTACCTTGCTCGCGACCCT 1151	Oy 318 uArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAs 338	Db 1152 GGCCGAGGAAATGGCCATGCTCGCACCGGAACTCACGC 1196	
Db 1888 1888	Qy 415 tGluLysMetThrLysLyslleLysLysLeuGluLysGluThrThrMetTyrArgSerAr 435	Db 1887 -GAGCGCCTGCAGGAGCGCGCCCTGCAGGAGGAGGCGTGGCCAGTTGGCGGCC 1831		Db 1830GACCCCGAGGACGCGGCGATCCTCGAACTCAACGAACAGGTGGCGATCGCCGAACT 1775	455 sGluLeuGluGlyLeuGlnValLyslleGlnArgLeuGluLysLeuCy	1774 GGCCCTGGAAGAACTGCAATTGCAGGAGCAGGCCAAGCCGAGGGACTCGAACAATTGCG	Oy 471 sArgAlaLeuGinThrGlukrgAshAspLe 481 ::: - sh. 1914 Charleshameda.charleshamada	1/4* CCASSANTISCASCASCIGGCCSCACACCASSGCGASSGCGASGIIGCASGCGCI 1037	1654 GAACGGGCGCATCGCTTCGCTGCAGCAGGCCCGCTCTCGATCCCGGACAGGG	lyAla- 5	1594 CGCCTTGGAGTGGTTGCGCGAGCAGGCCTGGAACAACGTCCGCGCCTTGGAAGGCTT	511GLIALIBEROSETSETFOATGARITINEGIA.	541	Db 1474 GGTCTTGCTGGACGGCTTCGACGGCTCGCCCTGGC 1439	Cy 541 roThrSerAlaArgAla 546	Db 1438 CGGCTTCGGCAAGGGCG 1422	RESULT 43 US-09-252-991A-15688	; Sequence 15688, Application US/09252991A ; Patent NO. 6551795 . Granpa, Taropamarion	CID SEQUENCES REL	ICS AND THERAP	CURRENT AFFLICATION NUMBER: 0299/02/18 CURRENT FILING DATE: 1999-02-18 - PRIOR APPLICATION NUMBER: 18.60/074.788	PRIOR FILING DATE: 19 PRIOR APPLICATION NUMB	; PRIOR FILING DATE: 1998-07-27 ; UNDER OF SEQ ID NOS: 33142 . SEG ID NO 15688	រុដិ៍		8.13e-11 Length:	243.0	: 23.13% Mismatches: 8.73% Indels:	4 Gaps:	-10-023-523-44 (1-546) x US-09-252-99.A-15688 (1-3606)	OY SETPTOGLOGINGINGINGINGINFGFIOSTINGIN	

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95 ProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArg 114
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          COMPUTER: TELOPOY disk
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
SOFTWARE Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 1:
SEQUENCE HARACTERISTICS:
LENGTH: 3489 base pairs
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Mismatches:
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44.22%
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APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
338 palarysLeuGlnGlnalaGlnGluMetLeuLysGlualaGlu--
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CORRESPONDENCE ADDRESS:
CADDRESSEE: COOPER & DULP
STREET: 1185 Avenue of the Americas
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Patent No. 5948676
GENERAL INFORMATION
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
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Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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Best Local Similarity:
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LeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCys 193
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APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 3
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 1, Application US/09298568 Patent No. 6322792

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Ver.
                                                    TYPE: DNA
ORGANISM: Kaposi's
                                                                                                                                               Percent Similarity:
Best Local Similarity:
              PatentIn
SOFTWARE: Pater
SEQ ID NO 1
                                                                                                           Alignment Scores:
                                                                                 US-09-410-399-1
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                                                                   AlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg
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APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit on
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NONBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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Patent No. 6482587
GENERAL INFORMATION:
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1774 CGGGAGCCACAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAG
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93
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sarcoma-associated herpesvirus
                                                                       Length:
Matches:
Conservative:
Mismatches:
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                                                                       1.39e-10
240.00
44.22%
18.53%
8.62%
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Pred. No.: Score: Sanda and Sanda	60	OY 118 AAGGASHOLYGUINFOURTHTOYALVAINALASHOLYGUUFS-GIUPTOSELLYSG 138 3241 AGGCGTGGGCATCCTCAGCGCGCTGCAGGAGGCCCTCGGGGCCAAGGAGGTG 3297 OY 138 LYASPFOASHTHGLUGLUILEARGINSETASPGLUVALGLYASPARGASP 155 3298 CGGACGCGAGCTGCGGCCCAGCTCCGAGCCCAGGCAGCAGCAGCAGCAGCTGGCTC 3357 OY 156HisargargProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrL 174 174 EULEUMAGGACCCTGGAGCCTGGAGCTGCAGCTGACAAAGCAAGACGCTGACAAAAGGAACTGCAGGCCTGAGCAGGCTGACAAAAAAAA	Qy 193 ysLystyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnM 210 Bb 3478 GGGAGAAGGTGGAGCTGGAGCTTCAAGAATCCAGAGGCTTTAGGAAGAAGAAGA 3537 Qy 210 etLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyG 230 Bb 3538 TAAACGCCTTGAGGAGTCAACAAGAACTTGGCTCTTGAATTAGAGCACGAGAAGGGA 359 Qy 230 luHisSerLysAlaValLeuAlaArgSerLysLeuGluS 243 Bb 3598 AGCTTACGGCCTCGGTCAGTCCAACGAGCACACACACACA	
274 ThrSerHisPheGlnValThrLeuAsnaspIleGlnLeuGlnMetGluGlnHisAsnGlu ::: ::: :::	Oy 374 GluLeuMecLysGlnGlnGuThrHisleuLysGlnGlnLeuAlaLeuTyrThrGluLys 393 Db 2278 GAGCAGCAGGAGCAGGACTAGAGGAGCAG	Db 2506 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	GENERAL INFORMATION: APPLICANT: Buchbinder, Jenny TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US CURRENT APPLICATION NUMBER: US/09/976,594 CURRENT FILING DATE: 2001-10-12 FRIOR FILING DATE: 2000-10-12 NUMBER OF SEQ ID NOS: 1143 SOFTWARE: PERL PROGRAM SOFTWARE: PERL PROGRAM SEQ ID NO 735 LENGTH: 5467 TYPED DNA CORRAISM: Home sapiens FEATURE: NAME/KEY: misc feature CORRENTED MA CORRENTED NO 735 US-09-976-594-735 Alignment Scores:	

us-10-023-523-44.rni

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7 A	CACTAGAGA A GGA A GGA A GA A GGA A GA A	; Sequence 30, Appl.
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DP 43	3838 TGGAAGCCGGGCATAACCGCCGCACTTCAAGGCGGCCTCCTTGGAGCTGAGGTGAGG	APPLICANT: Berauch APPLICANT: Ohas Designation of the Applicant Cartes of the
ò	lleGluGlnTyrGluLeuArgGluGluHisIleAspLysValP	APPLICANT: VAIS
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ò	327 heLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluM 347	; TITLE OF INVENTICAL ; FILE REFERENCE: CTIPDENN PROFITCAL
qq	3933	CURRENT FILING DI
8 8	etLeuLysGluAlaGluGluArgHisGluArgGluLysAspPheLeuLeuLysGluAlaV	; PRIOR APPLICATION PRIOR PATE ; NUMBER OF SEQ ID
o O	3955 ACCTTCAGATTCGGGAGGGAAACATTCCCAGGAGATAGCACAGTTCCAAGGAGAGCTGG 4014	SOFTWARE: FastSEC
δλ	367 alGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnL 387	LENGTH: 8257
셤	4015 CCGAGGCCCGGGCACAGCTCCAGCTCCTGCAGAAGCAGCTGGACGAGCAGC 4065	CRGANISM: Human
ò	387 euAlaLeuTyrThrGluLysPheGluGluPheGluBsnThrLeuSerLysSerSerGluV 407	
qq	4066 TCAGCAAACAGCCCGTGGGAAACCAAGAGATGGAAAAT4103	Pred. No.:
ò	407 alPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLleLysLysLeuGluL 427	Percent Similarity:
Ωp	4104CTCAAATGGGAGTGGATCAGAAAGAAAAGAGAAATCCAGTCCTTGAAGG 4152	Query Match:
ò	427 ysGluThrThrMetTyrArgSerArgTrpGlu	
qq	4153 AGCAGCTGGACTTGACGGAGCAGGAAGGAACTGGAAGGACTACAGCAGCTGC 4212	-10-023-523-
δy	438SerSerAsnLysAlaLeuLeuGluMetAlaGluGiuLysThrValArgA 454	
Db	4213 TGCAGAACGTCAAGTCTGAGTTGGAGATGGCCCCAGGAAGACCTGTCCATGACCCCAGAAGG 4272	Db 2275 CTABAT
ò	454 splysGlubeuGluGlybeuGlnValbysIleGlnArgLeuGluLysbeuCysArgAlab 474	Qy 16 ProLys
QQ	4273 ATAAATTTATGCTCCAGGCAAAAGTGTCGGAGCTGAAGAACAACAAGAGCCC 4326	Db 2335 TTGAAA
ò		Qy 36 GlnAla
đ	TGGACCTACGCGGCCAAGACGAAAGGAG	Db 2395 GAGCTC
ò		Qy 56 GluGly
Db	4387 CCGAAAGCGCAGGCTCTTCCAACCCTGCCACGACCAAGATCCCGGACTGCCCA 4446	Db 2455 AGTAGA
ò	502	Oy 76 SerArg
op	GCCCGCCGTGAGCAAGGAGCCC	Db 2485 GGGAAA
ò		Qy 96 GlyGlu
Dþ	CAGCTGCCTCCAGCAGCTCAAGCAGAGATGGACAGCCTGCAGCGC	Db 2536 GATCAA
ò		Oy 116 Tyrval
QQ	4567 CAGAIGGAGGACCACGCCTGACGGIGCACGAGTCTCTGICCTCGIGGACGCCGCTGGAG 4626	Db 2593 ATGGTC
λŏ	520 luAlaProCygTyrProGlyAla-ProSerThrGluAlaSerGlyGlnThrGlyProGln 539	Oy 136 SerLys
QQ	4627 CCAGCCACTGCCAGCCTGTGCCCCGGGGGGTCACGCCGGCCCACGGGGGGGCGACCCACAG 4686	Db 2653 CAAAAA
ò	540 GluProThrSerAlaArgAla 546	Qy 145 IleArg
DP		Db 2713 CTTCAG

RESULT 48

-09-595-6848-10 Sequence 30, Application US/09595684B Patent No. 6544766 APPLICANT: Beraud, Christophe APPLICANT: Baraud, Christophe APPLICANT: Sakowicz, Roman APPLICANT: Sakowicz, Roman APPLICANT: Waisberg, Eugeni APPLICANT: Wod, Kenneth APPLICANT: Whisberg, Eugeni APPLICANT: Wod, Kenneth APPLICANT: Wod, Kenneth APPLICANT: Wod, Senenth APPLICANT: Whisberg, Eugeni APPLICANT: Whisperge, US/09/595,684B CURRENT FILING DATE: 2002-06-24 NUMBER OF SEQ ID NOS: 105 BRIOR FILING DATE: 2000-04-20 NUMBER OF SEQ ID NOS: 105 BENGTH: 8257 TYPE: DNA ORGANISM: Human ORGANISM: Human	int Scores: 4.85e-10 Length: 8257 io.: 240.00 Matches: 115 Similarity: 41.80* Conservative: 112 cal Similarity: 21.18* Mismatches: 224 atch: 4 .62* Indels: 17	3-523-44 (1-546) x US-09-595-684B-30 (1-8257)	1 MetlysasnglnasplyslysasnglyalaalalysglnSerasn 15	ro c	36 GlnAlaAlaProA	GGAG 2	56 GluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeu 75 	76 SerArgGinLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyPro, 95	96 GlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThr 115 	uLysGluPro 135 TAAAGAAGCC 265	6 SerLysGlyAspProAsnThrGluGlu 144	GATTCGAGTTTGGGTGCTTTGAA	145 IleArgGInSerAspGluValGIyAspArgAspHisArgArgArgFroGInGluLysLys 163 ::::::::	164 LysalaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSer 183 	
US-09-595-684 Sequence 30 Patent No. Patent	Alignment Pred. No. Score: Percent S Best Loca Query Math	US-10-023	<i>\$</i>	\dot \(\frac{1}{2} \)	3 - <i>8</i>	qq	SP GS	දු දු	Qy	oy Qu			S A	λο ;	

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Query Match
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TTAGAAATAGAGATTCTCCGCTGCAA 2802
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                              ThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHis 203
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OP INVENTION: No. 6569662el Nucleic Acids and
OF INVENTION: Polypeptides
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PEDIJGATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
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Sequence 130, Application US/09620312D Patent No. 6569662
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PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SCFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 130
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240.00
41.80%
21.18%
8.62%
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
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Chen, Rui-hong
                                                                                                                                                                                                   Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                    Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Best Local Similarity:
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (91)
US-09-620-312D-130
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3712 TTACAGAAGTCATTTGAAACAGAGAGAGACCACCTTAGAGGATATATAAGAGAAATTGAA 3771
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                                                                   430 ThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGlu
                                                                                                               -GAACATATGGAAACAGAGAGGCTTGAGTTGGCTCAGAAA
                                                                                                                                                         450 LysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
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93
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-770-379-20/c
; Sequence 20, Application US/08770379
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Rasso, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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TITLE OF INVENTION: HE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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GENERAL INFORMATION:
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7.13 CTTCAGGAGAAAACACGTGAGGTTCAAGAAAGACTAAATGAGATGGAACAGCTGAAGGAA 2772
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                                                                                                                                                                       ----ThrGlugin 144
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GlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThr 115
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                                         2536 GATCAAGAA---TTCCAAAATTTCAAAACCCTTCATATGGACTTTGAGCAAAGTATAAG
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                                                                                      TyrvalAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluPro
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14-JUL-2000; 2000US-00616289.
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-Q=/cgp12_1/USPTO_spool/US10023523/runat_08062004_063748_29931/app_query.fasta_1.1422
-Q=/cgp12_1/USPTO_spool/US10023523/runat_080FEX=ng -MINMATCH=0.1_-LOOPECL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1-MATRIX-bilosum62 -TRANS-human40.cdi
-LIST=50 -DOOALIGN=200 -THR SCORE=pet -THR MAX=100 -THR MIND -ALIGN=50
-USER=US10023523_GCGA1_1_755_Grunat_08062004_063748_29931 -NCFU=6 -ICFU=3
-NONEL-COLL -CUTFWT=pto -NORM-ext -HEAPSIZE=500 -MINLENE -MAXLENE=200000000
-USER=US10023523_GCGA1_1_755_Grunat_08062004_063748_29931 -NCFU=6 -ICFU=3
-NONEL-COLL -CUTFWT=pto -NORM-EXT -NGFD=COLL -LONGLOG
-DEV_TINECUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEX=0.5_-FGAPOP=6
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Acc46153 Human dit
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Aay32839 Human low
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Aay32836 Rabbit low
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Score

Result

The present sequence is that of the coding region of the human gene (see also AAH26496) encoding novel human low density lipoprotein binding protein 2 (LBP-3, see AAH82808). The gene was isolated from a genomic DNA library using LBP-3 cDNA as probe. The LBP-3 protein predicted from the present sequence differs from that predicted from a cDNA clone (see AAB82804) in that it concains an additional 16 amino acids at its N-terminus (the cDNA is a 5' truncation) and has Asn at amino acid position 130 rather than Tyr. LBP-3 nucleic acids are among claimed to polymucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP colymucleotides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. CC wethods of determining if an animal is at risk for atherosclerosis, methods for treating a cell having an abnormality in structure or companient of LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed. New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis. Arjona AA; Claim 8; Fig 8A; 143pp; English Law SW, WPI; 2001-565505/63. P-PSDB; AAB82808. Lees RS, Lees AM,

Sequence 1638 BP; 490 A; 417 C; 520 G; 211 T; 0 U; 0 Other;

ASH 180 AAT 540	Leu 200 CTG 600	 CTG 660	Lys 240 AAG 720	val 260 GTG 780	Thr 280 ACA 840	Gln 300 CAA 900	Glu 320 GAG 960	Lys 340	Asp 360 GAT 1080	Glu 380 GAG 1140	Thr 400	Lys 420 PAG 1260	Asn 440 AAC 1320		crd 1380	ASP 480 GAC 1440	GGC 1500	Glu 520	GAA 1560 Glu 540
GCAGACATT	rralagluber \TGCTGAACT	rsGlnserGl) AGCAGAGCCA(analaargse:	rsGluGluGl rGGAAGAAGG	SPheGlnVa.	arLysLeuAr	rglubeuar \TGAGCTGCG	uValAspala GGTGGATGC	nArgGluLy: \GCGGGAGAA(tLysglngl) GAAGCAGCA	uPheGlnAsi \GTTCCAGAA	.uLysMetTh: \AAAGATGAC	rpGluSerSer GGGAGAGCAG	uleuGluG]	Acticaacce	nrGluargasi agagcgcaa	uThraspse: CACTGACAG	oArgValTh	cagggrcac irGlyProGl
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LysglyLeug] 	slugluLysLe sAGGAGAAGC	Serginiysg] CACAGAAGC7	HisLeuargG] 	Argglubeug] 	3luGluGluLy saggaggaga	LeuGlnMetG] 	AlaGluArgLe GCTGAGAGGC1	valPheLysHi 	SluMetLeuLy 	Alavalgluse GCAGTAGAGTC	SlnLeuAlaLe	SluvalPherb 	slulysgluth sagaaagaaa	MetAlaGluG]	Ardecraade	Argleugluly 	31nAspleuse 	31uG1yProG]	3AGGGCCTGC 3lyAlaProSe
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03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. Drmanac RT; 2001-457740/49. (HYSE-) HYSEQ INC Tang YT, Liu C, WPI; 2001-457740/ P-PSDB; ABB11764. WO200157188-A2 11-JAN-2002 1561

cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. Hyman, cytokine; cell proliferation; cell differentiation; growth fandamentopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; bone disorder; osteoporosis; vascular growth disorder; ciscoporosis; vascular growth disorder; ciscoporosis; vascular growth disorder; ciscoporosis; vascular growth disorder; ciscoporosis; one disorder; antiatian d Human LDL binding protein homologue-encoding cDNA, SEQ ID NO:784. 1621 CCCACCTCCGCCAGGGCC 1638 546 ABA09008 standard; cDNA; 2523 05-FEB-2001; 2001WO-US003800. ProThrSerAlaArgAla

Human proteins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject e.g. and cancer.

Claim 1; Page 693-694; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0822-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of detecting the nucleotides, corporates against the polypeptides, methods of detecting the nucleotides of the invention and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; including cytokine, cell proliferation or cell facentialation activities; stem cell growth factor activity; differentialation activities; stem cell growth activity; climunomodulatory activity; tissue growth activities; chemokinetic activities; hemostatic, thrombootic or thrombolytic activities; the means activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of

the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemachopielte disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, carterial ischemaia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound communomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Co promote cell growth, For example, such polypeptides may be used to commune disorders. Co promote cell growth, For example, such polypeptides may be used to confine stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, cutoimmune disease or accidental damage. The polypeptides and nucleotides cautoimmune disease or accidental damage. The polypeptides and in drug screening techniques. The present sequence represents a cDNA encoding a covel human polypeptide of the invention 99999999999999999988

BP; 666 A; 626 C; 794 G; 437 T; 0 U; 0 Other; Sequence 2523

Alignment Scores:

101 GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn 120 239 GTAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAGGGGGCTCAAGCC 1 MetLysAsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro 119 ATGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAGCAGCCCA GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla 121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro 81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyBroGlyGluAspGlyAla 419 CAGGGIGAGCCGGCIGAACCCGGAGAIGCAGAGAGTCCCGGACCIAIGIGGCAAGGAAI 141 AsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln 539 AACACAGAAGGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCATCGAAGGCCACAG 61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu Length:
Matches:
Conservative:
Mismatches:
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161 GlulysLysLyslysAlalysGlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeuAsn 181 ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeu

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GluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu

659 ACTCTGAGTACCCCAGAGGAGAAGCTGGCTGCTGTGCAAGAAGTATGCTGAACTGCTG

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AAK52874 standard; cDNA; 2523

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                                                                                                    GTGCAAGAGAAGGACCACCTGCGCGGTGAGCACAGCAAGGCCCGTCCTGGCCCGCAGGAG
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RESULT 3

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW8329-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, manumomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activity inchibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM60020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptidde therapy, stem cell growth factor; haematopoiesis; tissue growth factor; mmunomodulatory; cancer, leukaemia; nervous system disorder, arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V, Zhou P, Xu C, Cao Y;
J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
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Matches:
Conservative:
Mismatches:
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Zhao QA, Wang D, Waus
- v. Wejhrman T, (
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2000US-00620325.
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15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                               (first entry)
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Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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To All Andrews

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Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging; extracellular signalling; gene; ss.
                            1259 ACCCACCTGAAGCAACAGCTTGCCCTATACACAGAAGTTTTGAGGAGTTCCAGAACACA
                                                                          CTTTCCAAAAGCAGCAGGAGTATTCACCACATTCAAGCAGGAGATGGAAAAGATGACTAAG
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                                                        LeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLys
                                                                                                                 LysileLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsn
                                                                                                                                          <u>AAGATCAAGAAGCTGGAGAAAGAAACCACCATGTACCGGTCCCGGTGGGAGAGCAGCAAC</u>
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ThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr
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29-WAR-2001, 2001US-0280067P.
16-WAY-2001, 2001US-0291280P.
17-WAY-2001, 2001US-0291829P.
17-WAY-2001, 2001US-0291849P.
19-UUN-2001, 2001US-029948P.
20-UUN-2001, 2001US-0299476P.
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                               GGACAACCGGAAGCACCCGAGGGAGCCCCAGGAGGGGGCCCCAGGCCCAGGCGCTCCTGCA
                                                                      ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla
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(INCY-) INCYTE GENOMICS INC.

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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
             Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panaer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                      WPI; 2003-129518/12.
P-PSDB; ABR41210.
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The invention relates to novel human diagnostic and therapeutic polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP, ABR41812). The invention also relates to polymucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and cransgenic organisms comprising a dithp mucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation of probe. Dithp mucleic acid sequences, methods of assessing the toxicity of test compounds using a dithp hybridisation of for compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation of for a bithp mucleic acid sequences and DITHP proteins may be used in the compounds which specifically bind an DITHP protein; and other cell aspense or proble. Dithp mucleic acid sequences and DITHP proteins may be used in the city in upon or parasitic infections; hormonal disorders; bacterial, visual or parasitic infections; hormonal disorders; bacterial, citycapers; neurological disorders; gastrointesfinal disorders; transport disorders; and connective tissue disorders. They may also be used in the proteins can additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of antisense sequences, as a source of antisense content of the printed of individuals, in toxicological testing, and in transcript imaging. The present sequence represents a dithy cDNA encoding a DITHP protein which has extracellular signalling activity. Who are the sequence data for this patent did not form part of methods of the sequence of the English Claim 2; SEQ ID NO 74; 591pp;

Sequence 5085 BP; 1178 A; 1310 C; 1407 G; 1190 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

		339	399
5 0 8 5 8 6 8 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		1 MetlysasnGlnasplyslysasnGlyalaalalysGlnSerasnProlysSerSerPro 20	21 Glyglnproglualaglyprogluglyalaglngluargproserglnalaalaproala 40
Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-5085)	AsnGlyAlaAlaLysGln AaCGGGCTGCCAAACAA	GluGlyAlaGlnGluArg
9.43e-153 2785.00 100.00% 100.00%	6) x ACC46153	nGlnasplyslys CCAAGACAAAAAC	oglualaglyPro ggaagcaggaccc
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-023-523-44 (1-546) x ACC46153 (1-5085)	1 MetLysAs: 280 ATGAAGAA	21 GlyGlnPr 340 GGACAACC
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1239 1539 1359 1419 1000 crrcadadectrareccercaderecedededecacecercecercaagaagaagarere 1059 240 340 400 380 440 220 939 819 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro 140 160 AACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCATCGAAGGCCACAG 759 940 graczasakakakacakonecacacacakakakakakakakaka o 999 GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn ValGinGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys GluHislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys 1480 CTTTCCAAAAGCAGCAGGTATTCACCACATTCAAGCAGGAGATGGAAAAGATGGACTAAG GAGAAGAAAAAGCCAAGGGTTTTGGGGAAAGGAGATCACGTTGCTGATGCAGACATTGAAT ThrieuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeu 820 ACTCTGAGTACCCCGAAGGAGAAGCTGGCTGCTGTTGTGTGCAAGAAGTATGCTGAACTGCTG 880 GAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAAGAGCCAGCTG 281 LeuAsnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGln GluasnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGlu 1180 GAGAACATGGAGCTGGCTGAGAGGTCAAGAAGCTGATTGAGCAGTATGAGCTGCGGGGG 361 PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGluGlnGlu LeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLys Lys11eLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsn GACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGATGGGGCA GluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu 1120 creanteacarreacrecacarecacacacacarreaccecaacrecaacrecaacrecaa 341 LeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAsp 381 ThrHisLeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla AsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln GlulyslyslysalalysGlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeuAsn LeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVal GlnArgAlaArgGluGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr 421 301 321 401 141 241 261 81 520 580 121 200 161 760 201 221 101 181

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ValGluAlaGluGlyProGlySerSerGlnAlaProArglysProGluGlyAlaGlnAla

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                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACAAGAGGGTACAGGACCTGAGTGGCTGGCCAGGGCTCCCTCACTGACAGTGGC
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                                                                                                                                                                        GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp
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, 2001US-0291280P.

, 2001US-0291829P.

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, 2001US-0291849P.

, 2001US-0299428P.

, 2001US-0299476P.
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29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
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19-JUN-2001; 2
20-JUN-2001; 2
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The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP, ABRA1136-ABRA1812). The invention also relates to proteins (DITHP, ABRA1136-ABRA1812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transpants comparising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; attribodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP protein; and cher cell cards avariate; infections; hormonal disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; transport disorders; and connective tissue disorders. They may also be used to ascent for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the protecome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of artisense agence can an additionally be used in analysis of thuman disease or knock in humanised animals, in toxicological testing, and in transgenic and mals, in toxicological testing, and in transgenic and which has extracellular signalling activity. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                          polypeptide useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 ATGAAGAACCAAGACAAAAAGAACGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCCA 339
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                     Novel human diagnostic and therapeutic polypeptide useful for identitest compound which specifically binds to a polypeptide encoded by hidagnostic and therapeutic polynuclectide, and to induce antibodies.
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Conservative:
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                                                                                                                   Claim 2; SEQ ID NO 51; 591pp; English.
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Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J; Dufour GB, Hillman JL, Yu JY, Thason O, Yap PB, Amshey SR; Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin E Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

WPI; 2003-129518/12. P-PSDB; ABR41186.

(INCY-) INCYTE GENOMICS INC.

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LeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGly
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3. .1595
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159. .179
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97US-0048547P.
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03-JUN-1997;
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                                   geegagccreaaccaacreagreardsaagaaagaaacccreaaggggarcca
                                                        AsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln
                                                                            AACACAGAAGAGATCCGGCAGAGGTGAGGAGGTCGGAGACCGAGACCATCGAAGGCCACAG
                                                                                                  GluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsn
                                                                                                              GAGAAGAAAAAAGCCAAGGGTTTGGGGAAAGAAGAACGATGCTGGTGCTGATGCAGAATTGAAT
                                                                                                                                              ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeu
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               GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro
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                                                                                                                                                                                                                                                                                                                                                                                                  1720 CTGAACAAGAGGGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGTGGC
                                                                                                      ProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu
                                                                                                                                                                                                                                                                                                                        AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu
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                       GAGCTGCGCGAGGAGCATATCGACAAAGTCTTCAAACACAAGGACCTACAACAACGCGGCG
                                                                   ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet
                                                                                                                                                                  AAGCAGGAAGAGACCCACCTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAG
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                                                        ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln
                                                                                                                                                       LysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu
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          GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu
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                       C; 1289 G; 1113 T; 0 U; 0 Other;
                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
recombinant LBP
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host cells used to produce
                       Sequence 4697 BP; 1097 A; 1198
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99.81%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 3 (LBP-3, see AAB82804). Clones were isolated from human foetal brain, liver and acrta cDNA libraries using rabbit LBP-3 cDNA as probe. A full-length cDNA clone is given in AAH26501, and a genomic DNA sequence is given in AAH26497. LBP-3 nucleic acids are among claimed polymelectides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPR. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in gruncture or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions.
                                                                                                                                                                                                                                                                                New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                           Law SW, Arjona AA;
                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 17; 143pp; English
                                                                                                                               (BOST-) BOSTON HEART FOUND INC.
                                                              02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
                       28-FEB-2001; 2001WO-US006356.
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P-PSDB; AAB82804.
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Sequence 4697 BP; 1097 A; 1197 C; 1290 G; 1113 T; 0 U; 0 Other;

t Scores: 1.95e-147 Length: 4697 2693.00 Matches: 529 Similarity: 99.81\$ Conservative: 0 al Similarity: 99.81\$ Mismatches: 1 tch: 5 Gaps: 0	3-44 (1-546) x AAH26496 (1-4697)	17 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 36	3 AAAAGCAGCCCAGAACAACCGGAAGCAGCCCGAGGAGCCCCAGGAGG	37 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 56	63 GCGGCTCCTGCAGTAGAAGCAGAGAAGGTCCCGGCAGCCAGGCTCCTCGGAAGCCGGAG 122	57 GlyalaGinalaArgThrAlaGinSerGlyalaLeuArgAspValSerGluGluLeuSer 76		77 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 96	3 CGCCAACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGCCCCGGC 242	97 GluAspGlyAlaGluGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 116	3 GAGGATGGGGCTGAGCTGAGCCGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTAT 302	7 ValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer 136	3 GTGGCAAGGAATGGGGAGCCTGAACCCAACTCCAGTAGTCTATGGAGAAGGAAG	7 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 156	3 AAGGGGGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCAT 422
ment S No.: : nt Sim Cocal Match	US-10-023-523	-		м	9	S	123	7	183	σ	243	117	303	137	363
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	ò	257 GluGluGlyValGlnArgAlaArgGluGluGluGl	nGluLysArgLysGluValThrSerHis 276
	q	723 GAAGAAGGTGTGCAGCGGGCCCGGGAGGAGGA	sakakkacackadakatakacrodaka 782
	ζŏ	277 PheglnValThrLeuAsnAspIleGlnLeuGl	MetGluglnHisAsnGluArgAsnSer 296
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	ò	297 LysLeuArgGlnGluAsnMetGluLeuAlaGl	Argleutysteutleglughnyr 316
	qq	843 AAGCTGCCAAGAGAACATGGAGCTGGCTGA	saggercaagaagergarrgageagrar 902
	λō	317 GluLeuArgGluGluHisIleAspLysValPh	
	qq	903 GAGCTGCGCGAGGAGCATATCGACAAAGTCTT	zaacacaaddactacaacadcagcig 962
-	λõ	337 ValAspAlaLysLeuGlnGlnAlaGlnGluMe	
	qq	963 GTGGATGCCAAGCTCCAGCAGGCCCAGGAGAT	sciaładdagdcagaddagcgdcaccag 1022
	δλ	357 ArgGluLysAspPheLeuLeuLysGluAlaVa	
	qq	1023 CGGGAGAAGGATTTTCTCCTGAAAGAGGCAGT	AGAGTCCCAGAGGATGTGTGAGCTGATG 1082
	λo	-	
	q d	1083 AAGCAGCAAGAGACCCACCTGAAGCAACAGCT	GCCCTATACACAGAAGTTTGAGGAG 1142
	ò	397 PheGlnAsnThrLeuSerLysSerSerGluVa	PheThrThrPheLysGlnGluMetGlu 416
	QO	1143 Trcchgaacacacrtrccaaaagcagcgaggr	vricaccacatrcaagcaggaggaggaa 1202
	λõ	417 LysMetThrLysLysIleLysLysLeuGluLy	
	qa	1203 AAGATGACTAAGAAGATCAAGAAGCTGGAGAA	GAAACCACCATGTACCGGTCCCGGTGG 1262
	λo.	437 GluSerSerAsnLysAlaLeuLeuGluMetAl	GluGluLysThrValArgAspLysGlu 456
	ηρ	1263 GAGAGCAACAAGAGCCCTGCTTGAGATGGC	CAGGAGAAAACAGTCCGGGATAAAGAA 1322
	δ	457 LeuGluGlyLeuGlnValLysIleGlnArgLe	GlubysLeuCysArgAlaLeuGlnThr 476
	qa	1323 CTGGAGGGCCTGCAGGTAAAAATCCAACGGCT	seagaadergreedededededededa 1382
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	qq	1443 ACTGACAGTGGCCCTGAGAGGAGGCCAGAGG	scridddcricaadcacccadcroccc 1502

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    Nucleic acid encoding low density lipoprotein binding proteins and talated vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying subjects at risk.
                                                                                                                                                                                                                                                                                                                                                                                                          LBP-2;
ss.
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                                                                                                                                                                                                                                                                                                                                                              Rabbit low density lipoprotein binding protein LBP-3 cDNA
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97US-0048547P.
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P-PSDB; AAW49039.
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GluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAla 339

Length:

2.91e-139

319

957

259

837

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777

279

Law SW, Arjona AA;

Lees RS,

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The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 3 (LBP-3, see AAB82801). The CDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynuclectides encoding novel bolypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, calls and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a call having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions are also claimed
                                                                                                                                                                              New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4722 BP; 997 A; 1332 C; 1430 G; 963 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     Claim 5; Fig 14; 143pp; English.
                                                      (BOST-) BOSTON HEART FOUND INC
 02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
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81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100 61 ATGAAGAATCAAGACAAAAGAACGGGCTGCCAAACAGCCCAACCCCAAAAGCAGCCCG 181 cgagaagccgaaggr---gccagcaagccaggcrccgggaggccgaggggggggcrcaagcc 1 MetLysAsnGlnAspLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro GinglyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro 21 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 238 AAAACTGCTCAGCCTGGGGGCCTCTGTGATGTCTCTGAGGAGCTGAGCCGCCAGTTGGAA GACATACTCAGTACATACTGTGGACAACAACCAGGGGGCCCCCGGGTGAGGATGGGGTC GlyGluProGluPro---ThrProValValAsnGlyGluLysGluProSerLysGlyAsp CAGGGTGAGCCCCCTGAACCTGAAGATGCAGAGAAGTCTCGCGCCTATGTGGCAAGGAAT Length:
Matches:
Conservative:
Mismatches: US-10-023-523-44 (1-546) x AAH26491 (1-4722) 2.91e-139 2552.50 93.19% 91.04% 91.65% Best Local Similarity: Percent Similarity: Alignment Scores: 41 61 862 101 358 121 418 140 Query Match: DB: 셤 ઠે g ò g ò g 8 임 엄 원 8 à

Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

Location/Qualifiers

Oryctolagus cuniculus.

/*tag=

WO200164874-A2

07-SEP-2001

28-FEB-2001; 2001WO-US006356.

Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.

(first entry)

12-NOV-2001

AAH26491;

BP

AAH26491 standard; cDNA; 4722

AAH26491

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1618 GGGGCTCAAGTACCCAACTCTCCAAGGGCCACACAGACGCTTCCTGCTGCTGCGCGGTGCACCC
GlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaPro
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23-AUG-2000; 2000US-00649167.
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              GlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeu
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (I). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treapy techniques to restore normal activity of (II) or to treap disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
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AGCACAGAGGCATCAGGCCAGACAGGGCCCCAGGAGCCCACCACCACCACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder,
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499 rGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValTh 519
IleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLys 164
                                                                                                                                                                                                                                                 GCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCA
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Wang
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J, Zhang J, Ren F, Chen
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27-AFR-2000; 2000US-00560875.
20-UTN-2000; 2000US-00598075.
19-UTL-2000; 2000US-0063025.
01-SEP-2000; 2000US-0064936.
15-SEP-2000; 2000US-0063561.
20-CCT-2000; 2000US-0069325.
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tao QA, Wang D, Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid upregulated/downregulated in osteogenesis, useful for bone disease therapy in subject.
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Bushnell SE,
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antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                 Human, adenosine receptor, low adenosine antisense oligonucleotide, phosphorothioate, impaired respiration; inflammation, allergy, allergic disease, bronchoconstriction; inhibitor; antiinflammatory;
Human adenosine receptor related polynucleotide 2nd SEQ ID NO:92.
                                                                                                                                                            99WO-US017712.
                                                                                                                                                                               98US-0095212P.
                                                                                                                                                                                                (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                      WPI; 2000-205971/18.
                                                                                                                       WO200009525-A2.
                                                                                                      Homo sapiens.
                                                                                                                                                            03-AUG-1999;
                                                                                                                                                                               03-AUG-1998;
                                                                                                                                          24-FEB-2000.
                                                                                                                                                                                                                   Nyce JW;
                                                                                                                                                                                                                                                                                    cancers
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New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

Disclosure, Page 1259-1260, 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets conclete acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c.g. isolaemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive culmonary disease (CODP), and cancers such as leukaemiss, lamphomas, pulmonary disease (CODP), and cancers such as leukaemiss, lamphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down which the crelease of deoxyadenosine which activates adenosine receptors causing concented sequences given in the sequence listing from the present the invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 185, but the sequence of from the previously named sequences. SEQ ID NO:1 to 185, but the sequence of from the present invention. N B. Sequences given in the disclosure of the present invention. N B. Line of the present invention. On the previous of the present invention. The libration of the present invention. isting.

Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;

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	2.01e-89	1688.00	9.12	99.12%	0.61	э
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205 AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys 224

US-10-023-523-44 (1-546) x AAA35218 (1-1793)

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RESULT 14 AAA35217/c

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& ଶ	225 AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu 244
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\$ Q	285 GInLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGlu 304
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셤	3GCTGAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGCATATCGAC 14.
& £	325 LysValPheLysHisLysAspLeuGlnGlnGlnEuValAspAlaLysLeuGlnGlnAla 344 [
ð	5 GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLys 364
q	CAGGAGATGCTAAA
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ð	25 LeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla
QD	CAACAAGGCCCTGCTT 10
ò	45 GluWetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGluValLysIle 464
đ	GGCTGAGGAGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAATC 10
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets conclide acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, cuseful for the treatment of diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating confidence conditions, pulmonary vascociatriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive carcinomas, and cancers which may metastassise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the carcinomas, and cancers which activates adenosine receptors causing chronicocartriction and inflammation. AAA3333 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 1860 (AAA3233 to AAA3392) are specifically claimed ONS from the present invention. N B. Sequences given in the disclosure of the present invention. N B. Contain the test of the present invention. N B. Contain the test of the present invention. N B. Contain the present invention. N B. Contain the sequences given in the sequences.
                                                                                                                                                                                                                                                          antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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                                                                                                                                            Human adenosine receptor related polynucleotide 2nd SEQ ID NO:91
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  AAA35217 standard; DNA; 1793 BP
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EAST CAROLINA

Length: Matches: Conservative: Mismatches:

2.01e-89 1688.00 99.12% 99.12%

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:

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AGGGCC ArgAla

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense cligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activity and peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adhesion molecules and their receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensine, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allsenge or surfactors of the contraction and/or bronchoconstriction) are sociated with a disease or such and sociated s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                    human; airway disorder; bronchoconstriction; lung inflammation; human; airway disorder; bronchoconstriction; lung inflammation; bronchoconstriction; lung inflammation; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma, RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                             Human low adenosine antisense oligonucleotide related sequence #2907
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                                                                                   AAF21340 standard;
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condition selected from pulmonary vasoconstriction, inflammation, assurance, astbma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergic thintis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

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           and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification
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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
ValGlnAspLeuSerAlaGlyGlnGlySerLeuThrAspSerGlyProGluArgArg 504
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                                                                                                                                                                                                                                                                                          952 GTACAGGACCTGAGTGCTGGCCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGAGG
                                                                                                                                                                                          892 CCAGAGGGGCCTGGGGGCTCAAGCACCCAGCTCCCCCAGGGTCACAGAAGCGCCTTGCTAC
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nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vascoctive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergy(ies) and/or surfactant, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. ARF18434 to AARF1843 represent human polymucleotide fragments and antisense oligonucleotides used in the exemplification of
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with activating peptide factors and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central

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                                  CTGGAGAAAAGAAACCACCATGTACCGGTCCCGGTGGGAGAGCAGCAAGAAGCCTGCTT
   LeuGluLysGluThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeu
                                                                                                                   GluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIle
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Tang L, Shahabuddin S;
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junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchocomstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention as antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, ung allergies, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfaction, but was obtained in electronic format directly from MIPO set fitp.wipo.int/pub/published_pot_sequences

Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:

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                                                                072 GAGATGGCTGAGGAAAAACAGTCCGGGATAAAGAACTGGAGGCCTGCAGGTAAAATC
                                                  445 GluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIle
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                       1132 criscacaaadaaaccaccargraccogreccogrecagagagcagcaacaaggcccriscrr
                                                                                                  GlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArg
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                                    AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys
                                                                                                    225 AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

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Aguilar

E, Pabalan J,

Katz

Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S;

Nyce JW, 1 Miller S,

WPI; 2003-229219/22

24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC.

23-APR-2002; 2002WO-US013135

31-OCT-2002

The invention relates to a novel pharmaceutical composition, which has first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

Disclosure; SEQ ID NO 12275; 872pp; English

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cell
  growth factor which stimulates B cell proliferation and inhibits B cell differentiation, termed interleukin 14. IL-14 can be used to interfere with the replication of B cells and to treat B cell non-Hodgkin's lymphoma, systemic lupus erythematosus and systemic necrotising vaculitis. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                 4.09e-84
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non-Hodgkin's lymphoma; systemic lupus erythematosus;
systemic necrotising vasculitis; transplant; ss.
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                  LeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeu
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proliferation and inhibit B cell differentiation, useful to treat
systemic lupus erythematosus.
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US DEPT HEALTH & HUMAN SERVICES.
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non-Hodgkin's
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Mismatches:
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5.59e-66 1286.00 67.49% 53.99% 46.18%

Percent Similarity: Best Local Similarity:

Query Match: DB:

US-10-023-523-44 (1-546) x AAH15042 (1-2045)

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                                                                                                                                                                                                                                                  CAACCGAGCACAGAAGCATCAGGCCAGACTGG-CCTCAAGAGCCCACCTCCGCCAGGGCC
LeuSerAlaGlyGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu-Gl
                                                    yProGlyAla-GlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyA
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Sugiyama T, Wakamatsu A, Nagai K,
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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GluGlyAlaGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly
                                                          SerSerGlnAlaProArgLys-----ProGluGlyAlaGlnAlaArgThrAlaGlnSer
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The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonnclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonuclectide comprises a least 15 nucleotides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence of an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence of the comprises a 3'-end sequence of complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide sequence and sequence of an oligonuclectide sequence of a polynuclectide sequence of comprises a 1'-end sequence, where the oligonuclectide sequence of sequence of primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length and any action and sequences; AAH13632 to AAH13632 represent thuman amino acid sequences; and AAH13629 to AAH13632 represent

Claim 8; SEQ ID NO 13025; 2537pp + Sequence Listing; English.

'tumor lung proteins and nucleic acids encoding the proteins, us vaccines and for treating, preventing, diagnosing or monitoring

Lodes MJ;

Mohamath R,

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Claim 1; Page 175-176; 189pp; English
                                                                 New tumor lung proteins
         (CORI-) CORIXA CORP.
                                             NPI; 2002-372001/40
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868 GGGGAGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAGGCACATTGATAAG 927
                  ValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGln
                               928 GTGTTCAAACGTAAGGAACTGCAACAGCAGCTCGTGGATGCCAAACTGCAAACGACA
                                                         346 GluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGlu
                                                                                                                                                                          GluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLysLeu
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The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the polypeptides. Also included are an expression vector comprising the polynucleotide operably linked to an expression control sequence; a host cell transformed or transfected with an expression wector of, an isolated antibody, or its antigen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient of its antigen-binding fragment that specifically binds to the polypeptide; an expression wector of; a fusion protein comprising at least the polypeptide; and cancer in a patient of stringent conditions, a method for stimulating and/or expanding T cells prepared from the method of above, a composition comprising a first component consisting of carriers and immunostimulants, and a second component selected from the polymucleotides, proteins, artibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polymethod; methods for stimulation and minumen response or treating cancer in a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotic of, or an antibody and detection reagent consisting of a reporter group. The polymucleotides are useful as vaccines for the treatment or prevention of tung cancer, and for diagnosis and minitoring of such cancer. The comprise in a patient by diagnosis and minitoring cells can be used to stimulate or expand T cells specific for a tumorous protein. The collymucleotides may be used as probes or primers for nucleic acid acid control inhibiting expression of tumour polypeptides and proteins in tumour cells. The present sequence is one of the 183 lung cancer associated
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BP; 672 A; 421 C; 506 G; 446 T; 0 U; 0 Other; Sequence 2045

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Mismatches:
Indels:
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Matches:
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2000US-0234837P.

22-SEP-2000;

20-SEP-2001; 2001WO-US042232

10-OCT-2000; 2000US-0239440P. 29-JUN-2001; 2001US-0301928P.

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modulating agent, by contacting an assay system comprising a purified HM polypeptide: (human orthologue of genes that modify the p53 pathway in for sosphila) or nucleic acid with a test agent under conditions; where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a IM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising to a nucleic acid) and diagnosing (M4) expression; (c) comparing the results with a control; and (d) determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to identifying (M1) a candidate p53 pathway
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                                                                                                                                                                                                                                                       Funke RP;
  Aspleu
                                                 1408 GAAGTCCTGAAAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCGAACAGGGÄTTTÄ
                                                                                                           489 SerAlaGlyGlyGlnGlySerLeuThr----AspSerGlyProGluArgArgProGlu
                                                                                                                                                             1468 GCAACACCIGIGAIGCAGCCCIGIÁCIGCCCIGGAÍICICACAAGGÁGCIGAACACTICC
                                                                                                                                                                                                                    -----GlyAlaGlnAlaProSer-SerProArgValThrGluAlaProCy
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antianglogenic; antiapoptotic; p53 pathway; breast cancer; colon
kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cy
apoptotic disorder; cell proliferation disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA encoding a p53 modifier, SEQ ID 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                     1588 CAAAAGCCCCCGTCCA 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACD13396 standard; cDNA; 1618
                                                                                                                                                                                                                                                                                                                                sTyrProGlyAlaPro 528
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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                                                                                                                                                                                                                       GlyPro---
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antiarteriosclerotic; anticonvulsant, noctropic; neuroprotective; stroke; cerebroprotective; anticonvulsant, noctropic; neuroprotective; cancer; antidiabetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epllepsy; Huntington's disease; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; diabetes; hypothyroidism; Cushing's syndrome; endocrine disorder; infection; gene;
                                                                                                                                                                        ATTAAAAAACTGGAAAAAAGAAACAATAATTTGGCGTACCAAATGGGAAAACAATAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neurotransmission-associated protein NTRAN-14 cDNA SEQ ID NO:39.
                                                                             AlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGln
                                                                                                                                                                                                                                                                                                                                                                                 909 ATAAAACTGGAACGGTTAGAAGGTGTGTGCAGGGCTCTTCAGACAAGAAAGGAATGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              969 ANTGAGAAGTGGAAGTCCTGAAAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgargProGluGlyPro-----GlyAlaGlnAlaProSer-SerProArgValTh
  CAACTAAAACAGCAGCTTTCTCTTTATATGGATAAGTTTGAAGAATTCCAGACTACCATG
                                                  SerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLys
                                                                                                                                                                                                                                                                                         GCACTTCTGCAAATGGCTGAAGAGAAAACAGTCCGTGATAAAGAGTACAAGGCCCTTCAA
                                                                                                                                                                                                                                                                                                                                         462 VallysileGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 -----AspLeuSerAlaGlyGlyGlnGlySerLeuThr-----AspSerGlyProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1029 AACAGGGATTTAGCAACACCTGTGATGCAGCCCTGTACTGCCCTGGATTCTCACAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmission-associated protein; NTRAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1149 AGAAGCGCTGTGCAAAAGCCCCCGTCCA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 rGlualaProCysTyrProGlyAlaPro 528
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309. .2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC68992 standard; cDNA; 4174
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2001US-0326096P.
2001US-0327446P.
2001US-0345837P.
2001US-0343903P.
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02-NOV-2001; 2
27-NOV-2001; 2
07-DEC-2001; 2
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28-SEP-2001;
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whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, anglogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as anglogenic, apoptotic or cell proliferation disorders. The present sequence is an HM nucleic acid encoding a p53 pathway modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGln 261
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                                                                                                                                                                                                                                                                                                                                                             Sequence 1618 BP; 558 A; 330 C; 363 G; 367 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Honchell CD, Warren BA, Borowsky ML, Griffin JA, Li JX, Lee SY; Yue H, Forsythe IJ, Marquis JP, Gietzen KJ, Baughn MR, Tran UK; Lahr-Mason PM, Tang YT, Ramkumar J, Emerling BM, Lee EA, Elliott VS; Hafalia AJA, Duggan BM, Chawla NK, Kable AE, Chang H, Khare R; Becha SD, Jin P, Lee S;
04-JAN-2002; 2002US-0345008P.
18-MAR-2002; 2002US-0365645P.
10-MAY-2002; 2002US-0379887P.
                                 (INCY-) INCYTE GENOMICS INC
                                                                                                   WPI; 2003-363137/34.
                                                                                                           P-PSDB; ABR43284.
                                                                                                                                                     or infections.
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New human neurotransmission associated proteins (NTRAN), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NTRAN expression e.g. cancer, AIDS, diabetes, epilepsy,

Claim 5; Page 230-231; 240pp; English

proteins given in ABR43271 to ABR43295, designated NTRAN-1 to NTRAN-25

(I). (I) have cytostatic, antiarteriosclerotic, anticonvulsant,

notropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
antinflammatory, thyromimetic and antidiabetic activities, and can be
useful in diagnosing, treating and preventing diseases or conditions
associated with the decreased expression or overexpression of NTRAN, such
as cell proliferative (e.g. cancer, attoke), immune/inflammatory (e.g. AIDS,
allergies), developmental (e.g. hypothyroidism, Cushing's syndrome) or
endocrine (e.g. diabetes) disorders, or infections. They are also useful
in assessing the effects of exogenous compounds on the arguesion of
nucleic acid and amino acid sequences of NTRAN. The NTRANS or their
fragments are useful in screening compounds for effectiveness as agonist
or antagonist of the polypeptides, or in altering the expression of the
target polymucleotide and compounds that specifically bind to or modulate
the activity of the polypeptide

Sequence 4174 BP; 1331 A; 924 C; 962 G; 957 T; 0 U; 0 Other;

		22	368	40	416	09	449	80	200	100	554
4174 277 ative: 94 .hes: 92 10		AsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGln 22		ProGluAlaGlyProGluGlyAlaGluGluArgProSerGlnAlaAlaProAla	369 AGTTCATCATTACCCAGTCACAATGGCCTGGAGAAGGAAG	ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla	ACCAGAGAAA	ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu	GAGGCAAGTGTGCACCCCGATATCTCTGAAGAGCTGAATCGACAGCTGGAA	AsplieLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100	
5.2e-65 Length: 1275.00 Matches: 12.42* Conservative 45.64 Mismatches: 17 Gaps:	US-10-023-523-44 (1-546) x ACC68992 (1-4174)	ysAsnGlyAlaAlaLysGl	 AATCACTCTGAAGGTCTCAGGGAAGGACGATCAACACTT	roGluglyAlagl		lyProGlySerSerGlnAl	GATTCTCCAACCCCAGTCCAACCACAGAGAA	erGlyAlaLeuArgAspVa	:: CAAGTGTGCACCCCGATAT	hrTyrCysValAspAsnAs	CTTATGGGTCTGC
y: rity:	1-44 (1-546) x	AsnGlnAspLysL	AATCACTCTGAAC	ProGluAlaGlyP	AGTTCATCATTAC	ValGluAlaGluG		ArgTh	;		
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-023-523	ο _Y 3	318	Qy 23	369 g	Oy 41	Db 417	Oy 61	Db 450	Qy 81	Db 501

101	GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn 120 ::: :::	
121	GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro 140 ::: GGGGACTGTGAGGAAACAGAGGCTGGAAGAGAACCCGTTGCTTGTGGAGAGCCA 665	
141	141 ASHTHrGluGlulleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln 160	
161	GlulyslyslysalalysglyLeuglyLysglulleThrLeuLeuMetGlnThrLeuAsn 180 	
181	ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysLyrAlaGluLeuLeu 200	
201	GlugluHisargasnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu 220 ::: gargaacatcGractgascaaaagaagtraaagcrccrccaaaaaaaaaacaogracaaatr 887	
221	Valginglulysasphisleuargglygluhisserlysalavalleualaargserlys 240 :::	
24 <u>1</u> 948	LeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVal 260 	
261	GINAYGAIAAFGGUGUGUULYSAYGLYSGUVAIThYSSYHISPHEGINVAITHY 280 	
281	LeuasnaspileGlnLeuGlnMetGluGlnHisasnGluargasnSerLysLeuargGln 300	
301	GluasnMetGluLeualaGluargLeuLysLysEeulleGluGlnTyrGluLeuargGlu 320 	
321	GluHisileAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys 340	
341	LeughnGinAlaginGiuMetLeuLysGiuAlagiuGiuArgHisGinArgGiuLysAsp 360 ::: :::	
361	PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlu 380 .::	
381	ThrHisteentysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr 400	
401	DeuserlyssersergluvalphethrThrPhelysglnGluMetGluLysMetThrLys 420	
421	LysileLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsn 440	
441	LysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeu 460 	
461	GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp 480	

10 A; 1038 C; 1025 G; 1150 T; 0 U; 0 Other;

Location/Qualifiers 196226 /*tag= a 197-A. 999. 997, 97JP-00331242. 997, 97JP-00331242. 997, 97JP-00331242. 997, 97JP-00331242. 9-379889/32. AAX17863. ein with neurite extending activity - useful for treating Page 5-8; 9pp; Japanese. ein with has neurite extending Radence encodes a protein (I) which has neurite extending readuence encodes a protein (I) which has neurite extending readuency and brain function. (I) is also used as a neurite- g agent
Mus sp. Loc CDS 196 196 196 196 196 196 196 196 197. A. CO-JUN-1999. 13-NOV-1997; 97JP 13-NOV-1999-379889/32 P-PSDB; AAY17863. The present sequence accivity: (I) may be calivity: (I) may be improve memory and improve memory and extending agent

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oglygludspglydla------GlnglygluProdlagluPro 107
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       Length:
Matches:
Conservative:
Mismatches:
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Ligenfelter C, Vuong TT;

Polakis P, PHARM INC

97WO-US013944 96US-0025601P

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WPI; 1998-193616/17.
P-PSDB; AAW37883.
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         06-AUG-1997;
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                                                                 LeulysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaVal 367
                                                                                                      GluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeu 387
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1030 AAGCTGAAAAGCATTATTGACCAGTATGAGCTGCGGGAAGAGCACCTTGACAAAATATTT
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                              LysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMet
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WO9810066-A1

12-MAR-1998

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sArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMe 176
                                                                                                                                                         This cDNA clone, designated 091-132020 (ATCC 98143), which is not full-length, codes for a 46 kDa BRCA1 modulator protein (see AAW37883) that binds to the tumour suppressor gene product BRCA1, and which is characterised by a single leucine zipper domain. 3 cDNA clones (see also AAV29062-63) coding for BRCA1 modulator proteins (see AAW37881-83) were isolated from a Hela-CDNA library using a yeast two-hybrid assay with a GAL4-BRCA1(8-1293) fusion as bait. Vectors and host cells comprising the isolated nucleic acid sequences are claimed, as well as a process for producing BRCA1 modulator protein by culturing these host cells. BRCA1 modulator protein acids can be used to diagnose diseases involving unwanted cell growth, e.g. breast cancer, and to identify compounds that alter BRCA1 interaction with BRCA1 modulators for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 TGGCACAATGGAAGAAGCTGGAATTTGTGGGCTAGGGGTGAAAGCAGATATGTTGTGTAA 170
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Breast cancer antigen 1 modulator protein - useful for diagnosing diseases involving unwanted cell growth, e.g. breast cancer, and producing therapeutics for treatment of such diseases.
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/note= "no termination codon given'
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                                                                                                                                   sGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLe 236
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                                                            429 GCAAGCCCTAAACACCCTTTCAACCCCAGAGGAGAAGCTGGCAGCTCTCTGTAAGAATA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                         909 CGTGGATGCCAAACTGCAGCAAACGACACAAGAAAGTGAAGGTGATGAAAAAGATGA 968
                                                                                                                                                                                                                                                                                               sPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSe
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                                   tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysTy
                                                                                    rAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLy
                                                                                                                                                                                     uAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA 091-132Q20 encoding a BRCA1 modulator protein.
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The present sequence encodes a modulator protein, that binds to and modulate the activity of the BRCA1 gene product (BRCA1). The BRCA1 protein has been characterized as a tumour suppressor protein.

Alterations in the amino acid sequence of BRCA1 causes breast and ovarian cancers by removing the controls on cell growth and proliferation. Research has shown that different regions on the BRCA1 molecule have different effects on cell growth and tumour suppression (e.g. full length truncated BRCA1 has no effect on breast cancer cell growth but will inhibit ovarian cancer cell growth. It has been suggested that different host cell factors (e.g. proteins) interact with different regions of the BRCA1 to control its function. The identification of these proteins (e.g. brothy) will facilitate the development of novel diagnostic methods and new therapeutics for identifying and treating cancers caused by changes in the expression or activity of BRCA1
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                                                                                                                                                                                                                                  Modulator proteins that bind to and modulate the activity of the BRCA1 tumor suppressor gene product, useful for the treatment of ovarian and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 TGGCACAATGGAAGAAGCTGGAATTTGTGGGCTAGGGGTGAAAGCAGATATGTTGTGTAA
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Polakis PG;
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                                                                                                       rLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHi
                                   sArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMe
                                              tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTy
                                                                               429 GCAAGCCCTAAACACCCCTTTCAACCCCAGAGGAGAAGCTGGCAGCTCTCTGTAAGAAATA
                                                                                               rAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLy
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Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.

(LUDW-) LUDWIG INST CANCER RES

WPI; 2001-025274/03.

Obata Y;

99US-0136526P. 99US-0153454P.

28-MAY-1999; 10-SEP-1999;

26-MAY-2000; 2000WO-US014749.

Homo sapiens. WO200073801-A2.

07-DEC-2000

Claim 50; Page 289-290; 799pp; English

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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                                                                                                                                                                                                                                         BP; 324 A; 155 C; 192 G; 149 T; 0 U; 3 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                         Sequence 823
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cancer associated antigen nucleotide sequence SEQ ID NO:48.

CDNA; 823

AAF22469 standard;

(first entry)

26-MAR-2001

AAF22469

Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.

or

vaccines

part

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cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                         :::
AGTCAGCACACTCCGATGAAGAGCCAGAGTCAAACGTCTCTGTGGATCAAGAGATTGAC
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polynucleotides and polypeptides are useful in gene therapy, vaccines peptide therapy. The polypeptides have various cytokine-like activitieg. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity at activity, tissue growth factor activity, immunomodulatory activity at activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system discorders, arthritis inflammation. Note: The sequence data for this patent did not form pic of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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polynucleotides or polypeptides of the invention, and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or meating a medical condition, kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention, methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide, and 767 contig sequences corresponding to the conk sequences of the invention and ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 (ADC33394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet
                                                                                                                                                                                                                                                                                                           disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                              TATGAGTGCTTTGTGATGAAAATCGGGAGGCTAGAGAACCTCTGCCGTGCTTTACAAGAA
GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu
                            GAGAACTGTAACAAGCTCTGTTGGACATGAAGAAGAAGCACTGAGAGCTAAAGAA
                                                           LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
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Wang Z, F
                                                                                                                                                                               ThrAspSerGlyProGluArgArgProGluGly------
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Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel cDNA sequence, SEQ ID NO:724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGCTGAACCTCCCTCCAAGGCC 1130
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Zhou P, Ghosh M, Wang D, Ma Y, Av
Haley-Vicente D, Drmanac RT;
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P-PSDB; ADC31613
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New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 724; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-CADC3088) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention, the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptides of the invention; and methods of computation and invention in methods of the invention. The invention further discloses methods for the invention; and encoded of invention further discloses methods of peventing, treating or ampliorating a medical condition; Kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention conting sequences corresponding to the compounds that modulate the expression or activity of the polypucleotide and/or polypeptide, and 767 contig sequences corresponding to the cDNA sequences of the invention are contig sequences corresponding to the cDNA sequences of the invention of mutations responsible for general disorders or other contigs. And dispensely in the contist, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as an analysis or and other mannoders and other mannoders and other mannoders and other mannoders and other mannoders. disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nuclei acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences.

Sequence 1782 BP; 564 A; 425 C; 445 G; 348 T; 0 U; 0 Other;

Alignment Scores Pred, No.: Score: Percent Similari Best Local Simil. Query Match:	Alignment Scores: Pred. No.: Porce: Percent Similarity: Best Local Similarity: Query Match:	2.35e-38 810.00 63.22% 47.70% 29.08%	Length: Matches: Conservative: Mismatches: Indels:	1782 166 54 68 60	
US-10-023	-523-44 (1-546	US-10-023-523-44 (1-546) x ADC30642 (1-1782)	-1782)		
λ̈	257 GluGluGly	ValGlnArgAlaArg	GluGluGluGluLys	GluGluGlyValGlnArgAlaArgGluGluGluLysArgLysGluValThrSerHis	276
qo	87 GAAGAGGCG	CTTCAGCGGGCACGT	GAGGAAGAAGAGAAA	GAAGAGCGCTTCAGCGCGCACGTGAGGAAGAAGAAGAAAGA	146
٥y	277 PheGlnVal	ThrLeuAsnAspIle	GlnLeuGlnMetGlu	PheGlnValThrLeuAsp1leGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer	296
qo	147 TTCCAGAGT	ACCCTCACGGACATC	CAGGGCCAGATCGAG	TICCAGAGTACCCTCACGGACATCCAGGGCCAGAGCAGCAGCGAGAGTATG	206
ζ	297 LysbeuArg	GingluAsnMetGlu	LeuAlaGluArgLeul	LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr	316
QC QC	207 AAGCTCTGT	CAGGAGAACACAGAG	CTTGCAGAAAAGCTG	AGCTCTGTCAGGAGAACACAGAGCTTGCAGAAAGCTGAAAAGCATCATCGATCAGTATA	266
δλ	317 GluLeuArg	GluGluHisIleAsp	LysValPheLysHis	GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu	336
d d	267 GAGCTCAGA	GAGGAGCATCTGGAC	AAAATATTTAAACAC	TGCAGCAC	326
oy Vo	337 ValAspAla	LysLeuGlnGlnAla	GlnGluMetLeuLys	ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln	356
qq	327 GIGGAIGCA	AAGCTTGAGCAGGCC	CAAGAAATGATGAAGG	GTGGATGCAAAGCTTGAGCAGGCCCAAGAAATCATGAAGGAAG	386

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proteins - derived for testes, brain, ovary,

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Racie LA,

ER,

oy JM, Lavallie Agostino MJ;

Mccoy

98WO-US006956. 97US-00837312

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The present sequence represents an expressed sequence tag (EST), and is a polymucleotide of the invention. The polymucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, cancelly cativity, receptor/ligand activity, ununu inhibition activity, oadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 529 BP; 151 A; 146 C; 168 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted human blood, kidney, foetal lung, placenta, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 381; 641pp; English
                                                                                                               GEMY ) GENETICS INST INC
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Spaulding V,
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                      ArgGluLysAspPhereuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet
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Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

BP.

CDNA; 529

AAV88391 standard;

entry)

(first

12-FEB-1999

AAV88391

EST clone GP232.

Homo sapiens WO9845437-A2

15-OCT-1998

RESULT 32

ACD13448;

ACD13448 standard; DNA; 115756

ACD13448

(first entry) 13-AUG-2003

Human DNA encoding a p53 modifier, SEQ ID 68.

Human, ds. gene, p53 modifier, cytostatic, cancer, cytostatic, antiangiogenic, antiapoptotic, p53 pathway, breast cancer, colon cancer, kidney cancer, lung cancer, ovarian cancer, angiogenesis, cell cycle; apoptotic disorder, cell proliferation disorder.

Homo sapiens

WO200299122-A1

12-DEC-2002,

03-JUN-2002; 2002WO-US017382.

05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P.

(EXEL-) EXELIXIS INC

Funke RP; Li D, Belvin M, Francis-Lang H, Friedman L, Plowman GD,

WPI; 2003-156859/15. P-PSDB; ABO07223 Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Example 2; Page 320-351; 678pp; English.

The invention relates to identifying (M1) a candidate p53 pathway

modulating agent, by contacting an assay system comprising a purified HM

polypeptide (human orthologue of genes that modify the p53 pathway in

Drosophila) or nucleic acid with a test agent under conditions, where but

for the presence of the test agent, the system provides a reference

activity, and detecting a test agent-biased activity of the assay system.

Contacting a cell defective in p53 function with a candidate modulator

Also included are modulating (M2) a p53 pathway of a cell (comprising

Contacting a cell defective in p53 function with a candidate modulator

Contacting a cell defective in p53 function with a candidate modulator

Contacting a cell defective in p53 function with a candidate modulator

Contacting a cell defective in p53 function with a condidate modulator

Contacting a cell defective in p53 function with a condidate modulator

Contacting a cell defective in p64 function with a control, and (M3) a p53 pathway

Contacting a patient (comprising: (a) obtaining a biological sample

Expression; (c) comparing the results with a control; and (M1) is useful

Contacting defection in dicates a likelihood disease). (M1) is useful

Contacting addiagnosing breast, colon, kidney, lung and ovarian cancer,

in a patient, where the cancer has greater than 25 % expression level.

Contacting the p53 pathway, such as an disponentic and

therapeutic applications, where disease or disorder prognosis is related

Confects in the p53 pathway, such as an disponent or

Confects in the p53 pathway, such as angiogenic,

Confects in the p53 pathway or a cell, thus restoring

Confects in the p53 pathway or a cell, thus restoring

Confects in the p53 pathway or a cell, thus restoring

Confects in the p53 pathway or a cell, approached the cell or cell world effects in the p53 pathway or as angiogenic or

Confection or progression through the cell undergoes normal

Confection or reading a p53 pathway such as angiogenic or

Confection or cell proliferat

115 res:
8.53e 11arity: 40.778 Similarity: 39.27% .:
-44 (1-546) x ACD13
MetlysasnglnasplyslysasnglyalaalalysglnSerasnProlysSerSerP:
GlyglnProgluAlagly
ValGluAlaGluGlyPr
CTCTGCGTTGCCAGCGGGCAGGAGGAGCTGTGGGGT
AGGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGG
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CGCGGTCCCCCTGCGCT
AGTTCTGGAGAGAAGCT
CAGGAAATCCAGGTCCCGTTAGAAACACCTCAGC
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ITGAGGCATTICIAGAATGATCTGAATGGCAAGAAATGGTTTTGTGGGGGGGAAGGAGA
GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT
AACAAATATGTTCGGGTGGTAGTGAGAAATAGTTGTGT
AAAGAAGTTAGGCAACGATTACTATATTT
TCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA
AAAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTTGGCTGGGCCTGAAAAATCCCA
ACCAGIGGIAIAAICG

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2100 ATGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAAGAAGCCGCA 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 3 (LBP-3, see AABS2080). The DNA was isolated from a human genomic library by screening with LBP-3 cDNA (see AABS2601). The open reading frame spans 10 exons. Human LBP-2 nucleic acids are among claimed applymucleotides of the invention that encode more! polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as biologically active fragments and analogues of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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Matches:
Conservative:
Mismatches:
Indels:
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14-JUL-2000; 2000US-00616289.
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P-PSDB; AAB82809.
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                                                                                                        pGlyalaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAl
                                                                                                                                                           aArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGl
                                                                                                                                                                                                               138 yAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgAr
                                                                                                                                                                                                                                        70814 GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACAGAGACCATCGAAG
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                                                    nLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAs
 aGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGl
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(HYSE-) HYSEQ INC
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                            SerThrProGluGluLysLeuAlaAlaLeuCys-----LysLysTyrAlaGluLeuLeu
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-- AAAACTATTCGTGATAAA
                                                                        GlubeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln
                                                                                                                                                        AATTATAAGGTCTTTCAAATAAATTGGAGCGGTTAGAGAAGCTGTACAAGGCTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                  -----GlnAspLeuSerAlaGlyGlyGlyGlnGlySerLeuThrAspSerGlyProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy; forensic, food supplement, medical imaging, diagnostic, genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAATGAATGAAGTAAATGCTACTCAAAAGCCCTCTCCACA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ValThrGluAlaProCysTyrProGlyAlaProSerThr
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                             ------GluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGln 217
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                                                                                                                                                                                                                                               GCCAAACTGCAGCAGGAGAACATGGAAATGGGAGAAAAAAGGTAAAGAAGCTCACTGACCAG
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                                                                                                                                                                                                                                                                                                                                              TCAAATTGCAGTGCCACAAGTAATAAACATTTATTGGAAGAAGAAGGCCGTGACTTT
                                                                                                   Sequence 1734 BP; 484 A; 404 C; 327 G; 519 T; 0 U; 0 Other;
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                                                                                                                                  456 GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln 475
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                                       306 AATTATAAGGTCTTTCAAATAAATTGGAGCGGTTAGAGAAGCTGTACAAGGCTCTTCAA
436 TrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 24947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
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genes from Drosophila and
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P-PSDB; ABB66052.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed carivity of (II) as useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and among sequences. Abs&4197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this for the invention of the invention, but was obtained in the content trains to be appear in the printed specification, but was obtained in the content trains and sequences.
                                                                              966 CACTCAGAGGGCCTGCAGAAGCAAATACAGCAGCTGCAGAAGCTACTGCGTGCTCTACAG 1025
                                           475
906 TACGAGAAAGCTAATGCCATGGTGATCGATTTAGCCACAGAAAAGAGTCTGCAGACGCAG 965
                                  456 GluLeuGluGlyLeuGlnValLysileGlnArgLeuGluLysLeuCysArgAlaLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                               Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                1026 CTGGAGAGACAACACTGCACAAGTGCCTGCGGGAT 1061
                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #2478.
                                                                                                                        476 ThrGluArgAsnAspLeuAsnLysArgValGlnAsp 487
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                                                                                                                                                                                                                                                AAS66674 standard; cDNA; 2526 BP.
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23-AUG-2000; 2000US-00649167.
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Sequence 2526 BP; 871 A; 536 C; 541 G; 578 T; 0 U; 0 Other;

Alignment Scores:

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Myers EW

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2001-656860/75,

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                             23-MAR-2000; 2000US-0191637P.
                                                                                      11-JUL-2000; 2000US-00614150
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         Drosophila melanogaster.
                                                                                                                        Venter JC, Adams M,
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                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elucatores for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS70737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 ValAspAsnAsnGlnGlyGlyProGlyGlu---AspGlyAlaGlnGlyGluProAlaGlu
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                                                                                                                                                                                                                                                                            Sequence 4307 BP; 1298 A; 971 C; 1016 G; 1022 T; 0 U; 0 Other
Claim 1; SEQ ID NO 24944; 21pp + Sequence Listing; English.
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 24944.

(first entry)

26-MAR-2002

Drosophila; developmental biology; pharmaceutical; gene; ss.

cell signalling; insecticide;

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2380 CTAATGCCATGGTGATCGATTTAGCCACAGAAAAGAGTCTGCAGACGCAGCACTCAGAGC 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce totipotence in one or more cells. Molecules which induce totipotence in one or more cells. Molecules which induce developmental none or more cells. Molecules which induce development in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGln 64
                                                459 lybeuGlnValbysIleGlnArgbeuGluLysbeuCysArgAlabeuGlnThrGluArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            taurus; EST; expressed sequence tag; totipotence;
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STACHE-CRAIN B.
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JONES L W.
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for

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identifying expressed genes or for physical mapping of the human genome, in forensias, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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27-AUG-1999;
11-JAN-2000; 2
02-MAY-2000; 2
09-JUN-2000; 2
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Yamamoto J; sogai T, Nishikawa T, Hayashi K, Saito K, Ya Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; Isogai T, Ishii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polymucleotides, particularly the 5602 full length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.

Claim 1; SEQ ID NO 4742; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonnclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination of a polynuclectide which comprises a S-end sequence and an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a S-end sequence and an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a S-end sequence. Oligonuclectide which comprises a S-end polynuclectide which comprises a least 15 nucleotides and the combination of the S-end sequence(3'-end sequence's where the reapy and in gene therapy. The primer set scan be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for AMH13612 and AMH13613 to AAH13612 and AMH13613 to AAH13622 to AAH13622 to AAH13622 to AAH13623 to AAH13623 to AAH13622 to AAH13623 to AAH13622 to AAH13623 to AAH oresent invention

Sequence 710 BP; 224 A; 144 C; 203 G; 136 T; 0 U; 3 Other;

710 97 25 89 16 Length:
Matches:
Conservative:
Mismatches:
Indels: 4.54e-13 368.00 53.74% 42.73% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: .. No.:

US-10-023-523-44 (1-546) x AAH07907 (1-710)

130 CGGCGACGCAGCCCGCGCGCAGAGTTTGAAATTGGCACAATGGAAGAAGCTGGAATTTGT 189 106 GluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro 125 86 TyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAla 105 250 CAA-----GGCTCAAATTGTGGTGGCACAAGTAACAAGCATTCATTGGAAGAGATGAA 303 126 ThrProValValAsnGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIle 145 -----GAAGCT 393 28 GluGlyAlaGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly 47 SerSerGlnAlaProArgLys-----ProGluGlyAlaGlnAlaArgThrAlaGlnSer 65 GlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThr 85 346 GCATACTGCACGCAAGAATCAAGAGGAAATCCCTGGGGGA----304 GGCAGTGACTTTATAACAGAGAACAGGAATTTGGTGAGC---48 99 à 임 à g $\stackrel{>}{\circ}$ g ò g à

g ò

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185
146 ArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysAla 165
                                                                                        507
                                                                                                                                                   567
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                                                                                                                                                                                                               627
                                                                                                                                                                                                                                        HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys 245
                                                                                                                                                                                                                                                                          687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                                                                                                                                        GAGGAGAAGCTGGCAGCTCTCTGTAAGAAATATGCTGATCTTCTGGAGGAGAACAAGAG
                                                                                                                                                                               206 SerGinLysGinMetLysLeuLeuGinLysLysGinSerGinLeuValGinGluLysAsp
                                                                                                                                                                                                394 CGAACAGATCCCCCTGATGGTCAGCAAGATTCAGAGTGCAACAGGAACAAAGAAACT
                                                         166 LysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrPro
                                                                                      154 -----TTAGGAAAGAAGTTTTATTACTGATGCAAGCCCTAAACACCCTTTCAACCCCA
                                                                                                                     186 GluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cardiovascular system antigen cDNA polynucleotide SEQ ID No 467.
                                                                                                                                                                                                                                                                                                       252
                                                                                                                                                                                                                                                                                                                                 688 ANAGAACTICANCGICACAAI 708
                                                                                                                                                                                                                                                                                                                                                                                              AAS35582 standard; cDNA; 405 BP.
                                                                                                                                                                                                                                                                                                     246 ArgGluLeuGlnArgHisAsn
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18-APR-2000;
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2000US-0249213P 2000US-0249213P 2000US-0249214P 2000US-0249214P 2000US-0249216P 2000US-0249216P 2000US-0249218P 2000US-0249218P 2000US-0246609P. 2000US-0246610P. 2000US-0246611P. 2000US-0246613P. 2000US-0249207P. 2000US-0249300P. 2000US-0250160P. 2000US-0250391P. 2000US-0251030P. 2000US-0251988P. 2000US-0256719P. 2000US-0251479P. 2000US-0251856P. 2000US-0251868P. 2000US-0251869P. 2000US-0249209P. 2000US-0249210P. 2000US-0249211P. 2000US-0246525P. 2000US-0246526P. 2000US-0246527P. 2000US-0246528P. 000US-0249264P 000US-0249265P 000US-0251989P 2000US-0246532P 000US-0246523P S-DEC-2000; 05-DEC-2000; 05-DEC-2000;

(HUMA-)

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-451930/48. P-PSDB; AAU22308.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system.

Claim 1; SEQ ID NO 467; 674pp; English.

Sequences AAS35126-AAS35740 represent cDNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polyncleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, detecting the presence or absence of a mutation can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune sheaps such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility,

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24-FEB-2000; 20-MAR-2000; 216-MAR-2000; 217-MAR-2000; 218-ARR-2000; 219-MAY-2000; 207-JUN-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cardiovascular system related polypeptide; cancer; proliferative disorder; foetal abnormality; developmental abnormality; haematopoletic disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma;
   renal disorders such
gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCCCCGGCGAGGATGGGGCACAGGTGAGCCGGCTGAACCGAAGATGCAGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cardiovascular system related polynucleotide #457
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Matches:
Conservative:
Mismatches:
Indels:
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352.00
80.00%
75.45%
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Best Local Similarity:
Query Match:
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Pred. No.:
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2000US-0198123P
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The invention relates to human cardiovascular system related polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies to the polypeptides are useful for diagnosing a data data the polypeptides are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, such as cancer of cardiovascular system tissues, proliferative disorders, foctal and developmental abnormalities, haematopietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheiner's disease, Parkinson's disease), cognitive disorders; controphrenia, asthma, skin disorders (e.g., psoriasis), sepsis, candorders, kidney disorders, gastrointestinal disorders, prequancy related disorders, endocrine disorders and infections. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mamping. The polypeptides and polymucleotides may also be used as food additives or preservatives to increase or come of the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 TCCCGGACCTATGTGGCAAAGGAATGGGGAGCCTTGAACCAACTTCCAKTAGTTCAATTGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yGlulysGluProSerLysGlyAsp-ProAsnThrGluGluI]e-ArgGlnSer-AspGl 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ovarian antigen, ovary, ovarian, breast, cancer, tumour,
ovarian cancer, breast cancer, tumour, reproductive system disorder,
infertility, pregnancy disorder, anovulation, polycystic ovary syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GluGluLeuSerArgClnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 uValGlyAspArgAspHis---ArgArgProGlnGluLysLysLysAlaLysGlyLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 AGTICGGAGCAAGGAACCATICGAAGGCCACAGGAGAAGAAAAAGCCAAGGITTITGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerArgThrTyrValAlaArgAsnGlyGluPro-GluProThrProValValAsn---Gl
                                                                                                                                                                                                                                                                                                                                                                 components. This sequence represents a human cardiovascular system related polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 405 BP; 123 A; 90 C; 126 G; 63 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian antigen HLTJA50 cDNA, SEQ ID NO:1238.
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Matches:
Conservative:
Mismatches:
Indels:
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                  Claim 1; SEQ ID NO 467; 262pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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DB:
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ID ABQ5
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2000US-0246474P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-743766/70.
P-PSDB; ADE46276.
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01-NOV-2000;
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08-NOV-2
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4228) and to CDMAs encoding them (ABD54131-ABD65305), and also encompasses polypeptides 99% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigens polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or preast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian orysts, and dysmenorinea, endocrine disorders, infertions (e.g., chlampadia, HIV, toxophasmosis, and toxic shock syndrome, ovary syndrome, conditions (e.g., mastitis, ophoritis and vaginately disorders, eurological disorders, gastrointestinal disorders respiratory disorders, neurological disorders, gastrointestinal disorders polynucleotides may also be used in screening for compounds which modulation or activity. The polynucleotides may further be used for gene therapy, chromesome mapping, in the control of individuals and in forensic analysis, and the control of individuals and in forensic analysis, and the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      usolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents CDNA encoding a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
PCOS; ovarian cyst, dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiowascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forenaci analysis; analysis; analysis; analysis; analysis; analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1238; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2000; 2000US-0209467P
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263 A; 122 C; 147 G; 176 T; 0 U; 17 Other; BP; 725 Sequence

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US-10-023-523-44 (1-546) x ABQ55358 (1-725)

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LeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHis 382
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                                                                                                                                                                                                                                                              LysIleGlnArg-LeuGluLysLeuCysArgAla-LeuGlnThrGluArgAsnAspLeuA 482
                                                                                                                                                                                                                                                                             The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing totipotence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for preventing a full term
                                                                                                                                                                                                                             334 TTAAANGAAGCGACAGAATCGAGGCACAAATACGAACAAATGAAACAGCANGAAGTACAA
                                                                 LeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer
                                                                                                      LysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIle
                                                                                                                    LysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla
                                                                                                                                                                                                             LeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taurus; EST; expressed sequence tag; totipotence;
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pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATACTGCGTGGACAACAGNNANNGGGGCCCAGGTNAGGATGTGGCANAGGGNGAGCCT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGlu 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 TAGATICCTGTACCAGNGATGAAGTTTGAGACCGANACCACCCAAAGCCNCNGGATANTAA 381
                                                                                                                                                                                                                                                                                          GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGln 64
                                                                                                                                                                                                                                                                                                                       derrecedececricingaactagrecarceece---edecrecedeannr-egecaceae 81
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Mismatches:
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                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating call signalling and cell-cell interactions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3611), expressed DNA sequences (ABL018175) and the encoded proteins (ABB57737-ABR3727). The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form part of the from WIPO at fip.wipo.int/published_pct_sequences
                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                 Claim 1; SEQ ID NO 5525; 21pp + Sequence Listing; English
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LeuGluGluHisArgAsnSerGlnLysGlnMet :: TTGAAAGAAAAAATCAAGGAAAGGAAAGAAG	1bysLysGlnSerGlnLeuValGlnGluLys	GGAGAAGGAACGAGAAGAAAGGATGAAG	LysalavalleualaargserlysleuGluseri AggagaagcaacgagaagaaaagcTaagagaaa	AsnArgSerLeuLysGluGluGluClyVal(::: 	LysArgLysGluValThrSerHisPheGlnValThrI	ctcccaaaagaaaaaaagaaaaaag	GluGlnHisasuGluarg/ 	MetGluLeuAlaGluArgLeuLysLysLeuIleGluC	GAAGAAAAGCTCAAGGAGGAAGGAAGCTGCTCAAG	IeasplysvalPhelysHislysAspleuGinGlnGinLeu 	GlnAlaGlnGluMetLeuLysGluAlaGluGluArgi :::: GAACGGGAAGGAAGCTCAAAAGGGAAAAAGGAAAAA	LeuLysGluAlaValGluSerGlnArgMetCysGluI	::: agggagagaagctaaaagagaaggggctgaaa	LeulysglnglnLeuAlaLeuTyrThrGluLysPheG ::	LysSerSerGluValPheThrThrPheLysGlnGluN 	aaggaaaaggagagagagagagagagagagagagagag	LysLysLeuGluLysGluThrThrMetTyrArgSerP 	LeuLeuGluMetAlaGluGluLysThrValA	GTCGTCGAGGATACTCCACCCAAACTGCCTGCGGTTC	aseccentrargedagecegagagagagageceggere	:gAsnAspLeuAsnLysArgValGlnA ::: ::::	100000000000000000000000000000000000000	erGlyProGluArgArg crcccrgcrcrcgaaco	13085 B
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5481 AACAAGCAAAAAGACCAGGGGAAAAGTCAGCGAAAAGAAGCCAGAGCAGAGCAAATCTGGCG 5422
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                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 5522.
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novel bone marrow polypeptide #14.
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
30-NOV-2000; 2000US-0250683P.
                                                                                                                                                                                                                                    AAS22920 standard; DNA; 5943
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P-PSDB; AAU14615.
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TTGCACGTGGAGATGAGTGCGGCGGATGCGGAGCAAGGCGAAGATGAAGAGATCGAAGGG
                        AlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArg
                                               5181 CTCGATGAGGAGCCA-----CCCAAAACAATGTCCAAAGAAGAAGAAGAAGAAAAAA
                                                                        120 AsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAsp
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                                                                                                                                                                        160 GlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeu
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                               GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln
  --Lys
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443 LeuLeuGluMetAlaGluGluLys-----ThrValArgAsp
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Bone marrow, diagnostic, therapeutic, gene therapy, antigenic, haematopoiesis, myeloid, lymph cell disorder; tissue regeneration, wound healing, nutritional supplement; immune disorder; severe combined immunodeficiency; SCID; ds.

Asundi ບັ

Xue AJ;

ď Zhou

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Nucleic acids encoding bone marrow polypeptides, useful in diagnostic and

polypeptides. The nucleic acids and corresponding novel bone marrow polypeptides. The nucleic acids and corresponding proteins may be used in the prevention, diagnosis and treatment of diseases associated with the inappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the patient's own production of the polypeptides, by inserting the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acid and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The proteins may also be used as antigens in the production of antibodies against bone marrow proteins and

us-10-023-523-44.rng

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in assays to identify modulators of their expression and activity. The anti-bone marrow protein antibodies and antagonists may also be used to computate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the protein in samples cc (e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins may be used to requlate haematopoiesis activity, and consequently in the creatment of myeloid or lymph cell disorders; in tissue regeneration, cc such as wound healing, as a nutritional supplement; and in treatment of immune disorders such as severe combined immunodeficiency (SCID)
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:888	treatment such as wo immune dis	of myeloid or lymph ce und healing; as a nutr orders such as severe	11 disorders; in tissue regeneration, itional supplement; and in treatment of combined immunodeficiency (SCID)	
X S	Sequence	5943 BP; 1437 A; 1594 C;	; 1783 G; 1129 T; 0 U; 0 Other;	
Alignmer Pred. No Score: Percent Best Loc Query Ma	gnment Scores: d. No.: re: cent Similarity: t Local Similari	res: 2.38e-07 286.50 arity: 36.11 nilarity: 22.27% 4	Length: 5943 Matches: 165 Conservative: 107 Mismatches: 238 Indels: 233 Gaps: 27	
US-10	-023-523	-44 (1-546) x AAS22920 (1	1-5943)	
ò	12	LysGlnSerAsnProLysSerSerProGly	ProglyGlnProgluhla 25	
qq	1152	AAAGAGGAAAATGAGAAGAATGAA		11
δ	26	GlyProGluGlyAlaGlnGluArg	aGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGly 45	
qq	1212	GACCCTACAGGC	AGTGAACCTGCCAAGCTCTGAAAGGAAGCA 129	56
à	46	ProGlyser	ysProGluGlyAlaG	
QQ	1257	 		16
ò	61	ArgThrAlaGlnSerGlyAlaLeu	enArgAspValserGluGlubeuserArgGlnbeuGlu 80	
g	1317	 CCAAAGAAGGCTTCTGCTCTG	CAAAGAAGGCTTCTGCTCTGGAAGAGGGGAGTTCAGACGCAGCCAAGAACTGGAA 137	76
ò	80		08	
QQ	1377	ATTAGTGAACACATGAAGGAACCA	TTAGTGAACACATGAAGGAACCACAGCTCTCAGACTCCATAGCTTCTGACCCCAAGTCC 143	36
ò	81		Asp 81	
ДQ	1437	TTCCATGGCCTGGACTTCGGTTTT	TICCAIGGCCIGGACTICGGITITICGCAGCCGGAICTCGGAGCACCTGCIGGAIGITGAI 145	90
à	82	IleLeuSerThrTyrCysValAsp	eLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGly 99	
qq	1497	::: Grecrrccccagrecressres-	::: GTGCTTTCCCCAGTCCTGGGTGG-AGCTTGTCGGCAGGCCCAGCAACCACTGGGAATAGA 155	55
ò	100	AlaginglyGluProAlaglu	11	м
Db	1556	AGACAAGGATGACAGCCAGTCCAG	 AGACAAGGATGACAGCCAGTCCAGCCAAGATGAGCTGCAGAGCAAGCA	15
δ	114	1	hrTyrValAlaArgAsnGlyGluProGlu-Pr 12	
qq	1616	GGAGGAGGTACCATAGGTTATC	GGAGGAGAGGTACCATAGGTTATCTCCTCCACTTCCACAGGGGGGGG	75
ò	125	oThrProValValAsnGlyGluLy	14	ı,
Dp	1676			35
à	145	eArgGlnSerAspGluValGlyAsp	15	en
Dp	1736	GAAGGAGGCAGAGGAGCTTGGGGA		95
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qq	1796	CCAGAGGAGCAGGCCCCAAGCCC	CCAGAGGGAGCAGGCCCCAAGCCCACCTGCTGAGAAAGGGCAAGGAGCAGCATTC 185	55
à	154		16	ம
QQ Q	1856	CCAGGCCGAGGAGCTGGGCCCTGG	AGGAAGAGCAGAGGATCCTGA	15

oy.	165 aLysGlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrPr 185
oy op	185 oGludlu
S S	201 uGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuVa 221
% da	221 1GlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSe 239
S da	
දු පු	259 yValGlnArgAlaArgGluGluGluGluLysArgLysGluValTh 274 2201 GCCCGGATGAGAGAAGAAAGCCAGAGGTATCCTGGCTCCGAGCTCAGGTCCA 2257
oy B	274 rSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGlu 289 2258 GTCCAGCACACAAGCAGATGAGGACCAAATCAGGGCTGAGCAAGAGGCTTCCCTGCAGAA 2317
දු දු	290
ò 8	302 nMetGluLeuAlaGluArgLeuLysLeuIleGluGlnTyrGluLeuArgGluGluHi 32
& 8	322 sileasplysvalPhelysHislysAspleuGlnGlnGlnLeuValAspAl 339 2438 TGCCCTGAATGCTGCAAAGGAGAAGCTCTGCAGCTGAGGAGGAGGAGGAA 2497
S S	339 aLysLeuGlnGlnalaGlnGluMetLeuLysGlu
· 강 원	351AlaGluGluArgHisGlnArgGluLysAspPheLeuLysGluAlaValGl 368
. y d	368 uSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLy 384
λ _o	384 sGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSe 402
्रे स	402 rLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIl 4
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8	442 aLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnVa 462
a 8	2835GCTGAGGAGAGGAGGAGGCGCGGGCTGAGCTTCTGGGGCACCTGATCGG 2881 462 llvs1leGlnArdLeuGluLvsLeuCvsArdAlaLeuGlnThrGluArdAsnAsple 481
qq	2 AGAGCTGGAGCGCCTGCAGGGGCCCATGAACGAGAACTGGAACTGGAGACTGTAGGGGAGGAGGA 29

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3107 TGACCT---GCAGGCCGAGGAGGACGTGTGAGCGCCTGACCAAGGCCAAGCTCCGGCT 3163
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Best Local Similarity:
        12-APR-2002;
16-APR-2002;
                            19-APR-2002;
                                     19-APR-2002;
02-JUL-2002;
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                                                         3001 ATTTAGAGTTGGACCTTGAAACCAGAGCTAAAGATGTCAAGGCCAGATTGGCTCTGCTGG 3060
                                                                                                                                                                                                  544
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                                                                                                                                527 aProSerThrGluAla-----SerGlyGlnThrGlyProGlnGluProThrSerAl
uAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSer----
                                                                                                                                                                                                                                                                                                                                                                                             wasting; cancer; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                              NOV; cytostatic; metabolic disorder; immune; neurodegenerative; circulatory; haemopoietic; wasting; cancer; gene therapy; vaccitransgenic; human; gene; ds.
                                                                              -GlyPro---GluArgArgProGluGlyProGlyAlaGlnAla
                                                                                                                    ----ProSerSer---
                                                                                                                                                            -----ProArgValThrGluAlaProCysTyrPro----
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2001US-0304016P.
2001US-0304502P.
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2001US-0308877P.
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                                                                                                                                                                                                                                                                                                                                                               Human NOV20 DNA.
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                                                                                                                                                                                                                                                             A 3301
                                                                                                                                                                                                                                         a 544
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05-MAR-2002;
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Gaps:

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--GluAspAlaGluLys-

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The invention relates to a novel isolated NOV polypeptide. The polypeptide of the invention demonstrates cycostatic activity and may be used for determining the presence of, or predisposition to a disease associated with altered levels of expression of the polypeptide, including metabolic disorders, immune disorders, neurodegenerative disorders, circulatory diseases, haemopoletic disorders, wasting diseases and cancer. The polypeptide may also be utilised during gene therapy procedures, vaccine development and transgenic animal production. The current sequence is that of the human NOV DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated NOVX polypeptide, useful for determining the presence of, or predisposition to a disease associated with altered levels of expression of the polypeptide, and for treating or preventing cancer.
                                                                                                                                                                                                                                                                                                                                                     Burgess CE, Casman SJ;
Bilerman K, Gerlach V, Gc
Malyankar UM, Miller CE;
Rastelli L, Shenoy S;
A, Stone DJ, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6149 BP; 1423 A; 1687 C; 2121 G; 918 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     Anderson DW, Berghs C, Boldog FL, Bur
Catterton E, Edinger S, Eisen AJ, Bli
Guo X, Jeffers M, Kekuda R, Li L, M
Padigaru M, Patturajan M, Pena CEA, I
Shimkets RA, Spaderna SK, Spytek KA,
Vernet CAM, Voss EZ, Zhong M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 95; 478pp; English
2002US-0363637P.
2002US-0372326P.
2002US-0372990P.
2002US-03738B1P.
2002US-0373921P.
2002US-0373921P.
                                                                                                                                                                                                                                                                                  CURAGEN CORP
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P-PSDB; ADC26271.
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3371 CGAGCAGCTCTTGGGGGCCCAGATGCAGAAGAAGAAGATCAAGGACTGCAGGCTGGGGGGGG	rLeuserThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr	: : : :	258	305 uAlaGludrgLeuLysLysLeuLleGluGlnTyrGluLeuArgGluGluHislleAspLy 325 1163 GCTGTCCAAGGCCAATGCCGAGGTGGAGGAGGAAGTACGAAGCAGATGC 4219 325 sValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGl 343 125 sValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGl 343 127 cATCCAGAGGACCGAGAGGAGGCCAAAAAAAAGGTGGCACTGCGGCTGCAGGA 4279 343 nAlaGlnGlu	

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The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. ABKAS5531-ABK35581 represent the human genes of the invention that are differentially expressed in breast cancer tissue
molecules or expression products that are differentially expressed in normal and malignant tissue.
                                                                                     Claim 1; Page 98-101; 219pp; English
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Sequence 5574 BP; 1610 A; 1394 C; 1752 G; 818 T; 0 U; 0 Other;

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ტ —	GlyAlaGinGiuArgProSerGinAlaAlaProAlaValGiuAlaGiuGlyProGlySer
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8	SerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAla
87	
8 Le	LeudrgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCys
3747 CC	CCACATCTCCACTCTCAGGTCTCCGACTCGAAGAAGAAGCTGCAGGACTTTGC
8 V	ValAspAsnAsnGlnGlyGlyGlyGluAspGlyAlaGlnGlyGluProAlaGluPro
07 C2	CAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATCGAGAACCT
80	GluAspAlaGluLys
67 CP	CACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACCAAGAACAG
Se	SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProVal
7	::: GCTTCAGCAGGAGCTGGACCTGGTTGTTGATTTGGACAACCAGCGGCAACTCGTGTC
ž 6	ValAsnGlyGluLysGluProSerLysGlyAspProAsnThr
87 CZ	CAACCTGGAAAAGAAGCAGAGGAAATTTGATCAGTTGTTAGCCGAGGAGAAAAACATCTC
143 G	GludlulleArgGlnSerAspGluValGly-AspArgAspHisArgArgProGlnGluLy
4047 T	TTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCAGAAGCCAG
62 8	<pre>sLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLe</pre>
4092 G	GGAGAAG
182 u	$\tt uSerThrProGluGluLysLeuAlaAlaLeuCysLysLysLyrAlaGluLeuLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu$

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202	uHisArgAsmSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValG1 222 ::::::: :::
222	sLeuArgGlyGluHisSerLysAlaValLeuAlaArgSer : :
242	userLeuCysargGluLeuGlnargHisAsnArgSerLeuLysGluGluGlyValGlnar 262
262	galaarggludlugludysarglysgluvalthrserhisph 277
277	eGInValThrLeuAsnaspIleGInLeuGlnMetGluGlnHisAsnGluArgAsnSerLy 297
297	sleuargglndluaenMetGlu
305	-LeualagluargLeuLysLysLeulleGluGlnTyrGluLeu 318
319	
329	-HistysaspleuglnglnglnleuValaspalaLys
341	
345	nglumetLeuLysGlualaGlualagHisGluargGluLysAspPheLe 362
362	uLeuLysGlualaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHi 382
382	sLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSe 402
402	rLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLys11 422
422	eLysLysLeudluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl 442 :::::
442	aLeuLeuGluWetAlaGluGluLysThrValArgAspLysGluLeuGluGl 459
459	y
467	uGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeu 481

5133 GGAGGAGCAGGTCGAGGAGGCCAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCA 5192

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AKS78043 Sequence
L15544 Human high
AK18010 Sequence
BD157034 Primer fo
AK002071 Homo sapi
AK002071 Homo sapi
AK0151988 Homo sapi
AL034248 Homo sapi
AL0537 Homo sapi
AL0534 Primer fo
AR05505 Homo sapi
AR05505 Homo sapi
AR10537 Human muscu
BK647477 Homo sapi
AK10537 Human muscu
BK64747 Human sapi
AK10537 Human sapi
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ALB32338 Home sapi
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AR199536 Sequence
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-MODEL=frame+ p2n.model -DFV=xlh
-MODEL=frame+ p2n.model -DFV=xlh
-Q=/Cogn_1/UGPFTO expo-1/UGS1023523/runat 08062004_063748_29937/app_query.fasta_1.1422
-Q=/Cogn_2_1/UGPFTO expo-1/UGS1023523/runat 08062004_063748_29937/app_query.fasta_1.1422
-DECALIGN=200 -TIVESCORE=pct -THR MATRIX=blosum62 -TRANS=human40.cdi -LIST=50
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2785
1 MKNQDKKNGAAKQSNPKSSP.....APSTEASGQTGPQEPTSARA 546
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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NT T CHANTENATIC	541	GGCTGCTGTGCAGAAGTATGCTGAACTGCTG
RESULT 1	OY 201 GIGGLWHISAFGAR 	GIGGLUATSAFGARBSECTATA GGLTAMELLYSBEULEUGLTATA GLYSBEGLTAGE GGLTAGE GGLTALEU 220 GAGGAGCACCGGAATTTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCAGCTG 660
LOCUS AR409338 1670m patent US 6632923. ACCESSION AR409338 07.4016013	Oy 221 ValGlnGluLyske 	ValgingiuLysAsphisLeuArgglygluHisSerLysAlaValLeuAlaArgSerLys 240
S Unknown. ISM Unknown.	Oy 241 LeuGluSerLeuC 	LeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVal 260
REFERENCE 1 (bases 1 to 1638) AUTHORS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A. TITLE Low density 1 poportoring inding profess and their use in	Oy 261 GlnArgAlaArgGl 	aArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr 280
JOURNAL Patent: US 6612923-A 46 14-OCT-2003; FEATURES Location/Qualifiers Source 1.1638	Qy 281 LeuasnaspileglnLo 	LeuasnaspileGlnLeuGlnMetGluGlnHisasnGluargasnSerLysLeuargGln 300
ORIGIN /mol_type="genomic DNA"	Qy 301 GluAsnMetGluLeuAlaGluAr	GluasnMetGluLeualaGluargLeuLysLysLeuIleGluGlnTyrGluLeuargGlu 320
Alignment Scores: Pred. No.: 1.92e-123 Length: 1638 Score: 2785.00 Matches: 546 Ercent Similarity: 100.00% Conservative: 0	Oy 321 GluHislleAspLy	GluHistleAspLysValPheLysHisLysAspLeuGlnGlnGlnClnLeuValAspAlaLys 340
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Leuglu	Oy 421 LysileLysLysLe 	LysilelyslysleuglulyysgluthrThrMetTyrArgSerArgTrpgluSerSerAsn 440
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301 CAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGTGGCAAGGAAT 360
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                                            PAT 26-SEP-2001
                                                                                                                                                                                                Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis
Patent: WO 0164874-A 46 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pobo, G., Han, M. and Wiemann, S.
Direct Submission

Direct Submission

Direct Submission

Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;

Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;

Reinrich-Heine-University, Duesseldorf/Germany) within the CDNA

Heinrich-Heine-University, Duesseldorf/Germany) within the CDNA

Sequencing consortium of the German Genome Project. This clone

(DKF2P451K215) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4851 bp mRNA linear PRI 13-MAY-2003
Homo sapiens mRNA; cDNA DKFZp451K215 (from clone DKFZp451K215);
ALB32338
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                                                                                                                                               ACCCACCTGAAGCAACAGCTTGCCCTATACACAGAGGTTTGAGGAGTTCCAGAACACA 1278
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1459 caddinananiccancederedadangererecedecenerecadendadadecenaridae 1518
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                                                    PheleuLeulysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlu 380
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4851)

Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wlemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1579 CCTGAGAGGCCAGAGGGCCTGGGGCTCAAGCACCCAGCTCCCCCCAGGTCACAAAA
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                                                                                                                                                                                            LeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLys
                                                                                                                         ThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr
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DH10B; sites Not1 + Sal1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGluAlaGluGlyProGlySerSerGlnAlaProArglySProGluGlyAlaGlnAla
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Mismatches:
Indels:
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/produci="hypothetical protein"
/protein_id="CAD91138.1"
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Matches:
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.03. .1743
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1. .4851
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Query Match:
DB:
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125. .1765
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                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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4852
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1. .4880
                                                                                            CCCACCTCCGCCAGGGCC 1740
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                                                                     541 ProThrSerAlaArgAla
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                                                                                                                                                                                                                             ValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys
                                                                                                                                                                                                                                                       GTGCAAGAGAACCACCTGCGCGGTGAGCACCAGCGAAGGCCGTCCTGGCCCGCAGCAAG
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4880 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DKFZp45110918 (from clone DKFZp45110918);
AL832636
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This close (DKF295110918) is available at the RZPD in Berlin.
Please context the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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QUQUBUDHIKOEHSKAVLARSKILESLOKELQHANKESIKEEGYBRAEBEEKKKYTSH
POYTLADI OLOMGOHNERNSKIROENMELAERLKKII EGYELAEEH DKVFKYTSH
POYTLADI OLOMGOHNERNSKIROENMELAERLKKII EGYELAEEH DKVFKYTSH
POYTLADI OLOMGOHNERAEBERHOREKOFILKEAVESORMCEINKOGETHIKOOLALYTSH
KVEBEQUATLSKSSEVFYTFEDGIMENYMYKKIKKILEKSTYNRSEMESSNKALLERAAERK
TYEDREL BGIGVKI OKALGKALOTERNDINKRYODILSAGGOSLTDSGPERRPEGP
GAQAPSSRYTEAPCYPGAPSTEASGQTGPOEPTSARA
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gpgssqaprkpegaqartaqsgalkdvseelsrqledilstycvdnngggpgedgadg
epaepedaeksrtyvarngepeptpvvngekepskgdpnteeirqsdevgdrdhrrpq
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Catarrhini; Hominidae; Homo.
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Submitted (17-UUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
On Apt 30, 2003 this sequence version replaced gi:21733212.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemanndekfz-haldelberg-de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the CDNA sequencing consortium of the
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/clone="DKFZp54110918"
/clone="DKFZp54110918"
/clone_ltppe="human spinal cord"
/clone_ltppe="human spinal"
/clone_ltp="451 (synonym: hlcc1). Vector pSport1; host DH108; sites Not1 + Sal1"
                                                                                    521 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu
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Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
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HSM803947 5023 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DXFZp451J0118 (from clone DKFZp451J0118).
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              Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I. (bases 1 to 5023)
Ansorge, W. Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
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Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
On Apr 30, 2003 this sequence version replaced gi:21733213.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                  TTTCTCCTGAAAGAGGCAGTAGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAGCAGAGA
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGlu
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                                       German Genome Project.
This close (DKF2p45170118) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: close@rzpd.de Further
information about the close and the sequencing project is available
at http://mips.gsf.de/proj/DNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codol_start=1
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EKKKAKGLGKEITLIMQTLNTLSTPBEKLAALCRKYAELLEERRNGGKKLLGKKO
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FLVTLNDIQLQMEQHNERNSKLRQENMELABRLKKLIEQVELREEHIDKVFYKHKDLQQ
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GAQAPSSPRVTEAPCYPGAPSTEASGQTGPQEPTSARA
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    sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                      /tissue type="human spinal cord"
/clone lib="451 (synonym: hlcc1). Vector pSport1; host
DH10B; sites NotI + SalI"
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// Agene="DKF22651J0118"

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Matches:
Conservative:
Mismatches:
Indels:
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Qy 117 ValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer 136 Dh 101	137 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis	17	p. 21— 4α ⊢	Db 483 CAGACTTGAATACTCTGAGTACCCCAGAGGAGAAGCTGGCTG	Db 543 GCTGAACTGCTGGGAGGAGGAATTCACAAAAAAGG 602 Oy 217 GlnSerGlnLeuValGlnGluLysAspHisleuArgGlyGluHisSerLysAlaValLeu 236	Db 603 CAGAGCCAGCTGCAAGAAGACCACCACGGCGGGGGAGACACGCCTCTG 662 Oy 237 AlakagserlysheuglusserleucyskrggluleuglukagdhisAsnkrgSerleulys 256	663 GCCGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGCACAACCGCCGCACAACCGCTAAGAGCTGCAGAACCGCACAACCGCAGAACCGCTAAAAAAGAGCTAAAAAAAA	23 GAAGAAGGTGCAGCGGGCCCGGGAGGAGGAGAAGAAGGCGCAAGGAGGA	Qy 277 PhedinValThrLeuAsnAspiledinLeuGinMetGluGinHisAsnGluArgAsnSer 296	Oy 297 LysLeuargGlnGluasnMetGluLeualaGluargLeuLysLysLeuIleGluGlnTyr 316	317	337	Qy 357 ArgGluLysAspPheLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 376	377	397	CCAGAACACACTTTCCAAAACACCGAGGTALICACCATTTAACACACACACACACACACACACACACACAC		GAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGAAAACAGTCCGGGATAAAGAA 13	Qy 457 LeuGluGlyLeuGlnValLys1leGlnArgLeuGlLLysLeuCysArgAlaLeuGlnThr 476 hp 1323 CTGGAGGGCCTGCAGGTAAATCAAGGGTGGAAAGCTGTGAGACACTGCAGACA 1382	477 GluArgAsnAspLeuAsnLysAr
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1602 AAGGCCCTGCTTGAGATGCCTGAGGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTG 1	inrgluargashasp 4 acagagggaargac 1	Qy 481 LeuAsnIySArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGly 500 [Oy 501 ProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 520	Oy 521 AlabroCysTyrProGlyAlabroSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 540		SULT 7 199336 4697 bp	ON Sequence 17 from patent N AR199536 AR199536.1 GI:20249610	KEYWORDS OORRCE OORCANISM Unknown.		diagnosing and treating atherosclerosis AL Patent: US 6355451-A 17 12-MAR-2002; S Location/Qualifiers	SOUICE	1.28e-118 Length: 2693.00 Macches: 99.81% Conservative:	Best Local Similarity: 99.81% Mismatches: 1 Query Match: 96.70% Indels: 0 DB: 6	US-10-023-523-44 (1-546) x AR199536 (1-4697) Qy	Db 3 AAAGCCCAGGACAACCGGAAGCAGGACCCAAGGCGCCCAGGGCGCCCAGCAG	63 GCGGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCCAGGCTCTCGGAAGCTCCGGAG	Oy 57 GlyalacinalaargThralacinserGlyalaLeuargaspValSerGluGluLeuSer 76		rgThrTyr 11	Db 243 GAGGALGGGGCACAGGGGGGGGGGGGGGGGGGGGGGGGG

157 ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuwet 176 	177 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysTyr 196	os croncalidariacilidad Ancoccadadadado (no control de la cadadada (no control de la cadada (no	GCTGAACTGCTGGAGGGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAA	217 GlnSerGlnLeuValGlnGluiysAspHisLeuArgGlyGluHisSerLysAlaValLeu 236	LeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 25 	101yValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis 27	77 Phecincario Control	297 LysLeuArgGlnGluAsnMetGlüLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 316	uglnglnglnLeu 33 	337 ValAspAlaLysLeuGinGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln 356 	357 ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 376 	377 LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 396 	397 PheglnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 416 	417 LysMetThrLysLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp 436	437 GluSerSerAsniysAlaLeuGluMetAlaGluGluIysThrValArgAspiysGlu 456 	457 LeuGluGlyLeuGlnValLySIleGlnArgLeuGluLySLeuCysArgAlaLeuGlnThr 476 	477 GluhrgasnaspleuasniysargValGinaspleuSerhlaGlyGlyGlnGlySerleu 496 	497 ThraspserdlyprogluargargprogludlyproglyalaginalabroserserPro 516 	
<i>&</i> 8	१	, <u>v</u>	Db	<i>≿</i> 8	S S	ර ස	8 8 8	<i>አ</i> 8	· & 점	S G	& 8	oy B	상 업	연	oy da	λο qq	& A	co do	
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REFERENCE 1 (bases 1 to 4697) AUTHORS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A. TITLE Novel low density lipoprotein binding proteins and their use in	ò	GInSerGinLeuValGinGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu
diagnosing and treating atherosclerosis JOURNAL Patent: JP 2011505983 29-NAY-2001;	qa (CAGAGCCAGCTGGTGCAAGAGGACCACCTGCGCGGTGAGCACAGCAAGGCCGTCCTG
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                                         1498 GACCTGAACAAGAGGGTGCAGGACCTGAGTGCCGGTGGCCAGGGCCCCGTCTCCGACAGC
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their
diagnosing and treating atherosclerosis
Patent: US 6605888-A 14 12-AUG-2003;
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AR374685.1 GI:40077500
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140 ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgFro 159	CACCGGAACTCGCGAAGCAGTGAAGCTCTGCTGCAGAGAAGAGCAGCCCGCCGCGCGCG		360 AspPheLeuLeuLysGlualaValGluserGlnArgMetCysGluLeuWetLysGlnGln 379	420 LysLysIlellysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSer 439 1318 AAGAGGATGGAGAAAGGACCACCATGCTTCCCGGTGGGAGAGCAGC 1377 440 AsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluLGGTGT 1378 AACAAGCTGCTTGAGAGAAAACACTCCGGGACAAGAGCTGGAAGGC 1437 460 LeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsn 479 1438 CTGCAGGTGAAAATCCAGCGGCTGGAGAAGCTGTGCCGGCACTGCAACAGCTGCAACAACAGCTGTAAAATCAGCTGGAGAAGCTGTGCCGGGCACTGCAACAACAGCTGAAAAAAGCTGTGAAAATCAGCGGCTGGAGAAGCTGTGCCGGGCACTGCAGAACAGCTGAAAAAAGCTGTGAAAAAAAA
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	RESULT 14 AR409320 LOCUS AR409320 AR409320 AR409320 DEFINITION Sequence 14 from patent US 6632923. MACCESSION AR409320 VERSION AR409320. AR40933. AR409320. AR40933. AR409320.	/organism="unknown" ORIGIN Alignment Scores: 5.6e-112 Length: 4722 Score: 2552.50 Matches: 508 Percent Similarity: 93.19\$ Mismatches: 12 Best Local Similarity: 91.04\$ Mismatches: 25 Query Match: 6 1.65\$ Indels: 3	MethysAsnGlnAspLysRasnGlyAlaAlaLysGlnSerAsnProLysSerSerPro	7 2 4 8 7 4 4 9 8 7 8 8 7 8 8 7 8 8 8 8 8 8 8 8 8 8 8

Oy 61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80 :::	Oy 81 AspileLeuSerThrTyrCysValaspAsnAsnGlnGlyGlyProGlyGlyAla 100 100 298 GACATACTGTACTGTGGGACAACAACCAGGGGGCCCCGGGTGAGGTC 35	101 GlnGlyGl 358 CAGGGTGA	121 GlyGluProGluProThrProValV	Oy 140 ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro 15	160 GlnGluLysLysLysAlaL 	180 ASNThrLeuSe	200 LeuGluGluHisA 658 CTCGAGGAGCACC	220 LeuValGlnGl 718 CTGGTGCAGGA	240	Oy 260 ValGlnArgAlaArgGluGluGluGluGluGluGlygArgLysGluValThrSerHisPheGlnVal 2	Oy 280 ThrLeuasnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerlysLeuArg 2:	Oy 300 GlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeuArg 31	Qy 320 GluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnGunleuValAspAla 3	Oy 340 LysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLys 35	Oy 360 AspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGln 37		Qy 400 ThrLeuSerIbysSerSerGluValPheThrThrPheLysGluGluMetGluLysMetThr 41
Oy 500 GlyProGluArgargPro	Qy 509 GlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaPro 528	Oy 529 SerThrGlublaSerGlyGlnThrGlyProGlnGluProThrSerAlaArgAla 546	RESULT 15 AX239571 LOCUS AX239571 AX239571 FAT 26-SEP-2001 DEFINITION Sequence 14 from Patent WO0164874.		SOURCE OTYCLOLAGUS CUNICULUS (TABDIL) ORGANISM OTYCLOLAGUS CUNICULUS (TABDIL) Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.	KEFERENCE AND AUTHORS Lees, A. M., Lees, R. S., Law, S. W. and Arjona, A. A. TITLE Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis TOWNS AND THE AUTHOR OF THE AUT	JOURNAL FACERIE: NO 12939-73-73-73-73-73-73-73-73-73-73-73-73-73-	/organism=-Orycolagus cuniculus /mol_type="unassigned DNA" /db_xref="taxon:9986" /cref="taxon:9986" /-ref="taxon:9986"	/note=uniamme process process / note=uniamme process / codon start=1 /protein_id="CAC88294.1" / db xref="G11979754" / db xref="G11979754" / db xref="G11979754"	/translation="MKNODKKNOAKOPNPKSSPGQPEAGAEGAGGRPGRPAPAREAE" /translation="MKNODKKNOAKOPNPKSSPGQPEAGAEGACOVGAEGASGAPGRPEGAPGARCAVGAEGAGATAQQARTAQQARTAQQARTAQQABGATAAVARNGEPPOTEBIRISDSVGDRDHRRPQEKKSRAYVARNGEPPERTAALAKKYARELLEBHRNSQKQMKLLQKKQS	QLVQEKDHLRGEHSKAILARSKLBSLCRELQRHNRSLKEBGYQRABEBEBKKKEVTGH POMTLANDIQLQMRENSKLIRGENNELLABELKKLIEQYELREEHIDKVFKHKDLQQ QLVDAKLQQAQEMLKRABERHQRENG LLKBAVESQRHCELMKQOSTHLKQQLALYTE KFBEPQYTLSKASEVFTIFKQENGEKOTKKIKKLEKETTWYRSRWESSNKALLEMAEEK	TLRDKELEGLQVKIQRLEKLCRALQTERNDLNKRVQDLSAGGGGYVSDSGPERRPEFA TTSKEGGVEGFGAQVENSPRATDASCCAGAPSTEASGGTGPQEPTTATA" ORIGIN	5.6e-112 2552.50 93.19%	est Local Similarity: 91.04% Mismatches: uery Match: 91.65% Indels: 6 Gaps:	SerPro 20	AGCCCG ProAla	Db 121 GGALAGCCGGAAGCAGGAGCGGAGCCCAGGGGCCGGCCGG

Oy 1 MetLysAsnGlnAsp 	121		238 81	298		14 1 4 18 14 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	OY 160 GlnGluLysLysLysl	180	200 8	DD 658 CTCGAGGAGCACCGG	718 CT	Oy 240 LysLeuGluSerLeuC 	260	Db 838 GTGCAGCGAGCCCGAC Qy 280 ThrleuAsnAspileC	Db 898 ACGCTCAACGACATTC	Oy 300 GlnGluAsnMetGluI	320	Db 1018 GAAGAGCACATCGACA 340 LysLeuGlnGlnAlaG	1078 AAGCTCCAGCAGCCCC
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GATCCGGACGAGCGATGAGGTCGGAGACCGAGACCACGGAGGCCA
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                                                                                                                              T---GCCAGCAGCCAGGCTCCCGGGAGGCCGGAGGGGGCTCAAGCC
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QLVQEKDHIRGEHSKAVLARSKLESLCRELQRHNRSIKEEGVQRAREEEEKRKEVTSH
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OLVDAKLQQAQEMLKBABBRHQRBKBFLLKBAVBSQRMCBLMKQQETHLKQQLALYTB
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KEGGVESPGAOPASSPRATDAPCCSGAPSTGTAGQTGPGEPTPATA"
                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDM Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: bento-soares@ulowa.edu; tom-casavant@ulowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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                                                                                                                  Submitted (20-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0.
Location/Qualifiers
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ycoduc="unknown (protein for MGC:77972)"
protein id="AAH60227.1"
db_xref="GI:38614271"
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                                                                                                                        Submitted (20-OCT-2003)
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                                                                                            Direct Submission
                                                            Strausberg, R.
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinamalia; L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Wolfelon, D.K., Maray, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halle, S., Carcia, A.M., Gay, L.J., Hulyk, S.W., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Kzzywinski, M.I., Schaus, M.A., Generation and mouse oDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                        1318 AAGAAGATCAAGAAGCTGGAGAAAAGAGACCACCATGTACCGTTCCCGGTGGGAGAGCAGC 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1378 AACAAGGCCCTGCTTGAGATGGCTGAGGAGAAAACACTCCGGGACAAAGAGCTGGAAGAGC 1437
                                                         GACTTTCTCCGAAGGAGGCCGTGGAGTCCCAGAGGATGTGCGAGCTGATGAAGCAACAG 1197
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Db 1417 ACACTTTCCAAAAGCAGTGAAGTGTTCACCACGTTCAAACA OV 420 LVSLVSIleLVSLVSLeuGlulySGluThrThrMetTyrAr	1477	440 ASILIYARIADELEGIATETETETETETETETETETETETETETETETETETETE	Oy 460 LeuGlnVallys1leGlnArgLeuGlüysLeuCysArgAi, [] [] [] [] [] [] [] [] [] [] [] [] []	480	Qy 500 GlyProGluArgArgPro	509	•	AX578043/C LOCUS LOCUS DEFINITION Sequence 165 from Patent W002081745.			AUTHORS CATEGRALY, TOMAN ROMENTS, DALLOW, CALLY, CONDOLLY, T., Jackson, A., Bushnell, S.E. and TITLE Genes involved in osteogenesis, and methods JOURNAL Patent: WO 2020B1745-A 165 17-0CT-2002, Aventic Pharms Q A (FP)	FEATURES Location/Qualifiers 1. 1793 Corganism="Homo sapiens" Corganism	/db_xref="taxon:9606" /noTe="Homo sapiens interleukin 14	2.09e-73 Length: 1727.00 Matches:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 62.01% Indels: 0 DB: 6	US-10-023-523-44 (1-546) x AX578043 (1-1793) Qy 205 AsnSerGlnLysGlnMetLysLeuLeuGlnLysGlnSe	Db 1791 AATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAG Ov 225 AspHisLeukrqGlyGluHisSerLysAlaValleuAlaAr	 1731 GACCACC
340 GCGGAAGCCGAAGGTTCCACAAGCCAGGCTCCTGGGAAGACCGAGGGGCTCGAGGT 396	61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80 :::	81 ASPITELEUSETThrTyrCysValASpAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100 	GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn	517 CAGGGTGAGCCCACTGAGGCGGAAGACACGGAAGATCCCGAACCTATGCAGGAAT 576 121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAsp 139 577 GRGGAGCCTGAACCAGGCATTCCAGTGCAAAGGAAGAAGAACACACTCTAAAGGGAGAG 636	ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro	GINGINLYSLYSLYSAIALYSCIYLeuGIYLYSCIUII=ThrLeuLeuMetGINThrLeu 	180 ASDTHALEUSETTHAFAGIUGIULIYSLEUAlaalaleuCysLysLysTyrAlaGluLeu 199 	200 LeuglugluhisargasnSerglnLysglnMetLysLeuLeuglnLystysglnSergln 219 	220 LeuvalGlnGluLysAspHisLeuArgGlyGluHisSerLysAlavalLeuAlaArgSer 239 	240 LysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGly 259	260 ValGinargalaargGluGluGluGluLysArgLysGluValThrSerHisPheGlnVal 279 	280 ThrleuasnaspliedInleuGlinmetGluGlihisasnGluargasnSerLysLeuarg 299 	300 GlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeuArg 319 	320 GlugluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAla 339 	340 LysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLys 359 	360 ASPPheLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGln 379 :::		ThrLeuSerLygSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThr 419
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SerGinLeuValGinGluLys 224
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                   ArgserArgTrpGluserser 439
                                                        ArgAspLysGluLeuGluGly 459
                                                                                              AlaLeuGlnThrGluArgAsn 479
                                                                                                                                   31nGlySerLeuThrAspSer 499
AGGAGATGGAAAAGATGACA 1476
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EUKARYOCTA, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Manmala; Etheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1793) AUTHORS ANDTUS, J.L. Jr., Pippin, J., Joseph, A., Xu, C., Blumenthal, D., Tamayo, A., Claypool, K., McCourt, D., Srikiatchatochorn, A. and Ford, R.J. TITLE Identification of a cDNA for a human high-molecular-weight B-cell growth factor JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (13), 6330-6334 (1993) BUBMED 83217675 REFERENCE 2 (bases 1 to 1793) AUTHORS Anbrus, J.L.T. TITLE Submitted (03-MAY-1993) Julian L. Ambrus, Jr., Department of Medicine, Washington University School of Medicine, St. Louis, MO 63110, USA COWMENT On May 25, 1995 this sequence version replaced gi:347605. COMMENT On May 25, 1995 this sequence version replaced gi:347605. FEATURES I. Location/Qualifiers Source Lext: Homo sapiens CDNA to mRNA. Mol type="mRNA" //mol type="mRNA" //mol type="	Alignment Scores: 1.46e-71	Qy 205 AsnSerGlnLysGlnMetLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys 224 Db 1791 AATTCACAGAAGCTCCTACAGAAAAGCAGAGCTGGTGCAAGAAAG 1732 Qy 225 AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu 244 Db 1731 GACCACTGGGGGGGGGCAGCAGCAGCAGCCCGCAGCAAGCTTGAGAGCCTA 1673 Qy 245 CysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArg 264 Db 1672 TGCCGTGAGCTGACGCACACCTCCTCAAGGAAGATGCAGGGGCCCGG 1611 Db 1672 TGCCGTGAGCTGACGCACACCTCCTCAAGGAAGAAGGTGTGCAGGGGCCCGG 1613	Oy 265 GluGluGluLuysArglysGluValThrSerHisPheGlnValThrLeuAsnAspile 284	305 LeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeuArgGluGluHislleAsp	Db 1432 AAAGICITCAAACGACCIACAACGAGCIGGAIGCCAAGCICCAAGCICCAGCAGCICCAGCAGGCC 1373 Qy 345 GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgHisGluLysAspPheLeuLeuLys 364 1372 CAGGAGATGCTAAAGGAGCAGAAGAGCGCACCAGCGGGAGAAGGATTTTCTCCTGAAA 1313 Qy 365 GluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlnGluThrHisLeuLys 384 Db 1312 GAGGCAGTAGAGTCCCAGAGGATGTGTGAGACCAGCAGCAGAGACCCACCTGAAG 1253
CysargGluLeuGlnargHisAsnargSerLeuLysGluGluGlyValGlnArgAlaArg 26 TGCCGTGAGCCGCACCGCTCCCTCAAGGAAGAGGTGTGCAGCGGGCCGG 16 GluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAsplle 28 GluGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAsplle 28 GluGluGluGluGluHisAsnGluValThrSerHisPheGlnValThrLeuAsnAsplle 28 GluGluGluGluGluHisAsnGluValThrSerHisPheGlnGluGluHisIll	385 385 1251 405 1191 425	1131 445 1071 465 1011	Db 951 GTACHGAGGCCGGGCCCCCCCCTCACTGACTGGCCCTGAGAGGAGG 892 Qy 505 ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr 524 Db 891 CCAGAGGGCCTGGGGGCTCCCCCAGCTCCCCCAGAGGCTCCAGAGGCTCTGCTAC 832 Qy 525 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla 544	b 831 C Y 545 A D 771 A	RESULT 19 HUMHWBGGF/c LOCUS LOCUS LOCUS LOCUS DEFINITION Human high molecular weight B cell growth factor mRNA sequence. DEFINITION Human high molecular weight B cell growth factor mRNA sequence. DEFINITION L15344 L15344.1 GI:832913 KENWORDS B-cell growth factor; interleukin 14. SOURCE Homo sapiens ORGANISM Homo sapiens

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Mus musculus clone RP23-239013, WORKING DRAFT SEQUENCE, 5 unordered
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GlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSer 404
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                      SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLys
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Mus musculus (house mouse)
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Signature, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cooke, P., Carum, B., DeArellano, K., Diaz, J.S., Dodge, S., Docoley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Grand Pierre, N., Hafez, M., Hafez, M., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kalls, C., Landers, T., Levine, R., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Micol, R., Mabbitt, R., MacLean, C., Noron, J., Peterson, K., Phunkhang, P., Peters, N., Nells, J., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Peters, N., Spencer, S., Schauer, S
.uopnam, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo.A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Birren B. V. L. 181547)
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Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project name: 120929
Center project name: 120920
Center project name: 120920
Center clone name: 120920
Center clone name: 120920
Center project name: 120920
Consensus quality: 180713 bases at least Q40
Consensus quality: 180705 bases at least Q20
Consensus quality: 180590 bases at least Q20
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Insert size: 181147; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 7.6 in Q20 bases; sum-of-contigs
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/organism="Mus musculus"	q	111281 TGAAAAATGTTCAACATGCTTAATCAGGGAAATGCAAATCAAAACAACCTGAGAT 111340
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	q	112361 TGCCCCAGTACAGGGGAACGCCAGGGCCAAAAAGGGGGGGG

113557	Db 113617 CTGACTGTGCAGAGGCTGGAGGG Qy 509 GLyAlaGlnAlaProSerSerPr Db 113677 GGGGCTCAGCCATCCATCTCTC Qy 529 SerThrGluAlaSerGlyGlnTP Db 113737 ATCACAGAAACAGCAGGCCAAAGCAAACCAAAAC	RESULT 21 AX878120 LOCUS LOCUS DEFINITION Sequence 13025 from Pater ACCESSION AX878120 VERSION AX878120 VERSION AX878120 CURCE Homo sapiens OURCE Homo sapiens ENKARYOCUS ENKARYOCUS FUKARYOCUS MAMMALIA; EUtheria; Prima REFERENCE TOTAL	Clahi, S., Suga Primers for s Patent: BP 10 Research Asso Research Asso (Applementation of the search Asso (Applementation of the search Asso	CDS 521638 //note="unnamed /note="unnamed /codon start=1 / /codon start=1 /brovein id="CAI / /db_xref="cl1:40" / /translation="NMT/LESENGOAREB /www.techwolkersengoarem // / / / / / / / / / / / / / / / / /	Scores:	1.66e- 1286.0 1286.0 11arity: 53.99% nilarity: 46.18% 46.18%	Qy 28 GluGlyAlaGlnGluArgPros Db 70 GAGCAGGGGGAAGAGCG
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ARTDPEDGODGBECNRANKEKTLGKEVLLLMOALNTLSTPEEKLAALC

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AREBERREATAAFOITLDEICAGLEGHDIHNAKLRGEN ELGEKL

BHIDNYRRKELQOGLVDAKLGOTYGLIKEADBEKHQREREFILKEAT

ENVOKKOLSLYMDKEBEFGTTWAKSNELFTFRQENEKMTKKIKKL

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Db 988 CAACTGATAAAAGAAGCTGATGAAAAACA Qy 366 AlaValGluSerGlnArgMetCysGluLe	Oy 426 GluLysGluThrThrMetTyzArgSerAr	486 GIN	Cy 5.23 STYFFTCGLIYALAFIC 5.28 RESULT 23 AK002071 LOCUS DEFINITION Homo sapiens CDNA FLJ11209 fis, AK012071 VERSION AK002071. GI:7023730 KEYWORDS Oligo capping; fis (full insert 5.000 AK02071. GI:7023730 KEYWORDS ONGO sapiens (human) ORGANISM Homo sapiens (human) BUKARYOCKS ORGANISM Homo sapiens (human) MAMMMalia; Eutheria; Primates; C	AUTHORS Isogai, T., Ota, T., Hayashl, K., Nishikawa, T., Nagai, K., Sugano, Wagatsuma, M., Hosolri, T., Kaku, Sugawara, M., Takahashi, M., Chik Ono, Y., Takiguchi, S., Watenabe, Ishii, S., Kawai, Y., Saito, K., Y Nakamura, Y., Nagahari, K., Masuh TITLE NEDO human cDNA sequencing proj AUTHORS Isogai, T. and Otsuki, T. TILLE Submission Clark Direct Submission JOURNAL Direct Submission TILLE Submitted (16 FFB-2000) Takao I Genomics Laboratory; 1522-3 Yar (E-mall:genomics@hri.co.jp, Tel COMMENT NEDO human cDNA sequencing proj International Trade and Industi sequencing: Research Associatic construction, 5'- & 3'-end one
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o Isogai, Helix Research Institute, fana, Kisarazu, Chiba 292-0812, Japan lel:81-438-52-3976, Fax:81-438-52-3986) coject supported by Ministry of Japan; cDNA full insert ion for Biotechnology; cDNA library to pass sequencing and clone selection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., Sugiyama, T., Otsuki, T., Suzuki, Y., ano, S., Shiratori, A., Sudo, H., Caku, Y., Kodaira, H., Kondo, H., Chiba, Y., Ishida, S., Murakawa, K., abe, S., Kimura, K., Murakami, K., ... Yamamoto, J., Wakamarsu, A., asuho, Y., Ninomiya, K. and Iwayanagi, T. project
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ATCAGAGAGAGAGAGTTTTTATTAAAAGAA 1047
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ESKTIIWRTKWENNINKALLQWAEEKTVRDKEYKALQIKLERLEKLCRALQTERNELNE
KVEVLKEQYSIKAA, TKAANRDLATPVWQPCTALDSHKELNITSSKRALGAHLEABPKSQ
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Helix Research Institute (supported by Japan Key Technology Ceretc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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clone lib="PLACE1"
note="cloning vector: pME18SFL3"
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Mismatches:
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note="unnamed protein product"
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                                                                                                                                                                                                   'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="PLACE1007946"
                                                                                            Location/Qualifiers
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                                                                   121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro
                                                                                                                                     141 AsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln
                                                                                                                                                                                                                                                                                                                                                                   221 ValGluGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVal
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                               338 GCCAGGCCCAGTGAGCAGCCTGAGAATGCAGAATCACCTGACAAC-----GAGGAT
                                                                                                                                                                       449 CCCACTGTCAAA-----GAGCCCGTCAGCAATAAGGAGCAAAAA----TTG
                                                                                                                                                                                                        GluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsn
                                                                                                                                                                                                                                       491 GAAAAGAAATCCTAAAAGGATTAGGCAAAGAAGCCAACCTGCTAATGCAAAATCTGAAC
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                                                                                                  389 GGGGACTGTGAGGAAACAACTGAAGGGGCTGGAAGAGAACCCGTTGCTTCTGGAGAGCCA
                                                                                                                                                                                                                                                                                                           551 AAGTIGCAAACACCGGAAGAAAGITTTGATTTTTTATTCAAGAAGTATGCTGAATTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlu
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                                                                                                                                                                                                                                                                                                             Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp451B326) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                        HSM807779 4625 bp mRNA linear PRI 30-AUG-2003
Homo sapiens mRNA; cDNA DKFZp451B226 (from clone DKFZp451B226)
BX647633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GAGGCAAGTGTGCACCCCGATATCTCTGAAGAGCTGAATCGACAGCTGGAA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLySProGluGlyAlaGlnAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom. Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 4625)

Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Miemann,S.

The German Human cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERWANY
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Indels:
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1276.00
61.42%
45.86%
45.82%
                                                                                                                                          Homo sapiens (human)
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JOURNAL
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/note="similar to 77K muscle-derived protein (Gallus gallus)" /codon start=2 /product="hypothetical protein" /protein id="CAD91140.1"	/ LATA STATE OF THE TO	LLOKKQVQIQKEKDQLQGEHSRAILARSKLESLCRELQRHNKTLKEEALQRAREEEEK RKELTISHFQSTLDIQGQIBQQSERNMKLCQENTELAEKLKSIIDQYELREEHLDKIF KHRELQQKLVAKLEQAQEMKREAERPHKREKEYLINQAAGMENGOETULQA	LOMILESCHEEFOSTITKSNEVFATFKOEMDKTTKKKKKLEKOTATWKARFENONKAL LDMILESKALRAKEYECFWKTIGRLENLCRALQEENNELHKKI RDAEISEKDDOSOHNS DEEPESNVSVOEDDAEEVNSVQTAVKNITHHEESTPHOSKETQPEIGSSOE SARAY KTERODEI I EGENGER DE HEESTERSKE SKAL		polyA_signal 45984603 /gene="DKFZp451G083" polyA_site 4620		Scores: 1.15e-51 Length: 1276.00 Matches: 61.42% Conservative: All Similarity. 45 R6% Mismatches	1: 45.82%	-10-023-523-44 (1-546) x HSM803295 (1-4640)	OY 3 ASNGINASPLYSLYSASNGLYALablaLySGINSerAsnProLySSerSerProGlyGln 22	Oy 23 ProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40 :::	uGlyAlaGlnAla	212GATTCTCCAGCCCCAGCCACCAGAGAA	Oy 61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80 	Qy 81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyBroGlyGluAspGlyAla 100 296 GACATCATTAACACTTAIGGGTCTGCCAGCAGAAGAGAGAAAAGAGGCTCT 349		121	401 GGGGACTGTGAGGAACAACTGAAGAGGCTGGAAGAGAACCCGTTGCTTGTGGAGGCCA	Oy 141 AsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln 160	161 GlutystystystatysGlyLeuGlyLysGlutleThrLeubeuMetGlnThrLeubsn	DD 503 GAAAAGAAAATCCTAAAAGGATTAGGCAAAGAAGACCAACCTGCTAATGCAAATTCGAAC 562	Oy 181 ThrieuserThrProGludluLygLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeu 200	
1391 GTGATGAAAATCGGGAGGTAGAAACCTCTGCCGTGCTTTACAAGAAGAAAAGAA 1450 Qy	ProGluhrgArgProGluGly	Qy 507 507 Db 1571 AATAGTGTCCAAACCGCGTGAAAAATCTGGCCACAGCCTTCATGATAATTCATCATCATCATGATAATTCATCATCATCATCATCATCATCATCATCATCATC	207	1631 GAGTCAACCCGCACCAGCAGCAAAGAAACCCAACCGGAAATAGGCAGTTCTCAGGAGAGT	OY 508ProdlyAlaGlnAlaProSerSerProArgvalThrGlu 520	Qy 521 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 540	541 ProThrSerAla 544	T 25 3295	LOCUS HSM803295 4640 bp mRNA linear PRI 13-MAY-2003 DEFINITION Home sapiens mRNA; cDNA DKFZp451G083 (from clone DKFZp451G083). ACRESTON AL81988	VERSION AL831988.1 GI:21732527 KEYWORDS SOURCE Homo saniens (human)	Homo sapiens Eukaryota, Me Mammalia, Eut	<pre>CE 1 (bases 1 to 4640) RS Wambutt,R., Heubner,D., Mewes, Fobo,G., Han,M. and Wiemann.S.</pre>	TITLE Direct Submission JOURNAL Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764	COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by ACOWA (Berlin/Germany) within the chall sequenced by ACOWA (Berlin/Germany) within the chall sequenced by ACOWA (Berlin/Germany) within the	consortium of the German Genome Project. This clone (DKPZp451G083) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059	BEILLH-CHAILOTTENDUIG, GEMMANY; EMAIL: CLONEGEIDG. GE FUTTHET information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.	rce 1.	/mol_type="mRNA" /db_xref="RZPD"DKFZp451G083" /db_xref="maxon-9606"		/clone_lib="451 (synonym: hlcc1). Vector pSport1; host /dm: sites Nor! + Sal!"	/ dev stage="adult" gene 1. 1646 / gene="DKRZp451G083"	CDS /32158 /32158 /9ene="DKFZp451G083"	

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Homo sapiens
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                                                        682
                                                                                  221 ValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys 240
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563 AAGTIGCAAACACCGGAAGAAAAGTITGATTITITATICAAGAAGTAIGCTGAAITGCTG 622
                             201 GlugluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu 220
                                                                                                              261 GlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr 280
                                                                                                                                                                                                                                                         LeuAsnAspileGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGin 300
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AB085905 2869 bp mRNA linear PRI 25-SEP-2003 Homo sapiens hMDP77 mRNA for muscle-derived protein 77, complete
                                                         1703 GCTGACGCCGCTCTCAAAGAGCCAGAGCAACCCCCTCTGATCCCTTCACGGGATTCAGAG 1762
                                                                                                                                                                           1763 AGTÓCÓCTGCCTÓCCTAACTÓCTCAGGCTGAAGCGCAAGGAGGCAGTGATGCTGAACCT 1822
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KFDFLFKKYAELLDEHRTEOKKLKLLOKKOVOIOKEKDOLOGEHSRAILARSKLESLC
RELORHNKTLKEBALORAREEBEKRKEITSHFOSTITDIOGOIEQOSERNMKLCOENT
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I HTHERSTHYPOSKETOPEIGSSGESADAALKKEBEOPELI PSROBSERPLEPELTPOGAEAE
GGSDAEPPSKASNSPAGIGAETTOGEGLPVGAQADQASKYBBAEASGQAPQAFTGASLO
KWEADVPAPACAAEEHVAAMVPACEPSRQPPRAAAEELPVGASAGPQPRNVADTNLEG
   -----ArgvalThrGlu 520
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LLNGAAEWKLGAKVLKEGETVLGAQLTLYSGRFEEFGSTLTKSNEVFATPKQEMDKTT
KKOKKLEKDTATWKARPENCNKALLDMI EEKALRAKEYECFVWKI GRLENI CRALGES
                                                                                                                  521 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 540
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PEKEASVHPDISEELNRQLEDIINTYGSAASTAGKEGSARASEQPENAESPDNEDGDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Uyeda.A., Fujimori,K. and Taguchi,T.
Direct Submission
Submitted (29-MAY-2002) Atsuko Uyeda, AIST, Div. for Human Life
Tech, 1 -8-31, Midorigaoka, Ikeda, Osaka 563-8577, Japan
(E-mail:uyeda atsukocka@aist.go.jp, Tel:81-727-51-9524,
Pax:81-727-51-9628)
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Molecular cloning of human homologue for MDP77
Unpublished
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/protein_id="BAC92688.1"
/db_xref="G1:35210318"
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Conservative:
Mismatches:
Indels:
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508 ----ProGlyAlaGlnAlaProSerSerPro---
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/db_xref="taxon:9606"
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	Oy 361 PheLeuLeuLysGlualaValGluSerGlnargMetCysGluLeuMetLysGlnGlnGlu 380	Qy 381 ThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr 400	1225 ACAGTCC	Oy 401 LeuSerLysSerSerGluValPheThrThrPheLysGluGluMetGluLysMetThrLys 420	1285 CTAACTAAAAGCAACGAGGTGTTTGCCACGTTCAAACAGGAAATGGACAAAACTAAG	OY 421 LYELIELYSLEUGILLYSGLUTHTTERMETTYTATGGERACTITTSGLUSETSETSEN 440	441 LysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeu	1405 AAAGCTCTGTTGGACATGATTGAAGAGAAGCACTGAGAGCTAAAGAATATGAGTGTTT		1465 GTGATGAAAATCGGGAGGCTAGAGAACCTCTGCCGTGCTTTACAAGAAGAGAAAACGAA	Qy 481 LendsniysArgYalGlinAspleuSerAlaGlyGlyGlyGluGlySerLenbrAspSerGly 500		1585 TCCGATGAAGGCCAGAGGCCAACGTCTCTGTGGATCAAGAGATTGACGCAGAGGAGGTT	ζογ 507 507	1645 ANTAGIGICCAAACCGCCGIGAAAAAICIGGCCACAGCCIICAIGAIAAIICAICAICCA	507	1705 GAGICAACCCCGCACCAGICCAAAGAAACCCGAAAIAGGCAGIICICAGGAGGI	OY 508Prodiyaladinalarioserserio	Qy 521 AlaproCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 540	1825 AGTCCCTGCCTC	Oy 541 ProThrSerAla 544 Db 1885 CCTCCAAGCC 1896	_	HSM805276 HSM805276 4631 bp mRNA linear PRI 17-JUN-2003 DEFINITION Home sapiens mRNA; cDNA DKFZp451F022 (from clone DKFZp451F022);	ACCESSION AL834248. VERSION AL834248.2 GI:30268572	SM Homo sapiens (human smither sapiens for the sapiens for the sapiens for the sapiens for the same sapiens for the sapiens	Mammalia; Butheria; Primates; Catarrhin; Hominidae; 1 (hases 1 to 4631)	Kam Fob	JOURNAL Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY COMMENT On Abr 30, 2003 this sequence version replaced qi:21739792.	Clone 1
	SerSerProGlyGln 2	CCAGGTGAC 225		aGlnAla	306	euSerArgGlnLeuGlu 80	GAATCGACAGCTGGAA 357		SAGGGAAGGGCTCT 411 NTVrValAlaArqAsn 120		coSerLysGlyAspPro 140	rfectrordeagagica 522			BUMECGINITATECASN 180	reTyralaGluLeuLeu 200					euLysGluGluGlyVal 260		erHisPheGlnValThr 280 	SnSerLysLeuArgGln 300	b = ==	AGTATGAGCTCAGAGAG 1044		lsGlnArgGluLysAsp 360	ACAAACGAGAAAGGAA 1164
3-523-44 (1-546) x AB085905 (1-2869)	3 AsnGlnAspLysLysAsnGlyAla	175 AATCACTCTGAACAGCTCTCAGCGGAACGACAGTCAACACCT	23 ProGluhlaGlyProGluGlyAlaGluGluArgProSerGlnAli 226 AGTTCATTACCAGTCACAATGGCCTGAAAGAAGAAAAAGAAGAAGAAGAAGAAGAAAGA		274GATTCTCCAACCCAGTCCAACCACCAGAAA	61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGl	307GAGGCAGTGTGCACCCCGATATCTCTGAAGAGCTG	81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGlyAspGlyAla	358 GACAICAITAACACITAIGGGTCIGCIGCCAGCACAGCA 101 GlnGlvGluProAlaGluProGluAspAlaG	412 GCCAGGGCCAGTGAGCAGCCTGAGAATGACCTGACAACGAGGAT	121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro	463 dedeacterdadeanacaacteaneaectedaaeaaacceerí	141 AsnThrGluGlu11eArgGlnSerAspGluValGlyAspArgAspHisArgArgProGln		161 GIULYSIYSLYSALALYSGIYLEUGIYLYSGIULLEINTLEULEUNGTGIIINTLEKASN 565 GAAAAGAAAATCCTAAAAGATTAGGCAAAAGAAAGGCAACCTGCTAATGCAAAAAC			201 GluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu		221 ValGlnGluLyshspHisheuArgGlyGluHisSerLysAlaValLeuAlaA; 745 CAAAAAAAAGGACAAGTTACAAGGTGAACAACAAGGAAAGGTTACCCTCCTCC	241 LeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVal	805 TTGGAGAGTCTGTGCCGGGAGCTGCAGAGACACAACAAGACTCTC	261 GlnargalaargGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr	281 LeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGli	0 -	985 GAGAACACAGAGCTTGCAGAAAAGCTGAAAAGCATCGATCG	321 GluHisTleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys	-	1105 CTTGAGCAGGCCCAAGAATGATGAAGGAAGCGGAGGAGCGACGACACA
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                                                                                          286 GACATCATTAACACTTAT-----GGTCTGCTGCCAGCACAGAGAAAGAGGCTCT
                                                                                                                                                    101 GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 GAAAAGAAAATCCTAAAAGGATTAGGCAAAGAAGCCAACCTGCTAATGCAAAATCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr
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                                                                                                                                                                                                                                                                                391 GGGGACTGTGAGGAAACAACTGAAGAGGCTGGAAGAGAACCCGTTGCTTCTGGAGAGCCA
                                                                                                                                                                                                                                                                                                                                                                    ------GAGCCCGTCAGCAATAAGGAGCAAAAA----TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 AAGTIGCAAACACCGGAAGAAAGTITGAITTITITATICAAGAAGTAIGCIGAAIIGCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ValGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 GAGAACACAGAGCTTGCAGAAAAGCTGAAAAGCATCATCGATCAGTATGAGCTCAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                             GlulyslyslysalalysglyleuglylysglulleThrleuleuMetGlnThrleuAsn
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                                                                                                                                                                                           340 cccacccacacaccaccicasaarccacacaccacac--
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Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGGWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ451F022) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOKLEKKIIKGLGKEANLLMONLNKLOTPEEKFDFLFKKYAELLDEHFTEQKKLKLLU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PESNVSVDOEIDABEVNSVOTAVKNIATAFMIIHPESTFHOSKETOPEIGSSOBSAD
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DH10B; sites Not1 + SalI"
1. 4631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="DKFZp451F022"
note="similar to muscle-derived protein MDP77 variant
(Mus musculus), differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AGTICATCATTACCCAGICACAAIGGCCIGGAGAAGGAAGAIGGCCAG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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45.86%
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Best Local Similarity:
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DB:
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, K., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Vieler Submission JUENT Submission JUENT Submission JUENT CALLE Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA RESERBUCE BITTEN, B., Wusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Gook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galgan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macden, C., MacJor, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Methews, C., Nicoll, R., Norbh, C., Norman, C., O'Connor, T., O'Donnell, P., O'Weil, D., Oliver, J., Peterson, R., Roman, J., Roy, A., Schauer, S., Scanan, S., Severy, P., Smith, C., Spencer, B., Stange, S., Travers, M., Taskers, M., Taskers, M., Tesfaye, S., Travers, M., Travers, M., Travers, M., Taskers, M., Tesfaye, S., Travers, M., Travers, M., Taskers, M., Taskers	TITLE Direct Submission JOURNAL Submitted (14-ANG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2002 this sequence version replaced gi:20531889. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1998) All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1998) All repeats ware identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1998) All repeats ware identified using RepeatMasker.html	**Consists of 13 contigs. Gaps between the contigs ** are represented as runs of N. The order of the pieces ** is believed to be correct as given, however the sizes ** of the gaps between them are based on estimates that have ** provided by the submittor. ** This sequence will be replaced ** by the finished sequence as soon as it is available and ** the accession number will be preserved. ** 28688 28787; gap of 100 bp ** 28788 30488; contig of 28687 bp in length ** 30589 110109; contig of 79521 bp in length ** 110210 113705; gap of 100 bp ** 110310 113705; gap of 100 bp ** 113807 113806; gap of 100 bp ** 113807 120823; contig of 7017 bp in length ** 113807 120823; contig of 7017 bp in length ** 120924 133081; contig of 12158 bp in length
	508ProGlyAlaGli 1693 GCTGACGCGCTCTCAA. 521 AlaProCysTyrProGly 1753 AGTCCCTGCCTCCCT. 541 ProThrSerAla 544 1813 CCTCCAAGGCC 1824 5010537/c ACL10537 FINITION Mus musculus clone F prees. ACL10537 ACCTCCAAGGCC 1824 ACC	TITLE Unpublished REFERENCE 1 to 242048) REFERENCE 2 (bases 1 to 242048) AUTHORS Birren, B. Litton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Colangelo, W., Colangelo, W., Collins, S., Collymore, A., Cock, A., Choepely Y., Colangelo, M., Collins, S., Collymore, A., Cock, A., Choepely Y., Colangelo, W., Callymore, A., Cardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gooke, P., Horton, L., Hulme, W., Iliev, I., Jorand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKernan, R., Maldrim, J., Meneus, L., Mihova, T., Morman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rosetti, M., Ribeck, M., Riley, R., Riese, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Seman, S., Schupback,

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87844 AAAGCATATCTCATGATGATGGTAGAGGACATCAAGAAGGACTTTAATAACTCACTTAAA
                                                            96 GlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThr
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                                                                                    100 bp
of 13682 bp in length
                                                                                                                         100 bp
of 21687 bp in length
                                                                                                                                                             100 bp
of 28189 bp in length
100 bp
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8 21997: gap of 100 bp
8 239952: contig of 28555 bp in length
2 24062: gap of 100 bp
3 242048: contig of 1996 bp in length.
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288
          bp
9685 bp in length
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Matches:
Conservative:
Mismatches:
Indels:
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11398. .239952
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note="assembly_fragment"
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mol_type="genomic DNA"
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                                                                                                         contig gap of
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gap of
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vector_side:right"
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61322. .183008
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note="assembly
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Best Local Similarity:
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183009
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Pred. No.:
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DB:
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/db_xref="taxon:9606" /clone="DKKZp451H216" /tissue_type="human skeletal muscle" /clone_lib="451 (synonym: hlcc1). Vector pSport1; host DH10B; sites Nor1 + SalI" /dev_stage="adult" /de	0y 3 AenGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGln 22 123 AATCATCTAACAGGGAACGGCAACACACACACACACACAC	Db 513 GHANAGARAATCCTAARGGCAAAGGCCAACCTGCTAATGCAAATCTGAAC 572 Qy 181 ThrLeuSerThrProGluGluLysLeuAlaalaLeuCysLysLysTyAlaGluLeuLeu 200
Oy 349 sGlualaGluargHisGlnArgGluLysAspPheLeuLeuLysGlualaValGlu 368 B6710 AGAAGCTGATGAAAACATCAGAGAGAGAGAGAGATTTATTATAAAGAAGAACAGAA 86651 OY 369 SerGlnArgMetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGluLeuala 388	449 GluLysThrVallargAspLysGluLeuGluGlyLeuGlnValLysIleGlnArgleuGlu 4	Fobo, G., Han, M. and Wiemann, S. The German Human cDNA Consortium Direct Submission and Wiemann, S. The German Human cDNA Consortium Direct Submission Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85; Neuherberg, GERMANN Neuherberg, GERMANN Neuherberg, GERMANN Neuherberg, GERMANN Research Center The German Genome Analysis, German Car Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Blomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the (sequencing consortium of the German Genome Project. This clo (DKFZp451H216) is available at the RZPD in Berlin. Please or (DKFZp451H216) is available at the RZPD in Berlin. Please or (DKFZp451H216) is available at the RZPD in Berlin. Please or (DKFZp451H216) is available at the RZPD in Berlin. Hernich-Heine-University, Duesseldorf/Germany) within the close or the RZPD in Berlin. Please or (DKFZp451H216) is available at the RZPD in Berlin. Hernich-Heine-University, Duesseldorf/Germany) within the close or the RZPD in Berlin. Hernich-Heine-University, Duesseldorf/Germany) within the close or the RZPD in Berlin. Hernich-Heine-University, Duesseldorf/Germany) within the close or the RZPD in Berlin. Hernich-Heine-University, Duesseldorf/Germany) within the close or the German Genome Project. This close or the RZPD in Berlin. Hernich-Herni

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813 281 301 301 321 933	341 1053 361 1113 381	401 1233 1292 1353 1353 441 1413 1413 1533 501	1593 507 1653 508 1713 521 1773 1833
8 6 8 6 8	6 6 6 6 6 6	8 8 8 8 8 8 8 8 8 8 8	8 6 8 6 8 6 8 6 8

RESULT 30 D89999

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D89999 4704 bp mRNA linear VRT 26-APR-2000 Gallus gallus MDP77 mRNA for muscle derived protein, complete cds. D89999
                                                                                                                                                                     1 (sites)
Uyeda,A., Fukui,I., Fujimori,K., Kiyosue,K., Nishimune,H., Kasai,M.
and Taguchi,T.
MDP7: A nowl neurite-outgrowth-promoting protein predominantly
expressed in chick muscles
Biochem. Biophys. Res. Commun. 269 (2), 564-569 (2000)
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-DEC-1996) Atsuko Uyeda, Osaka National Research
Institute, Department of Organic Materials; 1-8-31, Midorigaoka,
Ikeda, Osaka 563-8677, Japan (E-mail:au-uyeda@onri.go.jp,
Tel:*81-727-51-9524, Fax:+81-727-51-9628)
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with molecular mass 77 k"
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Matches:
Conservative:
Mismatches:
Indels:
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1. .4704
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                                                                                  Gallus gallus (chicken)
Gallus gallus
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2 (bases 1 to 4704)
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Db 1270 ACTCTCTACTCTGAGAGATTTCAGAAAACATTGACCAAAAGCAATGAAGTG 1329 Qy 408 PheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLys 427 1330 TTTGCTACCTCCAAACAGGAGAGAGAAAATGACAAGAAAATGAAAAGAAAAG Qy 428 GluThrThrMetTyrArgSerArgTrGAGAAAATGAAAATGAAAATGAAAAG 1390 GATACTCCTACAACAGGAGATGGAGAAAATGAAAATGAAAATGAAAAG Db 1390 GATACTCTACATGGAAATCCAGATTGAGAAAATGAAAATGAAATGAAAT 148 GluLysLeuCysArgAlaLeuGluLauGluGlyLeuGluValLysIleGlnArgLeu 467 148 GluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysLrGGAGAGTA 1509 Qy 488 GluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGlnAsp 487 1510 GAAACCTTTGCCGAGCTCTGCAGGAATGACAGAATGAAAATCCAGAGGCTA 1509 Qy 488 LeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyPrOGlu 502 Qy 488 LeuSerAlaGlyGlnGlySerLeuThrAspSerGlyPrOGlu 502 Qy 488 LeuSerAlaGlyGlnGlySerLeuThrAspSerGlyProGlu 502 Cy 63 ArgArgProGluGly-PrOGlyAlaGlnAlaProSerSerProArgValThrGluAlaPr 522 Qy 7630 ArgArgProGluGly-ProGlyAlaGlnAlaProSerSerProArgValThrGluAlaPr 522 Db 1530 ACAAACCCTTCCCGAGCAAGCAACCAATGAGCTATGTGCTGACAAACAGAACAGA 1689	522 1690 1729 N EZ	5533.1 GI:13026200 1999147897-A/1. identified ilassified. (bases 1 to 4723) (bases 1 to 4723) cent: UP 1999147897-A I 0 ENCY OF IND SCIENCE & TEC Unidentified UP 1999147897-A/1 02-UN-1999	PP 13-NG PR 13-NG PI TAKAH PI TAKAH PC COYKI PC AGING PC STREN PC C TOPOI PH KGY FT SOUTC	Source 1.4723 / Organism="unidentified" / Organism="unidentified" / Mol_type="genomic DNA" / Ab_xref="taxon:32644" / Abignment Scores: 1.78e-50 Length: 4723 / Score: 1251.00 Matches: 276
265 CAAAGCAAACCAGTCCCCGTCTACAGGCCCTTTCCCCCACAAACCAAAC	556 AAGGAGCCCAGTGCCAGGAACAAAAGCTGGAGAAAATCCTGAAAGGA 609 168 LeuGlyLyGGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGlu 187 [228 ArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGlu 247 :::		1150 ATGAAGGAAGCAGCATCAGAAGGAATATCTCCTGAATCAGCCGCA 1209 168 GluserGlnArgMetCysGluLeuMetLysGlnGlnCluThrHisLeuLysGlnGlnLeu 387 1210 GAATGGAAGCTACAGGCCAAAATGTTAAAGGAACAGTCCTGCAGGCACAGCAGCCCTGCAGGCCAAAATGTTAAAGGAACAGTCCTGCAGGCACACAGAGTC 1269 188 AlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluVal 407

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TGGAGCAGTCTCAGGAAATG 1149

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hrHisLeuLysGlnGlnLeu 387
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GAGCATTACTGGACATGATT 1449
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TGTACAGAAAATAAAACAA 1569
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GTGCTGCTGACAAGAACATG 1689
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                                                                                                                                                                                                                                      190 AlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln
                                                                                                                                                                                                                 MetLysleuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGly
                                                                                                                                                                                                                                                                                      GluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGln
                                                                                                                                                                                                                                                                                                                         GAGCACAACAGGCCGTCCTTGCTCGAAGCAAACTCGAGAGTCTGTGTCGGGAGCTACAG
                                                                                                                                                                                                                                                                                                                                                                250 ArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluLys
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                                  529 AAAGAGCCTGTCAGCAATAAAGAGCAAAAAGCTGGAAAAGAAAATCTTAAAAGGATTAGGT
                                                                                                     589 AAAGAAGCTAACTTGCTCATGCAAAACCTGAACAAGCTGCAAGCACCTGAAGAAAGCTT
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QEGSLHPEKGAHDVAEELSRQLEDIISTYGSAASPEEGDASETKEQPPNTEAPDNEDV
DYEETTEEIDREPTAPEEBPAAKEPVSNKEQKLIEKKIIKGGKRANLIANDNINKLQAP
EEKLDFLFKKYTTELIDEHRTEGKKLILLILKQQAQTQREKDQLGSEHNRAVLARSKLES
LCRELQRHNKTLKESTILGRAREEBEKKEITFGHFQTTLTDIOTQIEGGSERNMKLCQB
NTELAEKLKSIIDQYELREEHLDKIFKHRELQQKLVDAKLEEAQELMQEAEERHRREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTILHHEEFTPDQPTERQLAVMGPQSGBDVTHQHPETARLNHEGLPADGSSPRPVGA
QAVAEGVCEATPAPTASCTPAEAELQSQGLPAENTPGPKPHKPEANTSGQAFLSPAQG
SLSVVEAKYDISPSPESEGDSAVVPGCESREQPPPEVTDIPVGPSTGLPREFDACLNG
VD"
                                                                                                                                                                                                                                 note="muscle-specific; similar to Gallus gallus
uscle-derived protein encoded by GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYLLNQAAEWKLQAKVIKEQETVIQAQITILYŠGRFEBEOSTITKSNEVFATFKQENDK
TTKKMKKLEKDTATWKARFENCNKALLDMIBEXALRAKEYECFVMKIQRLENLCRALQ
BERKELYKKIREAKMSEKEDQVQRTSEEEPEPSVSENEEVDAEEANSFQKAVENLATA
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rotein_id="AAL33909.1"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                      Mtap7"
                                                                                  map="between Cni-rs2 and sex="female"
musculus"
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             mol_type="mRNA"
strain="C57BL/6J"
db_xref="taxon:10090"
chromosome="10"
                                                                                                                                                                                                                                                                                                                       protein_id="AAL33909...
db_xref="GI:17026374"
                                                                                                       /dev_stage="heart"
/dev_stage="adult"
/____2435
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organism="Mus
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Best Local Similarity: 49.07% Mismatches: 132 Query Match: 44.15% Indels: 63 DB: 8 US-10-023-523-44 (1-546) x AF422245 (1-4394)	n t	69ArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCys 87	108 GluAspalaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluProThrPro 127	ArgGlnSer::::GAAGAAACC	SUPSITION OF THE STANDARD OF T		230 GluHisSerLysAlaValLeualaArgSerLysLeuGluSerLeuCysArgGluLeuGln 249	270 ArglysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGnMetGlu 289 889 AGGAAGAGTCACTTICCACTTICCACACACACACACACACACACACAC	AAAAGCATCATTGACCAGTACGAGCTCAGAGAGGAGCATCTGGACAAAATATTCAA Lysaspleuglnglndlnleuvalaspalalysleuglnglnalaglnglumetle :::::: ::
	RESULT 33 AF422245 LOCUS LOCUS DEFINITION Mus musculus muscle-derived protein MDP77 variant 2 (Mdp77) mRNA, ACCESSION AF422245 DD DD	AF422245.1 GI:17026375 Mus musculus (house mouse) 1 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases i to 4394) Benson, K.F. and Chada, K.		Medical Genetics, University of Mashington, Seattle, WA 98195, USA	/organism="Mus musculus" /mol type="mRNA" /mol type="mRNA" /strain="CS7BL/GJ" /db_xref="taxon:10090" /chromosome="10" /monesome="10"	/ Lissue type="heart" / dev_stage="adult" / dev_stage="adult" 1. 4394	D89999" Codon_start=1 /codon_start=1 /product==muscle-derived protein MDP77 variant 2" /protein_id="Ad133910.1" /db_xref=="G1:17026376" /db_xref=="G1:	DERLOPLARY TELLOPERK ELONGARAL TO CRANCE SERVANCE AND CONTROL DE CRELOPERTANTIA ELONGARA ELONGAR ELONGARA ELONGAR ELONGA	ORIGIN

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 131 Row: i Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Stavanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Ihorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                      Direct Submission
Submitted (01-OCT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGly
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                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: agapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agancy, Vancouver, BC, Canada
info@bcgsc.bc.ca
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zoeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuti, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Mordey, K.C., Hange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Mallahy, S.J., Boask, S.A., McEwan, P.J.,
Norley, K.C., Malle, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergen, E.J., Lulyk, S.W.,
Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                             1309 ACTITCAAGCAGGAAATGGATAAGACAACTAAGAAAATGAAGAAGCTGGAGAAGGACCC 1368
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                        AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
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          GlnLeuGluAspIleLeuSerThrTyrCysVal --- AspAsnAsnGlnGlyGlyProGly
                          <u> AACAGAAATTTGGTGAGCTCAGTATTCTGTACACAGGAGAAAAGAGAAAATTCCTGGA</u>
                                                     117 ValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer
                                                                                                             137 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis
                                                                                                                                               ArgargProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMet
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   DNA
                                                                                               Unknown.
Unclassified.
3 1 (bases 1 to 1191)
5. Rubinfeld, B., Polakis, P.G., Lingenfelt Modulators of BRCA1 activity
AL Patent: US 5948643-A 5 07-SFP-1999;
Location/Qualifiers
1191
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 1191 bp
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Sequence 5 from patent
AR072731
AR072731.1 GI:9999495
                   5 from patent
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1048.50
69.01%
55.69%
37.65%
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Oy 236 uAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLy 256	nrSerHi 27 ::: CTGCACA 72 rgAsnSe 29 ::	296 rLysLeuArgGlnGluAsnMetGluLeuAlaGluAzgLeuLysLysLeuIleGluGlnTy 31	316 FGLUARGGARGGARGARGARGARGARGARGARGARGARGARGAR	OY 356 DAYGGLULYSASPHELEULEULYSGLUAAVIGUSEKGLUAARGAAGUTGATGA 968 OY 356 DAYGGLULYSASPHELEULEULYSGLUALAVAGLUGUSEKGLUAYGMETCYSGLULEUME 376	Oy 376 tLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGl 396	Oy 396 uPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGl 416	Oy 416 uLysMetThrLysLysIleLysLysLeuGluLysGlu 428	RESTLT 36 BD006992 LOCUS LOCUS DEFINITION Modulators of BRCAl activity. ACCESSION BD066992	VERSION BD006992.1 GI:18635363 KEYWORDS JP 2001502893-A/3. SOURCE unidentified ORGANISM unidentified	unclassified. REFERENCE 1 (bases 1 to 1191) AUTHORS Lubinfeld, B., Porakisu, P., Rigenferuta, C. and Buon, T.T. TITLE Modulators of BRCA1 activity	JOURNAL Patent: JP 2001502893-A 3 06-MAR-2001; ONIX PHARMACEUTICALS INC COMMENT OS Unidentified PN .TP 200150289-a / 3	E		CC Strandedness: Double, CC Topology: Linear; FH Key FT CDS 34 1191	

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LEKDTATWKARPENCNKALLDMIEEKALRAKEYECFYWKIGKLENLCRALQEERNELH
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LKSIIDQYELRESHLDKIFKHRELQQKLVDAKLEQAQEMMKEAEBRHKREKEKYLLAQA
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Matches:
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/gene="DKFZp451A175"
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Homo sapiens mRNA; cDNA DKFZp451A175 (from clone DKFZp451A175).
AL832332
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                                                                                                                                                                                                                                                                                                                         356
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                                                         908
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkf2-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf(Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKF2Q+51A175) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4154)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="human skeletal muscle"
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DH10B; sites NotI + SalI"
                                                                                                                                                                                  1029 GAAACAGCAAGAAGTACAACTAAAAAAGAGCAGCTTTCTCTTTATATGGATAAGTTTGAAGA
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                                                                                                                           cerecarecearacrecarecacacacacacrearararasacreareararara
                                                                                                                                                            nArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMe
                                                                                                                                                                                                                                                                                                      uPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="DKFZp451A175"
/note="similar to chicken 77K muscle-derived protein"
                                                                                                                                                                                                                                  tLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                   416 ulysMetThrLysLysIleLysLysLeuGluLysGlu 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="DKFZp451A175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="DKFZp451A175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
1. .4154
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JOURNAL
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300 326 360 346 420 366 480 386

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426 9 446

Db 62 CTTCTGGAGGAGGAGTGTTCAGAAGGAATGAAGATCCTGCAGAAGAAGCAAGC		Oy 379 GlnGluThrHisleuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGln 398	A AXX	Ki,T., Wakamatsu,A., Satc Y., Otsuka,K., Nagai,K., Kawa,T., Otsuka,M., Nagai SEP-2003; Lechnology (JP)
Oy 447 AlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArg 466 Db 721 ATTGAAGAAACACTGAGAGCTAAAGAATATGAGTGTTTGTGATGAAAATGGGGAG 780 Qy 467 LeuGluLysLeuCysArgalaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGln 486	961 GTGAAAATCTGGCCACAGCCTTCATGATAATTCATCAGAGTCAACCCCGCACAGG 508	823 bp DN 601 601 Chordata, Craniat Primates; Catarrh prostate cancer a 48 07-DEC-2000;	Coation/Qualifiers 1. 823 1. 823 1. 923 1. 103 1.	71.64% Mismacches: 33.23% Indels: 6

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------GluArgLeuLysLysLe 312
:
GGCAAGTCTTTGCCAACTGAGCTAGGCTGTTAT 1001
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                                                                                                                                                                                                                                                                                                         rctrcccattracaagagaarcagggacacaga 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATCCTGGGGTCAGAGATTTGAGTGTGTTTAT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A------AAGCTGACCTTCCAGAGACTTGG 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STCCATCATATCAGATTGAGATGGGGGGCTGGG 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHISTLASPLYSVALPheLysHisLysAsple 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | :::
rccataaaccargrectaacaaggrergaere 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCTACCCTGAGAAGGGAGCGCCTGACAAGCCG 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAGGCTCAGGCCCCAGGGTTGGGGGGGG 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTCATAGCCGGGTTATATGGGAGAGTCTG 1589
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1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 1979 | 197
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s, clone SMINT2001:114.
                                                                                                                                                                                                                                                                                                                                                                                                                            sGluGluGlyValGln----- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ArgAlaArgGl 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AsnGluArgAsnSerLysLeuAr 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rSerHisPheGlnValThrLeuAsnAspIleGl 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
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ro Found			
KEYWORDS SOIRCE	ANUSOSOS.1 G1:Z1:Debb1 Oligo Capping; fis (full insert sequence). Homo capriens (human)	qq	366 CAGGGTGAGCCGGCTGAACCCGAAGATCTGCCCTCTTAGGTTCATAGGCCGAAGTGATGA 425
ORGANISM	Homo sapiens	ò	115 rTyrvalAlaArgAsnGlyGluProGluProThrProValValAsn 130
REFERENCE	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.</pre>	qq	ACCTA
AUTHORS	Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., His Tanai H., Watanabe S., Ishida S., Ono V., Hotuta F.	à	131GlyGluLysGluProSerLysGlyAspProAsnThrGl 143
	Sugiyama, T., Titie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, R., Nishikawa, T.	QQ	486 TCCTCTGGGAACAAAGCTGCTTGTTTGGTTTGAGGGGGAGTTGGTTTGGTTTATCCCTC 545
	Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wadatsuma,M., Takahashi-Fhiji, A. Ochima A. Sucriyama A.	δχ	143 uGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGlu 161
	Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.	QQ	546 AGCGCTGAGACATAGAGGCTTCCTGGGCCACTACAGTGAGACACAGGAACTTCAAGAATCTG 605
TITLE	_	, VQ	162
REFERENCE	2 (bases	Ωp	606 AATACCCCCCTTTTCTCTCCCCGCCAAGGCAAAAAGGACTTAGTACTACC 656
TITLE		λŏ	175 uMetGlnThrLeuAsnThrLeuSerThrProGl 186
JOURNA	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan	· 6	::::: TGTGGAGAAGAAGAGGACTACCAGGCCCTGCTGCTTTACAGCCCTCCCCA
COMMENT	(E-mail:genomicsenfi.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	ò	186 uGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHis 203
	Research Association for Biotechnology (RAB); cDNA library	qq	:
	Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - & 3' -end one pass sequencing: RAB,	ò	204ArgAsn 205
	hki, and biorechnology center, National institute of rechnology and Evaluation; clone selection for full insert sequencing: HRI and	qq	::: 777 CCCCATCCAAAAAAIGGAGTTATTTTCCCTTATTTCAGCAAGTCCAGTTGATTTTACCT 836
FEATURES		ò	206SerGlnLysGlnMetLysLe 212
source		q ₀	
	/mol_type="mRNA" /db_xref="taxon:9606"	ò	212 uLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArqGlyGluHisSe 232
(/clone="SMINT2001114" /tissue_type="small intestine"	qa	4
	/clone_lib="SMINT2" /note="cloning vector: pME18SFL3"	ζō	232 rLysAlaValbeuAlaArgSerLysLeuGluSerLeuCysArg 246
OKIGIN		. · • • • • • • • • • • • • • • • • • • •	948 GTCTAGTCTTTGCCTAGATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTTAT 1001
Alignment Pred. No.:	Scores: 2.12e-34 Length:	Ã	
Score: Percent S	Matches: Conservative: Migmotoboo	q ₀	
Query Match: DB:	32.14.00 9.44.88	Š	247 uLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGln 261
US-10-023	6939 (1-2194)	qq	1062 AGTGAGGCTTCCAGCCCATAGGTGATCAATCCTGGGGTCAGAGATTTGAGTGTGTTTAT 1121
ò	1 MetLysAsnGlnAspLysLysAsnGlyAlaAlaAlaLysGlnSerAsnProLysSerSerPro 20	کم بر د	262Argalaargg 265
đ	6. ATGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCCA 125	3 8	717C0171700C077C017170T170T1707C077C077T1707T170
ð í	GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40	S	<pre>205 UGIUGIUGIUANASAIGAYSGIUVAIIINISGIHIBPIGGIIVAIIINILGUABRASDILGGI 285 1182 ACTGGGAGAGAAACGACGTGAGGTTGGAAAGCTGACCTTCCAGAGACTTGG 1232</pre>
QQ ·	GGACAACCGGAAGCAGGACCCGAGGAGCCCAGGAGCGGCCCAGGCGGC	ò	285 nLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuAr 299
& &	41 ValGluAlaGluGlyProGlySerSerGlnAlaProArglySProGluGlyAlaGlnAla 60 	qq	
δλ	61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80	8	gGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLe
ОЪ	246 AGAACGGCTCAGTCTTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCAACTGGAA 305	a à	
ර් ස්	81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100	장 <u>쉽</u>	1353 ACTGCTCCCACCATCTTTGTTGCAGCATATCGACAAAGTCTTCAAACACAAGGACCT 1409
3 &	300 sakanakisakekakanakisissakanakanaksessesekekeksesaksenissaka 355 101 GinglyGiuProAlaGiuProGiuAspAlaGiu-LysSerArgTh 115	Š	332 uGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGl 352
	· 1970年, 1980年,	1 m	

us-10-023-523-44.rge

rcent Sim st Local ery Match : -10-023-5	56 ATGAAGAACCAAGACAAAAGAACGAGGCIGCCAAACAAICCAAAICCAAAAAACCACA 11 21 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40 116 GGACAACCGGAAGCAGGAGGAGGAGGCCCAGGAGGCGGCCCAGGCGGGCCCAGGCGGC		296 101 356 121	1,	AL671759 141790 bp DNA linear Mouse DNA sequence from clone RP23-151A15 on chromos sequence. AL671759 AL671759.10 GI:22138725 HTG. MNS musculus (house mouse) Mns musculus		Center code: SC Web site: http://www.sanger.ac.uk Contact: htmquery@sanger.ac.uk Contact: htmquery@sanger.ac.uk Contact: htmquery@sanger.ac.uk
Db 1410 ACAACAGCAGCTGGTGGATGCCAAGGTCCAGCAGGAGATGCTAAAGGAGGCAGA 1469 Qy 352 uGluArgHisGluArgAspPhe	361 1590 361	1650 GGIGCTIGIGGCTAAAAACCAAACATAGCCCCTGGGGGCTTCTGACAGGATCTGGGGTTC 1 362LeuleulysGluAlaValGluSerGlnArgMetCysGluLeuMetL 3 1710 TGTCTTGGAAATACCTCCTGAAAGAGCACATAGAGTCCCAGAGGATGTGAGCTGATGA 1 377 ysGlnGlnGluThrHisLeulysGlnGlnLeuAlaLeulyyThrGluLysPheGluGluP 3	Db	SULT 41 060509 CUS CUS FINITION CESSION	KEYWORDS JP 2001518793-A/869. SOURCE Zea mays ORGANISM Zea mays ORGANISM Zea proper Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD Clade; Panicoideae, Andropogoneae, Zea. REFERENCE 1 (bases 1 to 529) AUTHORS Jacobs, K., McCoy, J. M., Lavallie, E.K., Racie, L.A., Merberg, D.,	Tracey, M., Spaliding, V. and Aggerino, M. U. TITLE Secreted expressed sequence tags (sESTs) JOURNAL Patent: UP 2001518793-A 869 16-OCT-2001; COMMENT PN UP 2001518793-A/869 PD 16-OCT-2001 PF 10-APR-1999 UP 1998843070 PR 10-APR-1997 US 08/837312 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC PI MAURICE TREACH SPAULDING, MICHAEL J AGOSTINO PC PI MICHAEL MIC	Pouble; CC Topology: Linear; FEATURES Source Source Accation/Qualifiers 1. 529 Accamise="Rea mays" Amol.type="qenomic DNA" Alignment Scores: Alignment Scores: C.18e-30 Antiches: 154 Score:

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given	OY 322 -HislleAsplvsValPhelvsHisLvsAspleuGlnGlnGlnLeuValAspAlalvsLe 341
in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the properties of the state of	61628 CCAGCGAGGAGATCTTCAAACATAAGGACCTGCAGCAGCTAGTGGACGCCAAGCT 341 uGlnGlnAlaGlnGluMetLeulysGluAlaGluGluArgHisGlnArgGluLysAspPh 61628 CCAGCAGGAGAGATGCTGAAGGAGGAGGCAGCGGCCCAGGAGAGAGA
	Qy 361 eLeu
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ent Scores: 2.96e-26	DD 0114.9 1G1CCAGACAGCAGCAGCAGCAGCACCAGGGCCGGGCCCAGGGCCTGGGGCCTGGGGCCGGGGCCGGGGGCGGGGGGGG
ore: 771.00 Matches: Conservative: 24.49\$ Conservative: 8t Local Similarity: 23.54\$ Mismatches: ery Match: 27.68\$ Indels:	Db 61389 AGGTCAGACATACCTCAGGGGCTTCTGACAGGTTCTGGGGTCCTGTCTTGGAAATAGCT 61330 Qy 363 - LeuLysGlualaValGluargNetCysGluLeuMetLysGlnGlnGluThrHi 382
UB: TIS-10-027-523-44 (1-546) x b1.671759 (1-141790)	Db 61329 CCTGAAGGAAGCGGTGGAGTCCCAGAGGATGTGCGAGCTGATGAAGCAGCAGGAGAGACCCA 61270
SAlaValLeuAlaArgSerL	Qy 382 sLeuLysGlnGlnLeu387
249 GlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluGluGluGluGluGluGluGluGluGluG	Oy 387 387 Db 61210 GCCCATCTGCAGGGCAGTGGAACAGGACTGTCATAGCCTGGCTTTGTGCCAGCTGGCCT 61151
268 GlulysArglygGluValThrSerHisPheGluValThrLeuAsnAsplleGluLeuGln 287	Qy 387 387 Db 61150 GTTGGTGGGCCAAGTCTTTTATTTATGTGTGTTTTGTTT
62228 GAGAAGCGCAAAGAAGTGACTICACACTICCAGGIGACACTGAAIGACATTCAGCTGCAG 6216 288 MetGludlihisAsnGluargAsnSerLysLeuargGluGluasnMetGlubeualaGlu 307 	Oy 387 387 Db 61090 CTGTGTAGCCCTGGCTGTCCTGAAACTTGCTTTGTACACCAGGCTGGCCTGGAACACAGA 61031
Db 62168 ATGGRACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAG 62109 Qy 308 ArgleuLysLysLysLeulleGluGlnTyrGluLeuArgGluGlu321	387
62108 AGCTCAAGAAGTTGATCGAGCAATACGAGCTTCGTGAGGAGGTGAGCTGCAGGCGATTG	Db 61030 GATTIGCCTGTCTTAGCCTCCTAAGTAATGGGATTAAATGTAGGCATGTGCCCATCATGCC 60971 Qy 387
CY 321 321 Db 62048 AGGCCAGCAGCTTGGGAGTCTGTAGTGACTGCCAGGGCCTGGGGCCCGCAACTGCAGGCCT 61989	60970 AGGCATTTTGTTGTTCTTTGAAGAACAGGTCTCTGAGTTTAGGTGTGGGCTACAACTAAC 6
Qy 321 321	QY 387 387 Db 60910 CCACAACTTACCTTGTACACCAGGTCTCTGTGAGGCTTTGAACTTGTGAACTGGAGGTCCTTGA 60851
61988 GGGCTTGCTTCCTTCAAGAGATGTATCCTGTAGATAAGGAGCTGAAATAAAT	387
Db 61928 AAGAGATTACACACACACACACACGTGTTATCCCTGGTGTCTGAACCGGACATCTGT 61869	60850 CTCCCAGATGCATGAGGCGTTAGCTACCAGGTCTAGCTCAATTCTGTCTACTTTTATTTT
ογ 321 321	Qy 387 3
Db 61868 AGAGTATTCAGTGCTAGAGTGGAGGCGTGTCCTCGTCCCAGCTCCGCATCAGACCTGTAC 61809	387
Qy 321 321	60730 CIGGIACCTITAGAGGITAGAATAGTTCCAGACAGTIGTGGTCTCCATGTAGGTGCTGGG
Db 61808 ATCAGACCATTCCCAAGGACATGGGTCGGCAGGAGACCGGATGAAGTGCCTTGTT 61749	387

consensus

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note="tRNA-Asp-GAC repeat: matches 1. .75 of
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note="match: GSS:
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to secret primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
This sequence is the entire insert of clone RP4-622L5 This sequence was finished as follows unless otherwise noted: all regions were circumble-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality == 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RR4-622L5 is from the library and relations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1957 of consensus"
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/clone="RP4-62115"
/clone lib="RPCT-4"
1645. .1810
/note="TIGGER1 repeat: m
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'db_xref="taxon:9606"
'chromosome="1"
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.1546 of consensus" consensus .790 of consensus" .263 of consensus" .728 of consensus" .2095 of note="11 copies 2 mer tt 100% conserved" note="32 copies 2 mer tt 70% conserved" '27 copies 2 mer tt 88% conserved" .85718 /note="16 copies 2 mer tc 87% conserved" Em: L29729 Em: L29763" match: GSS: Em:AQ376964" 38923. 39446 Note="LIMEc repeat: matches 1546. 39761. 39882 /note="LIMEc repeat: matches 1429. 'note="MER21B repeat: matches 718. 18985. .49173 note="MER21B repeat: matches 77. 19285. .49651 note="MER44C repeat: matches 1. Em:AQ091614" .75020) Em:L29744" omplement(66041. .66267) note="match: GSS: Em:AQ803288" note="match: GSS: Em:AQ040362" note="match: GSS: Em:AQ761532" 2462. .53177 note="match: GSS: Em:AQ040082" 4716. .54865 note="match: GSS: Em:AQ680771" note="match: GSS: Em:AQ514287" 28263. .28691 /note="match: GSS: Em:AQ317905" complement(29964. .30447) :omplement(29964. .30447) 'note="match: GSS: Em:AQ732256" omplement(43254. .43726) note="match: GSS: Em:AQ146371" 3527. .74249 note="match: GSS: Em:AQ892680" Em: AQ441232" note="match: GSS: Em:AQ812740" Em: AZ310334" Em: AQ536603" note="match: STS: Em:G20585" complement(66030. .66267) note="match: GSS: Em:B69239" note="match: STS: Em:G15744" Em:G09447" Em: G28385" 87612) Em:G06968" Em: G26511" 10465. .30718 'note="match: STS: Em:G58909 evidence=not_experimental 1427. .71448 .62382) 87579 74951 /note="match: GSS: E. note="no.".

296	Db 70274 AACAAATATGTTCGGGTGGTAGTGAAAATAGTTGTGTCATTTTACAAGTAAACAGACTT 70333	Qy 565	Db 70334 AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAAT 70393	95 56 56 VO	Db 70394 TCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA 70453	oy 56 56 56	Db 70454 AAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTGGCTGGGCCTGAAAAATCCCA 70513	57	70514 ACCAGIGGIATAATCGICTICTITCICACTCIACCCCICATCCICTCCIGGLGGGGG	CY 58 AGINALAARGINITALAGATALAGATATAGASPVALAGATATAGASTAGATAGATAGATAGATAGATAGATAGATA	Qy 78 nLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAs 98	Oy 98 pGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAl 118	/U094 IGGGGGACACAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AAGGATGGGGAGCCTCAACCAACTCCAGTAGTCAATGGAGAAGGAACCCTCCAAGGG	Oy 138 yAspProAsnThrGluGluIllArgGlnSerAspGluValGlyAspArgAspHsArgAr 158	Qy 158 gProGlnGluLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuWetGlnTh 178	aG1	70932	CAGAGCAGCAAGTCACTCTA	٠.	Db 71033 GTCTAATCAAGGCAG 71048	RESULT 44 AR409342		VERSION KEYWORDS	SOURCE UNKNOWN. ORGANISM UNKNOWN.		
misc_feature 9185692386 /note="match: GSS: Em:B85187"	repeat_region 911192122.			_teature	eature		at_region	eature	misc_feature 113362113450	match: GSS: Em:AQ806873" ORIGIN .	. }		US-10-023-523-44 (1-546) x HSDJ622L5 (1-115756)	1 MetLysAsnGlnAspLysLysBasnGlyAlaalaLysGlnSerAsnProLysSerSerPro 20	21 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla	69734 GGACAACCGGAAGCAGGACCCGAGGGAGCCCCAGGCCAGCCCAGGCGGGCGCGCTGGGA 99799 41 ValGlualaGluGlyProGlySerSerGlnAlaProArglySProGlu 56		TCTGCGTTGCCAGGGGGGGGGAGGAGGTGGGGGTCGGCCTTGGGACTTAC 6	929	69914 AGGCCGAGGCTGTTCCGGGAGGAGGAGTGTAGAATGAGAGGACAGTGCTGGGGGG 69973		69974 CGCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCTCTAAGCACAGAACAG 70033	AGTICTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGT	95	CAGGAAATCCAGGTCCCGGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGT	56	

58 AlaGinAlaArgThrAlaGinSerGlyAlaLeuArgAspValSerGluGluLeuSerArg	Db 3000 CT-CAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGGCGC 3058 Qy 78 GlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGlu 97	oGluproThrProValValAsnGlyGluLysGluProSerLys 	138 GlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArg	158 ArgProGlnGlubysLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuWerGl 	INTERNATION DE LA TRANSPORTINGE	Qy 198 GlubeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeu 213	214 GlnLysGlnSerGln 219	DD 3458 TAGICTAAICAAAGCCAG 3475 RESULT 45	AX239608 LOCUS AX239608 DEFINITION Sequence 51 from Patent WO0164874.	AX239608.1 G	SOURCE HOMO Sapiens (numan) ORGANISM Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Euthoria, Drimetae, Catarrhini, Haminidae, Homo	na, A.A. and their use	and treating atherosclerosis JOURNAL Patent: WO 0164874-A 51 07-5EP-2001; Roston Heart Roundation Inc (113)	FEATURES Location/Qualifiers source /22255 /organism="Homo sapiens"	/mol_type="unassigned_DNA" /db_xref="taxon:9606"	Scores:	1.19e-25 Length: 2 740.50 Matches: 1 40.56% Conservative: 7		10-023-523-44 (1-546) x AX239608 (1-22255)	Oy 1 MetLysAsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro 20	
/organism="unknown" /mol_type="genomic DNA"	res: 1.19e-25 740.50 arity: 40.56% milarity: 39.06% 6	US-10-023-523-44 (1-546) X AK409342 (1-22255) QY	21 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40	Qy 41 ValgluAlaGluGlyProGlySerSerGlnAlaProArglySProGlu 56	Oy 5656 YO	280	Db 2340 AGGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGC 2399 Qy 56	Db 2400 CGCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTCTAAGCACAGGAACAG 2459	Oy 56 56 Db 2460 AGTICIGGAGAAGCTCCGACGGATTAAGTCAGGTGGCAAACGAGGCACCCAGT 2519	95	Db 2520 CAGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGT 2579 Qy 56	Db 2580 TIGAGGCATTICTAGAATGATCTGAATGGCAAGAAATGGGTTTTGTGGGGGGGG	2640 TGGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATC	Cy 56 56 Db 2700 TAACAAATATGTTCGGGTGGTAGTGAAATAGTTGTGTCATTTTACAAGTAAACAGACT 2759	56	2760 TAAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAA	Db 2820 TTCTGACAGGAACTAGATTGCTGAATGATACTCCTTCTTCTCTGATTTCCATAAA 2879	29	Db 2880 AAAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTTGGCTGGGCCTGAAAAATCCC 2939	c	Db 2940 AACCAGTGGTATAATCGTCTTCTCACTCTACCCCTCATCCTCTCTGCTGGTGGGGG 2999

Oy 198 GluLeuLeuGluG] Db 3401 AGTCTGTCTGCCAGGATTCAAAGGA OY 214 GlnLysLySGlnSerGln 219		Eukaryota; Merazoa; G Mammalia; Eutheria; F Matalia; Eutheria; S Strausberg, R.L., Fein Alasner, R.D., Collin Alasner, R.P., Collin Alachenko, L., Marusi Stapleton, M., Soares, Scheetz, T.E., Brownst Carninci, P., Prange, C Abramson, R.D., Mullah McKernan, K.J., Malek, Worley, K.C., Halek, Wilalon, D.K., Mullah		AUTHORS Strausberg, R. TITLE Direct Submission JOURNAL Submitted (10-FEB-2003) Nati Gene Collection (MGC), Cance Institute, 31 Center Drive, USA REMARK NIH-MGC Project URL: http:// CONMENT Email: Gapbs-remail.nih.gov Tissue Procurement: ATC CDNA Library Preparation: Li CDNA Library Prayed by: The DNA Sequencing by: National Sequencing Center (NISC), Galthersburg, Maryland;
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1d.B.A., Grouse, L.H., Derge, J.G.,
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Y.R.W., Touchman, J.W., Green, E.D.,
Y.C., Grimwood, J., Schmutz, J., Myers, R.M.,
inski, M.I., Skalska, U., Smailus, D.E.,
Jones, S.J., and Marra, M.A.
ArgGlnSerAspGluValGlyAspArgAspHisArg 157
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AAGGGTTTGGGTGAGGGGGGGCTCTTTGTGA 3358
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he I.M.A.G.E. Consortium (LLNL)
I Institutes of Health Intramural
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Satou, Y. and Satch, N.
Direct Submission
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(E-mail:satoh@assidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095,
                                                                                                                                                                                                                     linear INV 30-NOV-2002 full insert sequence.
    528
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Ciona intestinalis
Eukaryota; Merazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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49 CAACCAAAGAGAGATGAAATAAATGAACAAGATTCAACTTCCGCTAAGTCCGACAATGAG 108
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  509 GlyAlaGinAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaPro
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                                                                                                                                415
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                                                                                       529 SerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAlaArgAla 546
                                                                                                                           362 AGCACAGAAGCATCAGGCCAGACTGGGCCTCAAGAGCCCACCTCCGGCCAGGGCC
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http://ghost.zool.kyoto-u.ac.jp/indexrl.html).
Location/Qualifiers
1. .2181
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Ciona intestinalis cDNA, clone:cits018c13,
AK117024
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/mol_type="mRNA"
/db_Xref="taxon:719"
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                Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 78 Row: p Column: II. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                              This clone has the following problem: The cds is short compared the longest cds in the locus.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGlnAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 ThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGlu
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Matches:
Conservative:
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Indels:
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/product=npxz9451J0118 protein"
/protein_id="AAH44555.1"
/db_xref="GI:283302156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="LocusID:200081"
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="LocusID:200081"
                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .3554
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue type="Uterus, le
clone lib="NIH MGC_71"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-3554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .3554
gene="DKFZp451J0118"
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Percent Similarity:
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Query Match:
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	Qy 484 ArgValGlnAspLeuSerAlaGly	Cy 504 ArgProGluGlyProGlyAlaGli :: 	SULT 48	EC029686 LOCUS BC029686 DEFINITION Homo sapiens, clone IMAGE ACTRESTON PC009686	2	DKGANISM THOMO SEQUENTS EUKARYOLE; MELEZOA; CHOTCH MAMMALIA; BUtheria; Primat REFERENCE I (Dases 1 to 3495) ATTWADES CTT. TO THE SECOND	TITLE Direct Submission JOURNAL Submitted (06-MAY-2002) N. Gene Collection (MGC), Can	REMARK NIH-MGC Project URL: http COMMENT Contact: MGC help desk	Tissue Procurement: ATCC CDNA Library Preparation: CDNA Library Prayed by: ONA Library Arrayed by: ONA Lower And Control of the Control of th	Sequenting Center Center code: BCN-HGSC Web site: http://www.hgsc	Gunaratne, P.H., Garcia, Yoon, V.S., Kowis, C.R., Richards, S., Gibbs, R.A.	Clone distribution: MGC C. through the I.M.A.G.E. Co. Series: IRAK Plate: 42 Rov	rce	/clone=limAcm.v9 /tissue_type="Pl /clone=lib="WIH"	CDS (1393 Actor: processed (1393 Actor: processed (1393 Actor) (1394 Actor) (13	/protein_id="AAH.ow /protein_id="AAH.or /db_xref="G1:209" /translation="RM	TEAPCYPGAPSTEASG	Alignment Scores: 5.75e-23 Pred. No.: 666.00 Score: 5imilarity: 100.00\$ Best Local Similarity: 100.00\$
104 ProblaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluPro 123	GluProThrProValValAsnGlyGluLysGluProSerLysGlyAspProAsnThrGlu	280 TCACCCATCCCA 291 144 GluileArgGinSerAspGluValGiyAspArgAspHisArgArgProGinGluLysLys 163		164 LysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSsr 183 	184 ThrProgluGluLysLeualaalaLeuCysLysTyralagluLeuLeuGluGluHis 203 :::	204 ArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysElysGlnSerGlnLeuValGlnGlu 223 :::	224 LysaspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGlaAser 243	244 LeucysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAla 263	264 ArgGluGluGluGluLysargLysGluValThrSerHisPheGlnValThrLeuAsnAsp 283	284 IleGInLeuGInWetGluGInHisasnGluargasnSerLysLeuargGlnGluasnWet 303 ::::::: ::: 682 GTTGAAGTCCAAATGAAAATGAAGTTGAAGTGAGCAACAAAATGAGGTCGGAAAATGAT 741	304 GluleuAlaGluArgLeuLysLysLeuIleGluGluTyrGluLeuArgGluGluHisIle 323 	324 AsplysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGln 343 :::	344 AlaGinGluMetLeuLysGluAlaGiuGluArgHisGlnArgGluLysAspPheLeuLeu 363	364 LysGlualaValGluSerGlnArgMetCysGluLeuWetLysGlnGluThrHisLeu 383 :::	384 LysGinGinLeualaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLys 403	404 SerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLbeLys 423 	424 LysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeu 443	LeuGlumetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLys
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AH29686.1"
09878362"
AMTKKIKILEKETTMYRSRWEŠSNKALLEMAEEKTVRDKELEGL
AMTKKIKVILOLLSAGGGGSLTDSGPERRPEGPGAQAPSSPRV
SGQTGPQEPTSARA"
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------GGGAAAACATGAAGGAAAAAAG 1305
                                                                                                                                                                                                                                                    3495 bp mRNA linear PRI 20-MAY-2002
iB:4993857, mRNA, partial cds.
                                                                    lyGlyGlnGlySerLeuThrAspSerGlyProGluArg 503
                                                                                                                                                                                                                                                                                                                                                                              data, Craniata, Vertebrata, Buteleostomi, ates; Catarrhini, Hominidae, Homo.
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Lawrence, S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institutes of Health, Mammalian.
Tancer Genomics Office, National Cancer
ve, Room 11A03, Bethesda, MD 20892-2590,
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The I.M.A.G.E. Consortium (LLNL)
or College of Medicine Human Genome
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| ATGCTCCTCTTCCAGA 1335
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993857"
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Matches:
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Query Match: 23.91% Indels: 0 DB: 9 Caps: 0 US-10-023-523-44 (1-546) x BC029686 (1-3495) 0 417 LysMetThityslyslleLysLysLeugluLysGluThrThrMetTythrgSerArgTrp (36 b) Cy 417 LysMetThityslyslleLysLysLeugluLysGluThrThrMetTythrgSerArgTrp (36 c) 60 Cy 437 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 456 c) Cy 437 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 456 c) Cy 457 LeuGluGlyLeuGluValLysTlGGluArgLeuGluLysLeuCysArgAlaLeuGluThr 476 c) Db 121 CTGGAGGCCTGCAGGTAAAAATCCAACGGCTGGAGAGCTGCGGGCACTGCAGGCACTGAGGC	SULT 49 047502 CUS CUS FINITION CESSION RSION RSION RSION RSION RSION RSION RATION RSION RATION REBREACE AUTHORS	Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., Gonzalez, M., Champe, M., Chamez, C., Dorsett, V., Farfan, D., Frise, E., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mung Munco, J., Pacleb, J., Parket, S., Phouanenavong, Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S., Phouanenavong, Submitted (19-JUL-2001) Berkeley Drosophila Genome Projec Lawrence Berkeley National Laboratory, Berkeley, CA 9472 Sequence Berkeley National Laboratory, Berkeley, CA 9472 Berkeley, CA 94720 Berkeley, CA 94720 Berkeley, CA 9420 This clone was sequenced as part of a high-throughput px.	sequence clones from Drosphila Gene Collection I (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyh tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular CDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, passe changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to

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REFERENCE
AUTHORS
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AUTHORS
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"Namin, V., Adams, C., Alder, J.,
"Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranike, D., Barber, M., Barnaed, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Draper, H., Duyan, Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
Esgen, A., Escotto, M., Edgene, C., Evans, C., A., Fall, F.T., Fan, G.,
Fernandez, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
Gunaratene, P., Haaland, W., Handerson, N., Hernandez, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-171G2, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln 475
296 Seriysi, eu Arg Gln Glu Asn Met Glu Leu Ala Glu Argi, eu Lysi, eu Ile Glu Gln 315
                               TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 335
                                                                                                                                                 ||||::: |||||||:::||||::::||||:::
TACCAAACGAGGGAGCAGCACCACGGAGAAGCTCAATGAACAGGTTCAGTTGGAGGCCCAG 585
                                                                                                                                                                                                                                                                                          586 criecaccageccaaecriecaaaaargccaegregaggcreccarggaaaageagararrg 645
                                                                                                                                                                                                                                                                                                                                                  GlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeu 375
                                                                                                                                                                                                                                                                                                                                                                                                          646 AGCAAGGAAAACCAGATTGGCCTGGAGAAACTGATGCAAGCGCAAGGTGCCATAAAGGAT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGlu 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 GluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 GlulysMetThrlysLysIlelysLysLeuGlulysGluThrThrMetTyrArgSerArg 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 TrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          886 TACGAGAAAGCTAATGCCATGGTGATCGATTTAGCCACAGAAAAAAAGAGTCTGCAGACGCAG 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                               LeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1006 CTGGAGAGACAACAGCACAAGTGCCTGCGGGAT 1041
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AC111774 GI:24818709
HTG: HTGS PHASE1; HTGS DRAFT; F
Rattus norvegicus (Norway rat)
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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, A., Jackson, J., Jacocob, L., Jiang, H., Ohnson, R., Johnson, R., Liu, W., Liu, W., Liu, W., Lordon, P., Lorgacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Lorgacre, S., Lopez, J., Liu, M., Liu, W., Lordon, R.J., Liu, X., Ma, J., Lorensuhewai, M., Martin, K., Martin, R., Perez, R., Rose, R., Rose, R., Rose, R., Rose, R., Rose, R., Rose, R., Rajas, P., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Valas, R., Valas, R., Wallson, R., W
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Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23321701.

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgso.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shocgun sequence reads. Both end sequences and whole genome shocgun sequence reads. Both end sequences and whole genome table.
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Submitted (19-FEB-2002) Human Genome Sequencing Center, Departmen
Submitted (19-FEB-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245095)
Rat Genome Sequencing Consortium.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center code: BCM
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2 (bases 1 to 245095)
Worley, K.C.
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        (see http://www.hgsc.born.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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3 6962: gap of unknown length
3 73689: contig of 63827 bp in length
3 73689: gap of unknown length
3 73689: gap of unknown length
3 73789: gap of unknown length
4 124713: gap of unknown length
14 179270: contig of 3666 bp in length
14 179270: contig of 54527 bp in length
17 179370: gap of unknown length
18 179270: contig of 54527 bp in length
17 22496: contig of 545126 bp in length
18 17 22496: contig of 45126 bp in length
19 224596: contig of 45126 bp in length
19 224596: contig of 45126 bp in length
19 228336: contig of 1229 bp in length
18 239565: gap of unknown length
18 243942: contig of 4277 bp in length
19 245095: contig of 4277 bp in length
10 2445095: contig of 1153 bp in length
10 241904: gap of unknown length
10 243045: contig of 1153 bp in length
10 241904: gap of unknown length
10 241905: contig of 1153 bp in length
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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91432. .93819
/note="wgs_contig"
116848. .118080
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39566. .240945
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24714. .126005
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Job time : 6777.85 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on:

June 8, 2004, 06:37:58; Search time 3984.89 Seconds (without alignments) 4091.647 Million cell updates/sec

US-10-023-523-44
2785
1 MKNQDKKNGAAKQSNPKSSP.....APSTBASGQTGPQEPTSARA 546 **BLOSUM62** Scoring table: Perfect score: Sequence:

Title:

Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext

55026578 Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

EST:* Database :

gb http://gb.http://gb.est1:*/gb-est4:* gb_est4:* gb_est5:* em_estfun:* em_estba:*
em_esthum:*
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mus: gss_phg:' hum: mam: dss plu: gss_pro: ea'

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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817 bp mRNA linear EST 15-MAY-2001 60271858381 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4858388 5', BG761234 BG761234.1 GI:14071887 EST. LOCUS DEFINITION ACCESSION VERSION KEYWORDS

RESULT 1 BG761234

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mus musculus
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/lab host="MUH MGC 49"
/clone lib="NTH MGC 40"
/clon
SM Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)

SINIH-MGC http://mgc.nci.nih.gov/.

Is NIH-MGC http://mgc.nci.nih.gov/.

National nasitutes of Health, Mammalian Gene Collection (MGC)

LUmpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC/CTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboration

Tissue Procurement: ATC/CTD/DTP

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

thup://image.llnl.gov

Plate: LLCM1712 row: f column: 21

High quality sequence stop: 766.
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121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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137 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 156
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QEKREEI PGREARTGPPDGQQDSECSRNKEKTLGKEVLLLMQALNTLSTPEEKLAALC
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Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical State (16-UUL-2001) Fire (18 Physical and Chemical State (18 Physical and Chemical Group, RIKEN Genomic Sciences Center (18 PREM Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (18-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212,
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EKETIIWRIKWĒDNNKALLQWABĒKTVRDKĒYKAFQIKLERLĒKLĒKLGRALQTĒRNEINĒ
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/dev_asage="11 days embryo"
29. .1603
                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
6 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2797)
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(evidence: rsCDS, ProCrest, decoder, NCBI CDS
Predictor, Longest-ORF)
                                             functional annotation of a full-length mouse cDNA
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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'strain="C57BL/6J"
                                                                         Nature 409, 685-690 (2001)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

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By Nature 420, 563-573 (2002)

Adachi J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Furuno, M., Harangaki, T., Harangaki, T., Hayashida, K., Hayatsu, M., Hirandach, T., Hayashida, K., Hayatsu, M., Hirandach, T., Kojima, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kohima, T., Miyazaki, M., Musata, M., Mushi, K., Nomura, K., Numazaki, R., Ohno, M., Ohato, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Tagawa, A., Tagawa, A., Takahashi, F., Takaku-Mahira, S., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Mahira, S., Direct Submission

AL Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genome Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi, Ru, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseascriken.go.jp, Wallintup://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Manton Baranda Baranda Genome Saranda Haranga Saranda Genome Genome Saranda Genome Genome Saranda Genome Genome Genome Saranda Genome Genome Genome Genome Genome Genome Saranda Genome Ge
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/dev_stage="10 days neonate"
64. 1638
                                                                                                                          the RIKEN Genome Exploration Research Group Phase II Team and the
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Nature 409, 685-690. (2001)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu
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High-efficiency full-length cDNA cloning
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Mus musculus (house mouse)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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AK030100 3810 bp mRNA linear HTC 18-SEP-2003
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4932441K18 product:hypothetical protein, full insert
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                                                                                                                                                                                                        ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln
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                                                            GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu
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High-efficiency full-length cDNA cloning
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AK030100.1 GI:26326082
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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EKETIIMRTKWENNNKALLOMAEEKTVRDKEYKAFQIKLERLEKLCRALQTERNELNE KVEVLKEQVSIKAADGDLVSPATQPCAVLDSFKETSRTLGWHLEARAKSVCEKSAAQ KPSSSGSPAQGIESVD" ORIGIN	No.: i nt Similar Local Simi	MACCN: 40.40% INGLES: 5	-10-023-523-44 (1-546) x AKG30100 (1-3810)	Oy 7 LysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGly 26	27 ProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGlu	Db 155 CCGCAGAAGTTTGAAATTGGCAAGAAGAAGCTAGAATTTGTGGGTTAGGAGTAAAA 214	43 AlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGln	GATATTCTTCAACATCAAGACCCCCAGTTGT	60 AlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArg		78 GlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 9	AACAGAAATTTGGTGAGCTCAGTATTCTGTACACAGGAGAAAAAGAGAAGAAATTCCTGGA	97 GludspGlyAlaGlnGlyGluProAlaGluProGludspAlaGluLysSerArgThrTyr	CGAGAAGCTCGAACAGGTCCTCTGATGGCCAGCAAGATTCAGAGTGCAGCAGG 44	Oy 117 ValAlaArgAsnGlyGluProGluProThrProValValAsnGlyGluLysGluProSer 136	Db 448 448	LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis		157 ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 1	449AACAAAGAAGAACTIIAGIIAGAAAAGAAGIIIIAGIIAGIIAGIIAGIIAGI	Db 491 CAAGGGTAAACACCTTTCAAGAGAGAGAGGGGGGTCTCTGTAAGATT 550	Qy 197 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 216	Db 551 GCTGATCTCCTGGAAGAAGCAGGAATGTTCAGAAACAAATGAAGATCTGCCAGAAGAAG 610	Oy 217 GinSerGinLeuValGinGluLygAspHisLeuArgGlyGluHisSerLygAlaValLeu 236	Db 611 CAAGCCCACATTGTGAAAGAAAGTTCACCTTCAGAACAGGAAGGCCATCTTG 670	Qy 237 AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 256	DD 671 GCAAGAAGCAAACTGGAATCTCTTTGCAGGAACTTCAGCGTCATAATAAGACCTTAAAG 730	Oy 257 GludluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis 276	1 ONGRAPHINIGHT OCHORNOGRAPHONIGHT ON	Oy 277 PheGlnValThrLeuAspAspIleGlnMeuGlnMetGluGlnHisAsnGluArgAsnSer 296	
TITLE RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer JOURNAL Genome Res. 10 (11), 1757-1771 (2000) MEDLINE 20530913 PURMED 11076861		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		JOURNAL Nature, 420, 563-573 (2002) REFERENCE 6 (bases 1 to 3110)	rudeni), nizawe, n., Animia, T., Aranawa, n., Calinini, Fukuda, S., Furuno, M., Hanagaki, T., Fara, M., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T.,	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,	λογα,δ., Λυτιπατά,, Ματευγαπα,ι., Μιγαζαλι,κ., Μιτατα,Μ., Νακαπυτα,Μ., Νίελι,Κ., Νοπυτα,Κ., Νυπαταλί,R., Ούπο,Μ., Ούδατο,Ν., Οκατακί,Υ., Saito,R., Saitoh,Η., Sakai,C., Sakai,Κ., Sakazume,Ν.,	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S.,		IIILE Direct Submission JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of	Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken	Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to	prepare mouse tissues.	.riken.go.jp/.riken.go.jp/.	FEATURES Location/Qualifiers source 13810		/strain="C57BL/6J" /db_xref="FANTOM DB:493241K18"	/db_xref="Md1:2342716" /db_xref="taxon:10090" /clone="4932441K18"	/sex="male" /tissue type="testis" //lone lib-merken fill-length enriched mouse onNa library"	TOTAL STORY	, , ,	Predictor, Longest-ORF)	/codon_start=1 /rotoin id="RaC26785 1"	/ processors / db // free = 0.000 // db // free = 0.000 // db // d	TCGLGVKADMVONSQANDILGED TRANSCAGOLERARANSKARKASFYRE TSFRENDALVEN TCGLGVKATANDALVEN TCGLGVKATAN	KKYADLILEESRANQROMKILONKQAQI YEEKYHLOSEEBAAI LAKSKLESLUKELOKH NKTLKEENMOQAREEEBRRKEATAHFOITLNEIQAGLEGHDIHNAKLRQENIELGEKL	KKLIEGYALREEHIDKVFKHKELQQQLVDAKLQQTTQLIKEADEKHQREREFLLKEAT ESRHKYEQMKQQEVQLKQQLSLYMDKFEEFQTTMAKSNELFTTFRQEMEKMTKKIKKL	

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TTCCAGATAACTCTAAATGAAATCCAAGCTCAGTTGGAACAACATGACATCCACATGCC 850
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Dr. Jim Lin, University of Icwa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                           GCACTAAGGGAAGAACATATTGATAAAGTATTCAAACACAAGGAATTGCAACAACAGCTT
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Location/Qualifiers 1. .798 /organism="Mus musculus"

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/note="Organ: Eye, Vector: pxx- Asc; Site_1: Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor , digested with NotI and then cloned directionally into pxx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Neurous System', supported by National Institute of Mental Health (NIMH)." 'organism="Mus musculus" Seq primer: pYX-5. Location/Qualifiers 1. .775 /mol_type="mRNA" /strain="C57BL/6"

CF735205 UI-M-HBO-ckc-l-18-0-UI.rl NIH_BMAP_HBO Mus musculus cDNA clone INAGE:30615737 5', mRNA sequence. 302 362 482 542 364 602 662 404 204 242 284 422 344 EST.

Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 122 224 244 264 304 324 62 363 CAGCTGCAGÁTGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAG 603 gaagcogrocacacacacacarereceasecercarcaecaccacacacaccaccacce CysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArg 265 GluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIle LeualadluargLeulysLysLeulleGluGlnTyrGluLeuargGluGluHislleAsp Lysval PhelysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAla 385 GlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSer 663 CAGCAGCTCGCCCTGTACACGGAGAGTTTGAGGAGTTCCAGAACACACTTTCCANAAGC 165 AlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThr 3 eccaagegreraeceaageagareaererererearecaeaeaeaeaeaeaeaeaeaeae 185 ProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArg 205 AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys 225 AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu 303 GAGGAGGAGGAGAAGCGCAAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATT GlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGlu 365 GlualaValGluSerGlnArgMetCysGluLeuMetLysGlnGluThrHisLeuLys 421 SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLys 775 254 1 2 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-775)US-10-023-523-44 (1-546) x CF728426 CF735205.1 GI:37631541 8.81e-72 1269.00 99.22% 98.83% Percent Similarity: Best Local Similarity: Query Match: DB: 285 305 325 405 245 VERSION KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION CF735205 RESULT a g g g g g g ð g ò g ò g ò 8 g à g Š 음 à ò ò ò ò

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/ Strain="CSTBL/6"
/ Strain="CSTBL/6"
/ db xref="caxon:10090"
/ clone="IMAGE:6817313"
/ tissue_type="whole brain"
/ tissue_type="whole brain"
/ dev stage="embryo" 13.5,14.5,16.5,17.5dpc"
/ lab host="DHIB (TI phage resistant)"
/ clone_lib="NIH BMAP_FW0"
/ note="Corgan: Brain; Vector: pYx- Asc; Site_1: EcoR I;
/ note="Corgan: Brain; Vector: px- Asc; Site_1: EcoR I;
/ site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
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Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
                                                                                               283 AspileGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGlnGluAsn 302
                                                                                                                                                                                                                         303 MetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHis 322
                                                                                                                                                                                                                                                                                                                                               323 IleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGln 342
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Dases 1 to 806)
NIH-MGC http://mgc.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                    302 GCCCGTGAGGAGGAGAGGGCGCAAAGAAGTGACTTCACACTTCCAGGTGACACTGAAT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 CTGAAGGAAGCGGTGGAGTCCCAGAGGATGTGCGAGCTGATGAAGCAGCAGGAGACCAC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 LeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 CTAAAGCAGCAGCTCGCCCTGTACACGGAGAAGTTTGAGGAGTTCCAGAACACACTTTCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 GACATTCAGCTGCAGATGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAT
                                                                                                                                                                                                                                                                                 422 Argenecraecencadecreandaderrearceaecaraceaecricerendedear
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UI-M-FW0-ccb-h-16-0-UI.rl NIH BMAP_FW0 Mus musculus cDNA clone INAGES:6817313 5', mRNA sequence.
   722 ANAAGCAGTGAAGTGTTCACCACGTTCAAACAGGAGATGGNAAAGATG 769
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/clone="IMAGE:30615737"
/tissue_type="whole eye."
/dev stage="mebry ol 2:5,13.5,14.5 dpc"
/dec lib="wintH_EMAP_HB0"
/clone_lib="wintH_EMAP_HB0"
/note="Organ: Eye: Vector: PXY- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-B06,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor , digested with Notl and then cloned
directionally into pYx-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH): "
                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Irisue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/imcousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGln 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlufysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGlu 242
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   1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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strain="C57BL/6"
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98,838
45,398
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                                                                                            Unpublished (1999)
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                         gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polya tail is AGCCAGACAC. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National program coordinator."
1996. Denatured RNA was size fractionated on a 1% agarose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeu 281
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Mismatches:
Indels:
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Matches:
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1251.50
97.39%
96.64%
44.94%
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BG827157 932 bp mRNA linear EST 22-MAY-2001
602751143F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4903690 5',
                       723 CTCCTGAAGGAAGCGGTGGAGTCCAN-AGGATGTGCGAGCTGATGAAGCAGCAGGAGACC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 316
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 932)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 GAAGAAGGTGTGCAGCGGGCCCCGGGAGGAGGAGGAAGCGCAAGGAGGTGACCTCGCAC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM1802 row: f column: 11 High quality sequence stor: 6 High quality sequence stor: 6 High quality sequence stor: 775.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
Indels:
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Matches:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                              382 HisteulysGlnGlnLeuAlaLeu 389
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                                                                                                       782 CACTA-AAGCAGCAGCTCGCCCTG 804
  BG827157.1 GI:14174744
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1250.50
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BG827157
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TITLE
JOURNAL
COMMENT
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BG827157
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TROPICALIS_SEQUENCE_ID: TGas088m24.q1kT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
CDNA was oligo dy primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with Bcorl at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site_2: NotI
Host: Escherichia coli XLI- blue.
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                                                                                                                                                                                                                                                                                /dev_stage="gastrula (stages 10.5-12 mixed)"
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/clome_lib="XGC-gastrula"
/none="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAsnGlyGluProGlu---ProThrProValValAsnGlyGluLysGluProSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysTyrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCAGCTTATTCAAGAAAAGGATCTACTTCGTAATGAGCACAGCAAGGCAATCCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 ArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 GlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArg
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2229
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TG8088m24"
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90.468
83.228
44.658
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Best Local Similarity:
Query Match:
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BX752507 BX752507.1 GI:39642575
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Silurana tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
 GAGCTGCGCGAGGAGCATATCGACAAAGTCTTCAAACACAAGGACCTACAACAAGGACTG
                                                                                                                           ValAspAlaLysLeu-GlnGlnAlaGlnGluMetLeuLysGluAlaGluArgHisGl
                                                                                                                                                                                                        nArgGluLysAspPheLeuLusGluAlaValGluSerGlnArgMetCysGluLeuMe
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                                                                                                                                                           246 GIGGATGCCAAGCTICCAGCAGGCCCAGGAGATGCTAAAGGAGGCAGAGAAGGGGGGCACCA
                                                                                                                                                                                                                                           306 GCGGGAGAAGGATTTTCTCCTGAAAGAGGCAGTAGAGTCCCAGAGGATGTGTGAGCTGAT
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                                                        GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeu
                                                                                                                                                                                                                                                                              tlysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGl
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Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
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Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: tropôsanger.ac.uk
Sanger Xenopus tropicalis BST project 2001
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Sanger Institute
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directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nerrous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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GlyGluProGluPro---ThrProValValAsnGlyGluLysGluProSerLysGlyAsp
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/mol_type="mRNA"
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AGENCOURT_8291711 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6308909
BQ714219
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapba-Tomail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: Reeden, Invitrogen Corp
CDNA Library Preparation: Reeden, Invitrogen Corp
CDNA Library Preparation: Rescence Corporation
CDNA Library Preparation: Rescence Corporation
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM19728 row: m column: 06
High quality sequence stop: 724.
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Sanger Institute
Hinkton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TGas127p15.p1kSP6
Sequencing primer: ESF from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 50n poly A+ RNA from stages 10-13
gastrulae. ECOR1-NotI cut CDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECOR1; Site 2: NotI
Host: Escherichia coli XLI- blue. AL961454 ... 945 bp mRNA linear EST 04-DEC-2003 AL961454 XGC-gastrula Silurana tropicalis cDNA clone TGas127p15 5', AL961454 159 531 591 199 LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln 219 LeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSer 239 772 AAGCTTGAGAGTCTGTGCCGGGAGCTGCAACGGCACAACCGNGTCCCTGAAGGAAGAAGAAG Silurana tropicalis (western clawed frog) Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; 1 (bases 1 to 945)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Nov 27, 2002 this sequence version replaced gi:25785049. 472 CCTGGAACAGAGGAACGAGCGAGTGATGAAGTTGGAGACCGAGACCATCGGAGGCCA 532 CAGGAGAAGAAAGACCAAGGGTCTAGGAAGAAGAAGTCACTCTGCTGATGCAGACACTG AsnThrLeuSerThrProGluGluGluJysLeuAlaAlaLeuCysLysLyrAlaGluLeu ProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro LysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg-SerLeuLysGluGluGl 259 yvalGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnVa 712 CTCGTGCAGGAGGACCATCTGCGAGGGGAACACACAGAAGGCTGTCCTGGCCCCGAGC

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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 AGAÁGCAAGCTCGAÁÁGTTTGTGCAGÁGAGCTACAGAGÁCACAACCGTACACTAAAGGAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 GInValThrLeuAsnAspIleGinLeuGinMetGluGinHisAsnGluArgAsnSerLys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 LeuargGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuVal 337
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/note="Vector: pCS107; Site_1: BCoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. BCoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAsp 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGGAAGATTT-CTTAGTACATATTGTGTTGCTTACTAGCAAGAAGAGGAGCAGGAGTTG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ---------GAGGAGACAGATAAGGGAGCCCAGGAGACACCA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 CAAGTGACGCTCAATGACATCCAGTCACAGATGGAGCAGCACAATGAACGTAATGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 CGAATGCAAGACAAAAAAGGCAAAGGGTCTGGGAAAGGAGATCACATTATTAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 ACTCTGAACACTCAGCACCCCAGAGGAAAAGCTGACTGCCCTGTGTAAGAAGTATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 SerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 ACCCAGCTTATTCAAGAAAGGATCTACTTCGTAATGAGCACAGCAAGGCTATCCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              621 CTGCGTCAAGAGAATGTTGAGCTTGCTGATCGACTTAAGAAGCTTATCGAGCAATATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlubeubeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GAAGGAGTACAGAGGGCTCGTGAGGAGAAGAAAGGAAGAAGAAGTAACCTCCCATTTC
                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-023-523-44 (1-546) x AL961454 (1-945)
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                                                                                                                                                                                                                                                                                                            2.28e-69
1233.00
85.06%
77.44%
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                       Alignment Scores:
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DB:
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/ Leasure_Type="windle Drain"
/ dev stage="wendry of 12.5dpc"
/ lab_host="bH10B (TI phage resistant)"
/ clone lib="WINH BMAP FIO"
/ clone lib="WINH BMAP FIO"
/ loote="Organ: Brain; Vector: pXx. Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs
ggl:First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYx.Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACCAC. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Haalth (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU701958
UL-M-FIO-bys-i-05-0-UI.rl NIH BWAP_FIO Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ogapbs-remail.nih.gov

CDNA Library preparation: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/Link at:
338 AspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArg 357
                                                                   741 GATGCAAAGCTTCAGCAAGCACAAGAATGTTGAAAGAAGAGTGGAAGAGCGTCACCAGCGG, 800
                                                                                                                                                        GlulysAspPheleuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLys 377
                                                                                                                                                                                                                                     378 GInGlnGluThrHisLeuLysGinGlnLeuAlaLeuTyrThrGluLysPheGluGluPhe 397
                                                                                                                                                                                                                                                                                                                                                                                     861 CAGCAAGAGCCCACCTCAAACAACAGTTAGCACTGTATACAGAGAAGTTTGAGGAGTTT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
/clone="IMAGE:5697868"
/tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 GlnAsnThrLeuSerLysSerSer 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU701958
BU701958.1 GI:23626281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: pYX-5.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 735)

RS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs: r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
This clone was contributed by the Brain Molecular Anatomy Project (EMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluileThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluIysLeuAla 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACTGTGCAAGAAGTATGCTGAGCTGCTGGAAGAGCATCGGAACTCGCAGAAGCAGATG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisserLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGluArg 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ATTGGAGACCGAGAGCCACAGGAGAGAAAGAAAGCCAAGGGTCTAGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 GAGATCACTCTGCTGATGCAGACACTGAACACGCTGAGTACCCCAGAGGAGAAGCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 AlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 LysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: pYX-5.
Location/Qualifiers
1. .735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
strain="C57BL/6"
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1207.00
100.00%
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Best Local Similarity:
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DB:
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                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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UI-M-FIO-byt-i-21-0-UI.rl NIH EMAP_FIO Mus musculus cDNA clone
                                                                                                                                                                                                                                       GlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGlyLysGlu 171
                                                                                                                                                                                                                                                                                                                             IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAla 191
                                                                                                                                                                                                                                                                                                                                                             LeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLys 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTGCAAGAAGTATGCTGAGCTGCAAAAGCATCGGAACTCGCAGAAGCAGATGAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHis 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCTGCAGAAGAAGCAGCAGCTCCAGGAGAAAGGACCATCTGCGAGGGAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480
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Mus musculus
Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                GGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAAGCCAAGGCTCTAGGGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGTAGAACAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 LeulleGluGlnTyrGluLeuArgGluGluHislleAspLysValPheLysHisLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGATCGAGCAATACGAGCTTCGTGAGGAGCATATCGACAAAGTCTTCAAACATAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 CIGCAGCAGCAGCTAGTGGACGCCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluLysArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAGAAG
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727
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                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                (1-725)
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BQ769910.1 GI:21978384
                                 5.72e-68
1209.00
100.00%
99.59%
43.41%
                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glu 392
         Alignment Scores:
Pred. No.:
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ζ	251 HisAsnArgSerLeulysGluGluGlyValGlnArgAlaArgGluGluGluGlulysArg 270	
Dp		
કે ક	LysgluvalthrSerHisPheGlnvalThrLeuAsnAsplleGlnLeuGlnMetGluGln	·
an an	AAAGAAGIGACIICACACIICCAGGIGACACIGAAIGACAIICAGCIGCAGAIGGAACAG	
à	HisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLys	
ф	431 CATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAG 490	
λŏ	311 LysLeuileGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLys 330	ORIO
gg	491 AAGTIGATCGAGCATACGAGCTTCGTGAGGAGCATATCGACAAAGTCTTCAAACATAAG 550	Alig
δλ	331 AspLeuGinGinGinLeuValAspAlaLysLeuGinGinAlaGinGinMetLeuLysGiu 350	8000
ΩÞ	551 GACCTGCAGCAGCAGCTAGTGGACGCCCAGGAGGCCCAGGAGATGCTGAGGAGGGGG 610	Best
	AlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGln	DB:
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NOTARE	IMAGE:30708497 5', mRNA sequence.	λο
VERSION	CF955807.1 GI:38512528	qa
SOURCE		ò
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REFERENCE	1 (bases 1 to 759)	ò
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	QC C
COMMENT	Contact: Janiela S. Gerhard, Ph.D.	ò
	National Cancer Institute / NIH	d d
	Email: cgapbs-r@mail.nih.gov	à
	Tissue Procurement: James Martin, University of lowa cDNA Library Preparation: M. Bento Soares, University of Iowa	q _C
	CUNA LIBRARY ARRAYED BY: INE 1.M.A.G.E. CONSORCIUM (LINE) DNA Sequencing by: Agencourt Bioscience Corporation	λõ
	Cione distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Link at:	q
,	http://image.llnl.gov Plate: NDAM1074 row: m column: 18	ζ
<u>й</u>	High quality sequence stop: 631. Location/Qualifiers	qa
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	/ MD_1	쉼
	/lab_host="DHIOB TonA" /clone lib="NHH MGC 221"	٥٨
	/note="Organ: mixed; Vector: pYX-Asc; Site_1: BcoRI;	අ <u>ධ</u> .

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Site 2: Not1; Library is oligo-dT primed and directionally cloned Donatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pXX-Asc vector. Average insert size 4-5Xb. Adaptors 5' (AATTCGGCACGAGG) 3' and 5'd (CTCGGCCCCGCGCGCGCGCGCCTGAGAGCC T18. Sequencing primers 3' end: T3 promoter primer 5'd (ATTAACCTCACTAAAGGA) 3'. 5' End: T7 promoter primer 5'd (TAATAACGTCACTAAAGGA) 3'. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 ArgasnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 LeuCysargGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAla 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 GluLeuAlaGluArgLeuLysLysLeuIleGluGluTyrGluLeuArgGluGluHisIle 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 GAGCTGGCTGAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGCATATC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AsplysvalPhelysHisLysAspLeuGInGInGInLeuValAspAlaLysLeuGlnGIn 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGTGGCCAAGCTCCAGCAG 428
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RIXEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp, Tel:81-45-503-922, Fax:81-45-503-9216, CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://fantom.gsc.riken.go.jp/.URL:http://fantom.gsc.riken.go.jp/.
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KEYLLNQAAEWKLQAKVLKEQETVLQAQLTLYSGRFBEFQSTLTKSNBVFATFKQEMD
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                    /tissue type="heart"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="16 days neonate"
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCATGATGTCGCGGAAGAGTTGAGCAGGCAACTGGAAGACATCATAAGCACGTAT---
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SPTR|AAL33909, evidence: FASTY, 99.1%ID, 100%length,
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                                                                                                                                                                                                                                                                                                                                   2480
262
82
1134
64
                                                                  prepare mouse tissues.
Please visit our web site for further details URL:http://genome.gc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                    /db_xref="FANTOM_DB:DB30027D20"

/db_xref="MG1.2423165"

/db_xref="Laxon:10090"

clone="DB30027D20"
                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Query Match:
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                                                                                                                                      uGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGlu-LeuAlaGluArgL
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                                               GATTTTTTTATCAAGAAGTATACTGAATTGCTGGATGAACATCGCACCGAGCAAAGAAA
                                                                                                                                                                                                                                                              TGAGCACAACAGGCCCGTCCTTGCTCGAAGCAACTCGAGAGTCTGTGTCGGGGAGCTACA
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190 AlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLys-Gl
                                                                                                       nMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGl
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520

160

400

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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 750)

2 NH-Moch http://mgc.nci.nih.gov/.

3 NH-Moch tip://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.go,

Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G. B. Onsortium/Libra at:

http://image.linl.gov.
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UI-M-FYO-ccy-g-01-0-UI.rl NIH_BMAP_FYO Mus musculus CDNA clone
IMAGE:6826106 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                               AGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCAACTGGAA 280
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/organism="Mus musculus"
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC-109"
/note="Organ: ovary, Vector: pOTB7; Site_1: EcoRI; Site_2: Xho1; cDNA made by oligo-dT priming. Directionally cloned into EcoRIX/Xho1 sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkaley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                              EST 16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gagbs-remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CONNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2830 row: I column: 10
High quality sequence stop: 566.
Location/Qualifiers
I. 799
/organism="Homo" sapiens"
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11 Masca 1 to 7990
NAH-MGC http://mgc.nci.nih.gov/.
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AGENCOURT_10437001 NIH_MGC_109 Homo sapiens CDNA clone
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/db_xref="taxon:9606"
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95.98%
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Homo sapiens
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/db_xref="taxon:10090"
/clone="IMAGE:5702161"
/clone="IMAGE:5702161"
/clone="IMAGE:5702161"
/dev_stage="whole brain"
/dev_stage="whole brain"
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/clone=lib="NH1B BMAP_F10"
/note="Organ: BFain; Vector: pVX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the DolyA tail
is CAGCCACGAC. This library was created for the University
lowa Brain Anatcmy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: Gapbs r@mail.nih.gov in University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing Strayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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11 HMG http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
602 GTGCAGCGAGCCCGTGAGAAGAAGAAGAAGAAGAAGAAGAAGTGACTTCACACTTCCAAGTG
                                                                                                                    662 ACACTGAATGACATTCAGCTGCAGATGGAACAGCATAACGAGCGANACTCCCAAGCTGCGC
                                                                                    ThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArg
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Location/Qualifiers
1. 727
/organism="Mus musculus"
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/strain="C57BL/6"
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Mus musculus
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                                              /dev stage="embryol 13.5,14.5,16.5,17.5dpc"
/lab host="mbH108 (T1 phage resistant)"
/lab host="mbH108 (T1 phage resistant)"
/clone lib="NH1 BMAP_PST, phage resistant)"
/clone lib="NH1 BMAP_PST, phage resistant)"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Ambral Health (NIMH), Hemin Chin, Ph.D.,
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Matches:
Conservative:
Mismatches:
Indels:
                                tissue_type="whole brain"
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406 GluvalPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLleLysLysLeu
                                                                                                                            1. .716
/organism="Mus musculus"
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                                                                                      Seq primer: pYX-5.
Location/Qualifiers
                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6".
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97.51%
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Query Match:
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Mus musculus

Bukarjota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Redentia; Sciurognathi; Muridae; Murinae; Mus.

I bases 1 to 716

III hases 1 to 716

INTH-MGC http://mgc.nni.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Umpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lih University of Iowa

Tissue Procurement: Dr. James Lih University of Iowa

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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                                                                                                                                                                                    67 GCGAGTGATGAAGTTGGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAGAAAGCCAAG 126
                                                                                                                                                                                                                       GlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGlu 186
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                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGCAGATGAAGCTCCTGCAGAAGAAGCAGAGCCCAGCTCGTGCAGGAGAAGGACCAT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAla 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 CAGATGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluArgleuLysLysLeulleGluGlnTyrGluLeuArgGluGluHislleAspLysVal 326
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                                                                                                          99
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                                                                                                            ccagregrenaegegagagagacereraagegagagetegaaekagagagagarega
                                                                                                                                                                                                                                                     GluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSer
                                                                                                                                                                                                                                                                                                                             GAGAAGCTGCACTGTGCAAGAAGTATGCTGAGCTGCTGGAAGAAGATCGGAACTCG
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                                                                                                                                                  nGluLysLysLysAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArg
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                                      US-10-023-523-44 (1-546) x BQ770181
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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/db xref="raxon:10090"
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/tissue_type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
/dev stage="embryo 12.5,13.5,14.5 dpc"
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/clone=lb="NTIE BMAD_HB0"
/clone=lb="NTIE BMAD_HB0"
/note="Organ: Eye, Vector: PXX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not1 and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NINH)."
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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61

94

153

173 301 193 213 421 233

361

253 541 601

312

481

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AK031023. 4452 bp mRNA linear HTC 18-SEP-2003 Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830498L23 product:hypothetical protein, full insert
                                                                                                                                                                                                                      722 Arcandcantaceangerregandenterrenteachanderer-anachragaeree 780
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AK031023 GI:26082107
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus (bazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                           ProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArg
                                                                                                                                                  CCGCTGAGGAGGACACAGGGTGAGCCCACTGAGCCGGAAGACACGGAGAGTCCCGA
                                LeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGly
                                                                   2 crdadccdccarricgaacarccrcadcracaracrcrcrcacacaacaarcagcaaca
                                                                                                                                                                                              ThrTyrValAlaArgAsnGlyGluProGluPro---ThrProValValAsnGlyGluLys
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                                                                                                                                                                                                                                                                             GluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAsp
                                                                                                                                                                                                                                                                                                                    182 GAGACCTCTAAGGGAGAGCCTGGAACAGAGAGATCCGAGCAAGTGATGAGGTTGGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                   242 CGAGACCATCGGAGGCCACAGGAGAAGAAGAAGCCAAGGGTCTAGGGAAGGAGGATCACT
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High-efficiency full-length cDNA cloning
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AUTHORS
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

B (Dases 1 to 819)

S NIH-MGC http://mgc.nci.nih.gov/.

I National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E: Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Conscitum (LINL)

DNA Sequencing by: The I.M.A.G.E. Conscitum (LINL)

CONDA Library Arrayed by: The I.M.A.G.E. Conscitum (LINL)

CONDA Library Arrayed by: The I.M.A.G.E. Conscitum (LINL)

CONDA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Conscitum/LINL at:

Plate: LiAM9852 row: 1 column: 10

High quality sequence stop: 758.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 12-JAN-2001
                                                                                                                                                                                                                                                       099
GAAGTGTTCACCACGTTCAAACAGGAGATGGAAAAGATGACAAAGAAGAAGATCAAGAAGCTG 480
                                                                                       540
                                                                                                                        MetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGln 465
                                                                                                                                                485
                                                                                                                                                                                                                                                                                        GlnAspheuSerAlaGlyGlnGlySerLeuThrAspSerGlyProGluArgArgPro 505
                                                                                                                                                                                                                                                                                                                               CAGGACCTGACTGCAGGGGC-----ATCACTGACATTGGCTCTGAGCGGAGGGCA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Butain=rup/m
/db/xref="twon:10090"
/clone="INAGE:4239513"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI_CGAP Kid14"
/nore="Organ kidney; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF783468 819 bp mRNA linear EST 12-JAN-2
602111238F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239513
                                       GluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuGlu
                                                                                   GAGAAAGAAACCACCATGTATCGATCCCGGTGGGAAAGCAGCAACAAGGCTCTGCTGGAG
                                                                                                                                                                                                       ArgleuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgVal
                                                                                                                                                                                                                                       CGGCTGGAGAAGCTGTGCCGAGCACTGCAGACCGAGCGCAATGACCTCAACAAGAGGGTA
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Matches:
Conservative:
Mismatches:
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Gaps:
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'strain="FVB/N"
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1148.50
92.05%
90.91%
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BF783468
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Best Local Similarity:
Query Match:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

.. No..

Pred. N Score:

DEFINITION RESULT 23 BF783468

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/tissue type="thymus".
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev.stage="adult"
1. 4452
/note="hypothetical protein (evidence:
rsCDS, ProCrest, decoder, NCBI CDS Predictor, Longest-ORF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1261 CTCTGTAAGAAATATGCTGATCTCCTGGAAGAAGAAGCAGGAATGTTCAGAAACAAATGAAG 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 GlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlu 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAla 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 SeriysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHis 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysVal---AspAsnAsn 91
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                                                                                                                                                                                                                                                                      4452
260
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                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Korno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazaam, M., Nishine, T., Harada, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yanjawka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Setten integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Pred. No.:
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/um.ktm="taxumiinuvav".
/clone="IMAGE:6833074"
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/lone_lib="mbryo 15:70"
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                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 727)
1 (Dases 1 to 727)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Oupublished (1999)
In Contact: Robert Strausberg, Ph.D.
Email: Gapba-remmali.nh.gov
Tissue Procurement: Dr. Jim Lin, Govares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

His clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                CB244426
UI-M-FYO-cdq-i-09-0-UI.rl NIH_EMAP_FYO Mus musculus cDNA clone
IMAGE:6833074 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AsnGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAsp 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GlutysSerArgThrTyrValAlaArgAsnGlyGluProGluPro---ThrProValVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GAGAAGTCCCGAACCTATGCAGCAGGAATGGGGAGCCTGAACCAGGCATTCCAGTCGTC
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723
132
133
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: pYX-5.
Location/Qualifiers
1.027
/organism="Mus_musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                        CB244426
CB244426.1 GI:28366070
EST.
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1135.50
96.28%
95.87%
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Best Local Similarity:
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                      ORGANISM
RESULT 26
CB244426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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/dev stage="munic Digital".
/dev stage="embryol 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="MINH BMAP FIO":
/clone lib="MINH BMAP FIO":
/note="Organ: Brain, Vector: pYX- Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CACCACGAC. This library was created for the University
lowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mentel Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGlu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 HisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLys 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TT-GGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAAGCCAAGGGTCTAGGGAAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GAGATCACTCTGCTGATGCAGACACTGAACACGCTGAGTACCCCAGAGGAGAAGCTGGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 AAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluileThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAla 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GCACTGTGCAGAGAAGTATGCTGAGCTGCTAGAAGAGCATCGGAACTCGCAGAAGCAGATG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 AlaLeuCysLysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 HisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 cácaccaagecrerececeaageaagerreagagrererecegegagerecegeaages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                 db_xref="taxon:10090"
clone="IMAGE:5721214"
'tissue_type="whole brain"
                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-023-523-44 (1-546) x BU701604 (1-699)
                       Location/Qualifiers
1. .699
                                                                                                               /mol_type="mRNA"
/strain="C57BL/6"
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1116.00
97.85%
97.00%
        Seg primer: pYX-5.
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Pred. No :
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UI-M-FIO-byp-e-23-0-UI.X1 NIH BMAP_FIO Mus musculus cDNA clone MAGE:5721214 5', mRNA sequence.
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Bmail: Ggapbs-r@mail.nih.gov
Trisue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Expendingly by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/Link at:
http://image.lnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                            185
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150 GluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGly 169
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                                                                                                         126 GAAGITIGGAGACCGAGACCATCGGAGGCCACAGGAAGAAGAAAAAGCCAAGGGTCTAGGG
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US-10-023-523-44 (1-546) x BX855901 (1-780)	Qy 170 LysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeu 189 :::	Oy 190 AlaAlaLeuCysLysLysTarlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln 209	22	Oy 230 GluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGln 249	OY 250 ArgHisAsnArgSerLeuLysGluGluGluAlglaArgAlaArgGluGluGluLys. 269	Qy 270 ArgLysGluValThrSerHisPheGlnValThrLeuAsnAsplleGlnLeuGlnMetGlu 289	GlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnWetGluLeuAlaGluArgLeu 30	QY 330 LysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLys 349	Qy 350 GlualadludludghisGlnargGluLysAspPheLeuLysGlualaValGluSer 369	OY 370 GlnargMetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGlnLeuAlaLeu 389	Qy 390 TyrThrGluLysPheGluGluPheGluAsnThrLeuSerLysSerSerGluValPheThr 409	Oy 410 ThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLys 427	EQ950691 930 bp mRNA linear EST 21-2	A AGENCOURT_8752844 NIH_MGC_130 Mus musculus cDNA clone IMAG 5, mRNA sequence. BQ950691 BQ950691.1 GI:22366169 EST.	Mus musculus (house mouse) This man amountus	ENGRAYOGA; MEGRAZOA; Chordate; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TILE Nutional Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Maconochie, Ph.D. and Nancy L. Freeman.
Db 480 CATAACGAGCGAAACTCCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAG 539	Oy 311 LysLeuileGluGlnTyrGluLeuargGluGluHisileAspLysValPheLysHisLys 330 	Qy 331 AspleuGinGinGinCeuValAspAlalysLeuGinGinAlaGinGiuMetLeuLysGiu 350 Db 600 GACCTGCAGCAGCAGCTAGTGGACGCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAG 659	Oy 351 AlaGludluArgHisGlnArgGluLysAspPheLeuLeu 363			_	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. REFERENCE 1 (bases 1 to 780)	INTA - SCRIBB Campus de beaulieu, RENNES cedex, 35042, France Tel: 02.23.48.50.09	Email: Yann.Guiguen@beaulieu.rennes.inra.fr Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this	Sequence: Plate: 0039 Seq primer: Loc	source 1.780 /organism="Oncorhynchus mykiss" /mol_type="mRNA" /db xref="taxon" = 1002" /db xref="taxon" = 1002"	/tissue_type="daipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine, kidney, liver, unsole, ovary, pituitary, testis" /dev stage="from embros to adults"	/lab_host="DH10B" /clone_lib="AGENAE Rainbow trout multi-tissues subtracted /library (tcay)"	/note="Wector: pTYT3D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction (tcay); Clone distribution : AGRNAE Resource centre. Francois PIUM1, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Edude du genome (LREG), Domaine de Vilvert, 78352,	ORIGIN	Alignment Scores: 7.09e-61 Length: 780 Score 1099.00 Matches: 215 Percent Similarity: 92.25% Conservative: 23 Best Local Similarity: 83.33% Mismatches: 20 Query Match: 39.46% Indels: 0 DB: 13.46% Gaps: 0

704 239 764

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AL637771 XGC-neurula Silurana tropicalis cDNA clone TNeu020c17 5', mRNA sequence.

AL637771 GI:38216372
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/lab_host="meurula"
/lab_host="meurula"
/lab_host="meurula"
/loone lib="xGC-neurula"
/note="Vector: pG$107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pG$107 with EcoRI at the 5' end and NotI at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                         Silurana tropicalis (western clawed frog)
Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
I Chases I to 702)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Nov 7, 2001 this sequence version replaced gi:16789750.
Contact: Huckle E
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EcoRI at
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                                                                                                                                                                                                                                                             259 lyVal-----GlnArgAlaArgGluGluGluGluLysArgLysGluValThr-SerHis
                                                                                                                                               200 LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln
                             220 LeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSer
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Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Arron M. Zorn.
constructed by Arron M. Zorn.
constructed of primed from Sug of poly A+ RNA from neurula.
EcoRI.Not1 cut cDNA was then ligated into pCS107 with EccRI at
S'end and Not1 at the 3' end.
Vector: pCS107, Site 1: EcoRI; Site_2: Not1
Host: Escherichia coli DH10B
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TROPICALIS SEQUENCE ID: TNeu020c17.plkSP6
Sequencing primer: 5P6.
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/mol_type="mRNN"
/db_xref="taxon:8364"
/clone="nReu020017"
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  Ph.D.

CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information ca

found through the I.M.A.G.E. Consortium/LINL at:

http://inage.llnl.gov

Plate: LLAM13798 row: h column: 19

High quality sequence stop: 560.
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Conservative:
Mismatches:
Indels:
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Query Match:
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358 GTCGTCAACGGCGAGAAGGAAGCTCTCTAAGGGAGAGCCTGGAACAGAGGAGATCCGAGCG 417
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy P (BMAP)
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Matches:
Conservative:
Mismatches:
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89.02%
86:99%
38.46%
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lih, Univeristy of Iowa cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
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                                                                                                              2 GGAAAGGAGATCACATTATTAATGGCAGACTCTGACACACTCAGCACCCCCAGAGGAAAAG
                                                                                                                                                                        189 LeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLys
                                                                                                                                                                                                 CTGACTGCCCTGTGTAAGAAGTATGCAGAACTGTTGGAGGAGGACAGGACACGAGGAGC
                                                                                                                                                                                                                                                          209 GlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArg
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                                                                                       GlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLys
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                                          US-10-023-523-44 (1-546) x AL63771 (1-702)
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/ loce="Organ: brain, Vector: pyx-Asc; Site_1: EcoR I;
/ note="Organ: brain, Vector: pyx-Asc; Site_1: EcoR I;
/ note="Organ: brain, Vector: pyx-Asc; Site_1: EcoR I;
/ note="Organ: brain, Vector: pyx-Asc; Site_1: EcoR I;
/ site_2: Not I; The library was constructed according to
/ Site_2: Not I ibrary was size fractionated on a 1% agarose
/ solicy-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mantal Health
(NIWH), Hemin Chin, Ph.D., program coordinator."
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BM455349

J318 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6406997 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5500322
S', mRNA sequence.
BM455349.1 GI:18504389
                                                                                                                                                                                                                           283 AspileGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGinGluAsn 302
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 1318)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                         263 AlaargGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsn
                                                                                                                                                                              142 GCTCGTGAGGAAGAAAAGGAAGGAAGTAACCTCTCATTTCCAAGTGACACTCAAT
                                                                                                                                                                                                                                               202 GACAACCAGTCACAGATGGAGCAGCAATGAACGGAATGCTAAACTTCGTCAAGAAT
                                                                                                                                                                                                                                                                                            MetGluLeuAlaGluArgLeuLySLySLeuIleGluGlnTyrGluLeuArgGluGluHis
                                                                                                                                                                                                                                                                                                                  323 IleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGln
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                   GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGlu
                                      22 GAGAAGGACCAACTTCGTAATGAGCATAGCAAGGCCATCCTGGCAAGAAGCAAACTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 TTGAAAGAGGCAGTGGAATCACAGCGCATGTGTGAACTTATGAAACAGCAAGAGACCCAC
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Tissue procurement: Lou standt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
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BJ618489 GI:37256314
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is available through the following
CTAGGGAAGGAGATCACTCTGCTGATGCAGACACTGAAACACGCTGAGTACCCCAGAGGAG
                                                                                                                                  LysG1nMetLysLeuLeuG1nLysLysG1nSerG1nLeuVa1G1nG1uLysAspHisLeu
                                                                                                                                                                                                                                                                      228 ArgGlyGluHisSerbysAlaValLeuAlaArgSerbysLeuGluSerLeuCysArgGlu
                                                                                                                                                                                                                                                                                              658 CGAGGGGAACACAGCAAGGCTGTCCTGGCCCGAAGCTAGGAAGCTTGAGAGCTGTGCCGGGAG
                                                                    LeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGlu
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/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8549, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes nim --
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 698
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:835s"
/clone="XL185e05"
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Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             248 LeuGlnArgHisAsnArg 253
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1070.00
96.89%
94.22%
38.42%
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Best Local Similarity:
Query Match:
DB:
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota, Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dases 1 to 861)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONDA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clond cistribution: MGC clonedistribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.j column: 21
High quality sequence stop: 738.
High quality sequence stop: 738.
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602888485F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043572
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                 ValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLleLysLeuGlu
                                                427 LysGluThrThrMetTyrArgSerArg-TrpGluSerSer-AsnLysAlaLeuLeuGluM
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Mus musculus (house mouse)
Mus musculus
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BI102887
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256
19
63.
98
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 LysLysTyrAlaGluLeuLeuGluGluHisArgAsn---
                              03
http://image.llnl.gov
Plate: LLAM12135 row: b column:
High quality sequence start: 90
High quality sequence stop: 669.
Location/Qualiflers
                                                                                                                            l. .1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-023-523-44 (1-546) x BM455349 (1-1318)
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1069.50
63.07%
58.72%
38.40%
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Pred. No.:
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/db_xref="taxon:10090"
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/clone="MAGE:685471"
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/dev stage="whole brain"
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/clone_lib="Dylane"
/clone_lib=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: gagbbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Genencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 647)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 GluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAla 190
                                                                                                                                                                                 CD578468 647 bp mRNA linear EST 09-JUL UI-M-FYO-cfs-n-14-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ValGlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGlyLys
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                                             755
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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/organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                    CD578468
CD578468.1 GI:31742859
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1060.00
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Query Match:
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                              DEFINITION
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TITLE
JOURNAL
COMMENT
                                                                                                                       RESULT 35
                                                                                                                                                    CD578468
LOCUS
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/db.rarie=lrach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.go=frach.ind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 GCTGGAGATGGCTGAAGAGAAAACCGTCCGGGACAAAGAGCTGGAGGGCCTGCAGGTGAA 481
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Mus musculus (house mouse)
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Email: cgapbs-remail.inh.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soarescaniowa.edu

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/strain="CS7BL/6"
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Matches:
Conservative:
Mismatches:
Indels:
/tissue_type="whole brain"
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99.54%
98.15%
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Best Local Similarity:
Query Match:
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155

242 195 255

482

235 422 275

602

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL MEDLINE PUBMED COMMENT

AUTHORS TITLE REFERENCE

LOCUS DEFINITION

RESULT 37 CA510893

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TCTAAGGGGGAGCCTGGCACAGAAGAGATCCGAGCAAGTGAGGTTGGAGACCGAGAC 182
                                                                                                                                                                                                                                                                                                                                                                                                            156 HisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluLleThrLeuLeu 175
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Email: Gagbbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Expending by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                     63 GCAGCCAGGAATGGGGAGCCTGAACCGGGCATTCCAGTCGTCAATGGCGAGAAGAGACC 122
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 784)
11 (bases 1 to 784)
National intriuctes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                            117 ValAlaArgAsnGlyGluProGluPro---ThrProValValAsnGlyGluLysGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr
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                                                                                         3 GAGGAGGAGCTCAGGGGGGGCCCACTGAGCTCAGAGACACAGAGAGTCCCGAACCTAT
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UI-M-FIO-cea-m-20-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:6837021 5', mRNA sequence.
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CB247697
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//
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Contact: Soares, MB
Contact Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9565
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
                                                                                                                    CA510893 722 bp mRNA linear EST 15-NOV-2002 UI-R-FJO-cpv-o-09-0-UI-R-FJO Rattus norvegicus cDNA clone UI-R-FJO-cpv-o-09-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
603 GCTGAAGGAGGCAGGAGCGCACCAGCGAGAGAAGGAGTTTGTG 648
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
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FEATURES

Мо..

Score:

ORIGIN

239 750

691

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BG975353 796 bp mRNA linear EST 12-JUN-2001 602842995F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4978775 5', mRNA sequence.
BG975353.1 GI:14362990
EST.
Wus musculus (house mouse)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases, 1 to 796)

Nath-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                           572 AACACGCTGAGTACCCCAGAGGAGGAGCTGGTGCACTGTGCAAGAAGTATGCTGAGCTG
                                                                                                                                                                                 LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln
                               160 GlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeu
                                                                                                         180 ASnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysAlaGluLeu
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/tissue_type="whole brain"
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/lote="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyX- Asc; Vector: Partial CDNA asc primer containing a Not I site. Double strand color of with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector: The library tag sequence located between the Not I site and the polyh tail is CACCACACAC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
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http://image.linl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAAP)
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Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                       organism="Mus musculus"
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                                                                                         Location/Qualifiers
1...784
                                                                                                                                                         mol_type="mRNA"
strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.79e-57
1046.00
87.65$
85.66$
37.56$
                                                                                 Seq primer: pYX-5
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Pred. No.:
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on replaced gi:2293 UK ct 2001 plkSP6 e Collection (XGC) f poly A+ RNA from	ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at 5' end and NotI at the 3' end. Vector: pCS107; Site 1: ECORI; Site_2: NotI HOST: ESCHERICHIA COLI XL1-blue. FEATURES Location/Qualifiers Source //orgalism="mbmh" June 1 1 1 1 1 1 1 1 1 1	/mol Type="mkNA" /db xref="taxon.8364" /clone="Tagg080c08" /dev stage="egg" /lab_host="Escherichia coli XL1-blue" /clone=lib="Scherichia coli XL1-blue" /clone=lib="SGC-egg" /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then licated into pCS107 with	ORIGIN Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Py.29\$ Conservative: 10 Bast Local Similarity: Py.75\$ Marches: Percent Similarity: Py.29\$ Manaches: Percent Similarity: Py.29\$ Manaches:	Uery March: 37.34% Indels: B: S-10-023-523-44 (1-546) x AL887857 (1-665) y 168 LeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnT b 1 CTGGGAAAGGAGATCACATTATTAATGCAGACTCTGAACA	188	Qy 208 LysGlmMetLysLeuleuGlnLysLysGlnGerGlnLeuValGlnGluLyaAspHisLeu 227	2 4 8 2 4 1 8 2 4 1 8 2 6 8 1	Db 301 GAGAAAGCAAAGAAGTAACCCATTICCAAGTGACACTCAATGACATCACAGTCACAG 360 Qy 288 MetGluGlnHisAsnGluArgAsnSerLysbeuArgGlnGluAsnMetGluLeuAlaGlu 307	Qy 308 ArgLeuLysLysLeulleGluGlnTyrGluLeuArgGluGluHis1leAspLysValPhe 327
Match: 12	aGlnAla ::: TCGAGCT nLeuGlu	AANGCAGCTCAGGCCCCCTCTGTGACGTCTCTGAGGGGCCTGAGCCGGGGAGCTGAGCCGGGGAAGCTGAGCCGGGGGAAGCTGAGCCTGGGGGAGGGGGGGG	GlyGlubroGlubroThrProvalValAshGlyGluLysGlubroSerLysGlyAsp	GINGLULYSILYSELYSALALYSGLYLEUGLYLYSGLULLETHYLEULEUWETGLITHYLLEU CAGGAGAGAGAGAGAGAGALTHINNINNINNINNINNINNINNINNINNINNINNINNINN	LeuGludluHisargasnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSer 21 	219 GInLeuValGlnGluLysAspHisLeuArgGlyGlu-HisSerlysAlaValLeuAlaAr 238 687 CAGCTCGTGGAAAGGACCTCTCGGGGGGGGAACCACAGCAGCAGCAGCTCTCCTGGCCCG 746 238 GSerlysLeuGluSerLeuCysArgGluLeuGlnArgHis 251 747 AACAAACCHTCACAAACGCTCTCACAACCTCTCAAAACCTCTCTCTCTC	A87857 XGC-egg Silurana tropicalis cDNA c	AL88/857.2 GI:38689228 EST. Silurana tropicalis (western clawed frog) Silurana tropicalis Gilurana, Tropicalis Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pippidea, Pipidae,	Xenopodinae; Silurana. 1 (Bases 1 to 65) Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenous tropicalis EST project 2001 (11 2003)

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862 bp mRNA linear EST 04-DEC-2002
AGENCOURT 11044319 NICHD XGC Embl Xenopus laevis cDNA clone
IMAGE:6865533 5', mRNA sequence.
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 GluGluPheGlnAsnThrLeuSerbysSerSerGluValPheThrThrPheLysGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 ArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAsp
                                                                                                 215 LyslysGlnSerGlnLeuvalGlnGluLysAspHisLeuArgGlyGluHisSerLysAla
                                                                                                                                                             235 ValleuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSer
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                                                                                                                                                                                                                                    295 AsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGlu
   4400
Conservative:
Mismatches:
Indels:
                                                                      (1-782)
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EST.
                                                                        US-10-023-523-44 (1-546) x BU231392
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1 (bases 1 to 862)
 91.51%
74.52%
37.24%
   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                       255
                             Query Match:
DB:
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CA793605
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p mRNA linear EST 22-MAY-2002
Silurana tropicalis cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Silurana.

1 (bases 1 to 654)
NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development; National
                                                                 401
                                                                                                                                                                                441
                                                                                                                                                                                                                                                                                                                              461
                                                                                                                                                    402 SerlysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLys 421
                                                                                                                                                                                                                                                                                  662 ATAAAGAAACTTGAAAAGGAAAGTGTTGTCTGGCGCACAAAGTGGGGAAAATAACAAAA 721
                                                                                                                                                                                                                                                                                                                                                          TIGITGAATGAGGCAACTGAAACAAGGCAAAAGTTTGAAGAATTAAAACAACAAGAAAGC 541
                                                              382 HisLeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu
                                                                                      422 ilelysiysieuGluiysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer Instruct,
Unpublished (2002)
Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
word-ng Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center (NISC)
Clone distribution. NCI-CCAP clone distribution information
found through the I.M.A.G.E. Consortium/LINL at:
info@image.llnl.go.
Plate: LLAM11780 row: E column: 11
Seq primer: M13RP1 reverse primer (ABI).
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204
9
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Embs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
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Silurana tropicalis
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IMAGE:5308018 5', mRNA sequence.
BQ389733
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/clone="IMAGE:5308018"
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TITLE
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                                     Tumor General institute, cancer denome Americany Figure (Correct Dupphlished (1997)

Umpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14488 row: a column: 20

High quality sequence stop: 687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo (stage 10)"

/tish host="DH10B (phage-resistant)"
/clone lib="NHIDB XGC Emb1"
/note="Vector: pCWV-SPORT6; Site_1: NotI; Site_2: SalI;
/note="Vector: pCWV-SPORT6; Site_1: Oligo dT. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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/db_xref="taxon:8355"
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                                                                                                                                                               /mol_type="name.corrections" //mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_mol_type="name.corrections" //mol_mol_mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections" //mol_mol_type="name.corrections" //mol_type="name.corrections" //mol_type="name.corrections"
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Matches:
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/organism="Mus musculus"
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Sciurognathi; Muridae; Murinae; Mus
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
                                                                                                                                                                                                                                            83 ATCCTGGCAAGAAGCAAGCTCGAAAGTTTGTGCAGAGAGCTACAGAGACACACAGAGA
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                                                                                                                                                     CAACTGGTGGATGCGAAGCTTCAGCAAGACACAAGAAATGCTGAAAGAAGAAGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPhe
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
I (bases 1 to 954)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BUJ51934
BUJ51934.1 GI:22665466
EST.
                              Gaps:
                                                                            US-10-023-523-44 (1-546) x BQ389733 (1-654)
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DB: US-10-023-523-44 (1-546) x CB247310 (1-777) OY 1 MetLysAsnGlnAspLysLysAsnGlyalaAlaLysGlnSerAsnProLysSerSerPro 20	41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla	Cy 101 GlnGlyGlubroAlaclubroAlacluLysSerArghrTyrValhlaArgAsn 120 11	Db 507 CAGGAGAAGGCCAAGGGTCTAGGGAAGGAGATCACTCTGTGATGCAGACACTG 566 Qy 180 ASHThrIeuSerThrProGluGluLySLeuAlaAlaLeuCySLySLySTyTAlaGluLeu 199 bb 567 AACACGCTGAGTACCCCAGAGGAGAAGCTGCTGCATGTGCAAGAAGTATGCTGAGTGC 626 Qy 200 LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln 219	RESULT 46 CA328385 LOCUS LOCUS LOCUS DEFINITION UI-M-FYO-cdb-1-19-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone NAGES:6827396 5', mRNA sequence. ACCESSION CA328385.1 GI:24546483 ACCESSION CA328385.1 GI:24546483 SOURCE Wus musculus (house mouse) Nus musculus (house mouse) SOURCE Nus musculus (house mouse) REFERENCE RATIONS REFERENCE I (bases 1 to 780) AUTHORS NIH-MAGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) COMMENT CONTENT
	RESULT 45 CB247310 CB		Seq primer: pVX-5. Location/Qualifiers 1. 777 organism="Mus musculus"	primer containing a Not I site. Double strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not1 and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator." Alignment Scores: 6.99e-55 Length: 777 Score: Conservative: 777 Best Local Similarity: 86.75\$ Matches: 30 Query Match: 36.10\$ Mismatches: 30

693

633

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/clone libs NCI CGAP_Mam4"

//clone libs NCI CGAP_Mam4"

//clone libs NCI Cloned Unidirectionally. Primer: Öligo dT.

Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.

Library constructed by Life Technologies Investigators

providing samples: Lothar Hennighausen/Priscilla Furth,

NIH Reference for transgenic model: Li et al., Cell Growth

and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI661586 890 bp mRNA linear EST 12-SEP-2001
603305711F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5351403 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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GlyGluProGluPro---ThrProValValAsnGlyGluLysGluProSerLysGlyAsp
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/dev_stage="5 months"
/lab_host="DH10B"
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/mol_type="mRNA"
/strain="NMRI"
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/clone="IMAGE:5351403"
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BI661586.1 GI:15575822
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH10B (TI phage resistant)"
/clome lib="NIH BMAP EyO"
/clome lib="NIH BMAP EyO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/clome lib="NIH BMAP EyO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaflo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mentel Health (NIMM), Hemin Chin, Ph.D.,
program coordinator."
         Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing-Dy: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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clone="IMAGE:6827396"
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Location/Qualifiers
1. .780
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/strain="C57BL/6"
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120 334 180 354 240 300 420 314 374 394 414 433 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 965)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) /tissue_type="lymphona, cell line"
/lab.host="DH1DB (phage-resistant)"
/clone lib="NIH MGC_88"
/note="Organ lymph, Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally, oligo-dT primed.
Average insert size 1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library." GlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGln GlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArg 241 CACCAGCGGAGAAGCCATTTTCTCTCTGAAAGAGGCAGTAGAGTCCCCAGAGGATGTGTGA GCTGATGAAGCAGCAAGAACCCACCTGAAGCAACAGCTTGCCCTATACACAGAGAAGTT eGluGluPheGlnAsn-ThrLeuSerLysSerSerGluValPheThrThrPheLysGlnG AsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGlu ACTCCAAGCTGGCCAAGAGAACATGGAGCTGGCTGGCTGAGAGGCTCAAGAAGCTGATTGAG 121 CAGTATGAGCTGCGCGAGGAGCATATCGACAAGTCTTCAAAAGCAAGGACCTACAACAG HisGlnArgGluLys-AspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGl uleuMetLysGlnGlnThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPh 361 TGAGGAGTTCCAGAACAACACTTTCCAAAAGGGGGGGGGTATTCACCACATTCAAGCAGG 181 CAGCTGGTGGATGCCAAGCTCCAGCAGGCCCAGGAGATGCTAAAGGAGGCGAGAAGAGGCGG Contract: Robert Strausberg, Ph.D.

Contract: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
 Tiscape Procurement: Louis Staudt, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 Clone Library Sequence stop: 557.
 High quality sequence stop: 557.
 Location/Qualifiers
 I. . 365
 I. . 365
 I. . 366
 /organism="Homo sapiens"
 /mol.Ltype="mRMA"
 /db xref="texon: 3666"
 /clone="IMAGE: 4342392"

•				ORIGIN	Alignment Scores: Pred. No.: Score: Percent Similarity	Best Local Similar Query Match: DB:	-10-023-523-	09 24 Glus	4 4	122	Qy 64 GlnS	84	 Db 239 AGTA	Oy 104 Proh	124	359	Oy 143 GluG	Db 419 GAGG	Oy 163 LysL	479	Qy 183 SerT	Db 539 AGTA	Oy 203 HisA	DD 599 CATC	Qy 223 GluI		KESULI SU
		433 gSerargTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValAr 453	453 gAspLysGluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAl 473	473 aLeuGinThrGluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGl 493	51.			537 lyProGlnGluProThrSerAlaArgAla 546 				Mus musculus (house mouse) Mus musculus			Unpublished (1999) Contact: Robert Strausberg, Ph.D.	묫	ento Soares, U Sares, Univers	Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:	<pre>nttp://mage.iiii.gov This clone was contributed by the Brain Molecular Anatomy Project 'name'</pre>	(BrAR) Seq primer: pXX-5. Location/Oualifiers		/ Organization into mice of the control of the cont	/ Strain = C1/20/ / A tref="taxon:10090" / A tref="taxon:10090"	/tissue type="whole brain" /tissue type="whole brain" /and the property of the	/dev_stage="embryo 12.5 dpc" /lab_host="DH10B (T1 phage resistant)" /רוסים ויה- מדוד האוד האוד האוד האוד האוד האוד האוד ה	rgan: brain; Vector: Not I; The library w	Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
	qq	Qy Db	cy eq	ð i	සු දුරු	\ \delta \delta \ \de	70	oy Oy	RESULT 49 BUOS4710	LOCUS	ACCESSION VERSION	SOURCE ORGANISM		REFERENCE AUTHORS TITLE	JOURNAL					FEATURES	source						

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1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGACACC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Alignment S Pred. No.: Scores: Scores: Scores: Scores: Seat Local Dest Local Dest Local Dest Cocal	### ##################################	### 15.92e-54 Length: ### 114: ### 114: ### 114: ### 115.93e ### 114: ### 115.93e ### 116.93e ### 116.93e ### 116.93e #### 116.93e #### 116.93e ####################################	5.92e-54 Length: 686 88.21% Conservative: 5 88.03% Mismatches: 25 35.55% Mismatches: 26 37.55% Mismatches: 26 38.55% Mismatches: 27 38.55% Mismatches: 26	erSerProGlyGlnPro GCAGCCGGGGGCACGG laProAlavalGluAla CTCCTGGGGGGGAGCC laGlnAlaArgThrAla [23 61 121 121 121 123 135 147 162 162 1762 1762 1763 1763 1763 1763 1763 1763 1763 1763
Qy Dp	3 Hisarga 9 CaTCGGA	SerglnLysglnMe TCGCAGAAGCAGAT	/sLeuLeuGlnLy GCTCCTGCAGAA	sLysGlnSerGlnLeuValGln 2 	222 658
상 연	223 GluLysasp 659 GAGAAGGAC	GlulysasphisleuargGlyGluhi 	uHis 231 ACAC 685		

296 SerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeulleGluGln 31	361 ATGAAGCTCTGTCAGGAACACAGAGCTTGCAGAAAAGCTGAAAAGCATCATCGATCAG 316 TyrGluLeuargGluGluHisIleaspLysValPheLysHisLysAspLeuGlnGlnGln	421	Db	Oy 396 GluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet 415	Qy 416 GluLysMetThriysLysIleLysLysLeuGluLysGluThrThrMetTyrArgSerArg 435 :::	Qy 436 TrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 455	Qy 456 GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln 475	Cy 476 ThrGluhrgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySer 495	496 LeuThraspSerGlyProGluargargProGluGly	Db 1021 GACGCAGAGGAGGTTAATAGTGTCCAAACCGCCGTGAAAAATCTGGCCACAGCCTTCATG 1080	Cy 507 507 Db 1081 ATAATTCATCACAGAGTCAACCCGCACCAGTCCAAAGAAACCCAACCCGAAATAGGC 1140	Qy 508 516 State of the control of the cont	517ArgValThrGlualaProCysTyrP ::: ::: 1201 TCACGGGATTCAGAGAGTCCCCTGCCTC	Cy 536 ThrGlyBroGlnGluProThrSerAla 544 ::::C ::: Db 1261 AGTGTGAACCTCCATCGAGGCC 1287	Search completed: June 8, 2004, 12:35:46 Job time : 4023.39 secs		
AY405165 1611 bp DNA linear GSS 1	ON Homo sapiens HOW2133 gene, VIRTUAL TRANSCRIPT, partial se genomic survey sequence. N AY405165 AY405165.1 GI:39761139	KEYWORDS GSS. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		PUBMED 14671302 REFERENCE 2 (bases 1 to 1611) AUTHORS Clark, A.G., Talanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Talanohaum, D.M., Civello, D.R., Lu, F., Murphy, B., Farriara S. Wang, G. Zhang, Y. White F. Shinek, J. Ferriara S. Wang, G. Zhang, Y.	TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		D D	<pre>/locus_tag="HCM2133"</pre>	Alignment Scores: Pred. No.: Score: Score: 988.00 Matches: Percent Similarity: Best Local Similarity: 48.02* Mismatches: 1611 Conservative: 56 Mismatches: 107	35.48% Indels: 29 Gaps:	US-10-023-523-44 (1-546) x AY405165 (1-1611) QY	Oy 196 TyralaGluLeuLeuGludluHisargAsnSerGlnLysGlnMetLysLeuLeuGlnLys 215	LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal 	Oy 236 LeuhlaargSerLysLeuGluSerLeuCysArgGluLeuGlnargHisAsnArgSerLeu 255	OY 256 LysgluglyValgInArgAlaArgGluGluGluGluGluLysArgLysgluValThrSer 275	Oy 276 HisPheGlnValThrLeuAsnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsn 295	

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Sequence 161, Appl
Sequence 162, Appl
Sequence 163, Appl
                    Sequence 46, Appl
Sequence 46, Appl
Sequence 784, Appl
Sequence 774, Appl
Sequence 17, Appl
Sequence 17, Appl
  Sequence 46, Al
Sequence 46, Sequence 46,
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APPLICANT: Lees, Robert S.
APPLICANT: Lee, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERBURG: 1079-7-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT APPLICATION NUMBER: US/09/976,789
FRIOR APPLICATION NUMBER: 09/616,289
FRIOR APPLICATION NUMBER: US 08/979,608
US-09-954-456-1602
US-09-967-768A-245
US-09-954-531-988
US-09-954-531-1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
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US-09-976-740-46
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                                                            June 8, 2004, 06:37:59 ; Search time 972.245 Seconds (without alignments) 2561.956 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2785
1 MKNQDKKNGAAKQSNPKSSP.....APSTEASGQTGPQEPTSARA
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                          - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                 2995936 seqs, 2280998010 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Jatabase

DB

Query Match Length

Score

Result No.

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

US-10-023-523-44

Title: Perfect score:

Sequence:

OM protein

on:

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                                                                  GlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThr
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US-10-671-242-46
US-10-671-242-46
Sequence 46, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORVATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
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Mismatches:
Indels:
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PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-10-37
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 1638
                                                                                                                                                                                                                                    7.68e-210
2785.00
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                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)...(1638)
US-09-976-740-46
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Best Local Similarity:
Query Match:
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APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2003-09-24
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR PELING DATE: 1090-11-26
PRIOR PELING DATE: 1090-11-26
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-27
PRIOR PELING DATE: 1997-11-27
PRIOR PELING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PELING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows. Version 4.0
SEQ ID NO 46
LENGTH: 1638
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ORGANISM: Homo sapiens
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US-10-671-242-46
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                                                                    RESOLUT 3
Sequence 46, Application US/10023529
Sequence 46, Application US/10023529
PUBLICANT: US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon W.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREASTITE OF INVENTION: APPLICANT: 2004-01
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREASTILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR PILING DATE: 2000-07-14
PRIOR PLILING DATE: 2000-07-14
PRIOR PLILING DATE: 1990-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-06-03
PRIOR PLILING DATE: 1997-06-03
PRIOR PLILING DATE: 1997-06-03
PRIOR PLILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 10.88
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Matches:
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Mismatches:
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; NAME/KEY: CDS
; LOCATION: (1)...(1638)
US-10-023-529-46
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Best Local Similarity:
Query Match:
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Oy 481 LeuAsnLysArgVa	Qy 501 ProGluArgArgPr Db 1501 CCTGAGAGGAGGCC	Oy 521 AlabrocysTyrBr 	Oy 541 ProThrSerAlaArgAla Db 1621 CCCACCTCCGCCAGGGCC	RESULT 4 US-10-023-523-46 ; Sequece 46, Application US/1002352; ; Publication No. US20020152485A1	; GENERAL INFORMATION: ; APPLICANT: Lees, Run M.; ; APPLICANT: Lees, Robert; ; APPLICANT: Law, Simon W.	; APPLICANT: Arjona, Aniba; IIILB OF INVENTION: NOVEL; ITILE OF INVENTION: PROT; ITILE OF INVENTION: ATHE	; FILE REFERENCE: 10797-004001 ; CURRENT APPLICATION NUMBER: US/10/023,523 ; CURRENT FILING DATE: 2001-12-17 ; PRIOR APPLICATION NUMBER: US/09/616,289	PRIOR FILING DATE: 2000-C PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-G PRIOR APPLICATION NUMBER:	; PRIOR FILING DATE: 1997-11-26 ; PRIOR APPLICATION NUMBER: US 60/031,930 ; PRIOR FILING DATE: 1996-11-27 ; PRIOR APPLICATION NUMBER: US 60/048,547	PRIOR FILING DATE: 1997-06-03 , NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: FastSEQ for Windows Version ; SEQ ID NO 46	-1 4 € ··	; NAME/KEY: CDS ; LOCATION: (1) (1638) US-10-023-523-46	Alignment Scores: 7.68 Pred. No.: 2785 Score: 2785 Percent Similarity: 100.	Best Local Similarity: 100. Query Match: 100. DB: 14	-10-023-52	Oy 21 GlyGlnProGluAl	

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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN AND TREATING
TITLE OF INVENTION: NOVEER: US/10/616,187
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-03-02
PRIOR PELING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/99,608
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1995-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTHARE: FRARESQ for Windows Version 4.0
SSEQ ID NO 46
LENGTH 143R
                                                                                                                                                                                                CCTGAGAGGAGGCCAGAGGGCCTGGGGCTCAAGCACCCGGCTCCCCCCAGGGTCACAGAA
                                                                                                                                                                                                                              AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu
                                        LysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGluGluVLeu
                                                                                      GlnValLys1leGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp
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Matches:
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                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/10616187 Publication No. US20040013668A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1638)
US-10-616-187-46
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Best Local Similarity:
Query Match:
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                                                                                                                    GTAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAGGGTGCTCAAGCC
                                                                                                                                                                                        301 CAGGGTGAGCCGGCTGAACCCGAAGATGCAGAAGTCCCGGACCTATGTGGGAAGTAT
                                                                                                                                                                                                                                                                                                                                                                                      361 GGGGAGCCTGAACCTCCAGTAGTCAATGGAGAAAGAAACCCTCCAAGGGATCCA
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Oy 1 MetLyshenGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro 20	нσ	Oy 41 ValGludlyBroGlySerSerGlnAlaBroArgLysFroGluGlyAlaGlnAla 60	Oy 61 ArgThrAlaGinSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGinLeuGlu 80	Qy 81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyBroGlyGluAspGlyAla 100	Oy 101 GlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsn 120	QY 121 GlygluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro 140	Oy 141 ASDTHIGHUT ASD ASD	OY 161 GluLysLysRalaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsn 180	Qy 181 ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysTyrAlaGluLeuLeu 200	QY 201 GludluHisArgAsnSerGlnLysGlnMetLysGlnMetLysLysGlnSerGlnLeu 220	Qy 221 ValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLys 240	LeuGluSerLeuCys	Qy 261 GlnArgAlaArgGluGluGluGluUshrghrgLysGluValThrSerHisPheGlnValThr 280	Oy 281 LeuasnaspileGinLeuGinMetGluGinHisasnGluArgasnSerLysLeuargGln 300	QY 301 GluasnMetGluLeualaGluargLeuLysLysLeuIleGluGlnTyrGluLeuargGlu 320	Oy 321 GluhisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys 340	Qy 341 LeuglnGlnalaglnGlnwetLeuLysGlualagluGluArgHisGlnArgGluLysAsp 360	
Oy 361 PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlu 380 	381	Oy 401 LeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLys 420	Qy 421 LysileLysLysLeuGluLysGluThrThiMetTyrargSerargTrpGluSerSerasn 440	Qy 441 LysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeu 460 	Oy 461 GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp 480	Oy 481 LeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlyGlyGlyGerLeuThrAspSerGly 500	Oy 501 ProGludrgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 520	Oy 521 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 540	Oy 541 ProThrSerAlaArgAla 546 Db 1621 CCCACCTCGGCAGGGC 1638	RESULT 6 US-10-276-774-784 ; Sequence 784, Application US/10276774	<pre>; Publication No. US20040053245A1 ; GENERAL INFORMATION: ; APPLICANT: Hyseq, Inc. ; APPLICANT: Tang, Y, Tom et al</pre>	; TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides; FILE REFERENCE: 21272-030; CURRENT APPLICATION NUMBER: US/10/276,774; CURRENT FILING DATE: 2002-11-18	; PRIOR APPLICATION NUMBER: 09/560,875 ; PRIOR FILING DATE: 2000-04-27 ; PRIOR APPLICATION NUMBER: 09/496,914 ; PRIOR FILING DATE: 2000-02-03	; NUMBER OF SEQ ID NOS: 2700 ; SOFTWARE: Custom ; SEQ ID NO 784 ; LENGTH: 2523	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-276-774-784	 >-	ty: 100.00% Mismatches: 100.00% Indels: 13 Gaps:	TIS-10-023-523-44 (1-546) × TIS-10-276-774-784 (1-2523)

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NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION NUMBER: 10797-002001 (formerly 3983/59818)
TELEPHONE: 617/542-5070
TELEPRA: 617/542-8906
INFORMATION FOR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4697 base pairs
TYPE: nucleic acid
STRANDENSES: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                      4697
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Matches:
Conservative:
Mismatches:
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LOCATION: 3...1592
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
 GlnValLyslleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp
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                                                                                             Acceaecteaageaacagerrececraracagagaagrreagagrrecagaacaca
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                                                            ThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThr
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STREET: WA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: 1885 CFO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
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US-09-962-055-17
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  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
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Matches:
Conservative:
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                                    FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 1000-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
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PRIOR FILING DATE: 1996-11-27
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Query Match:
DB:
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ORGANISM: HOMO
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NAME/KEY: CDS;
LOCATION: (3).
US-09-976-740-17
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                                                          GluGluGlyValGlnArgAlaArgGluGluGluLysArgLysGluValThrSerHis
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Sequence 17, Application US/09976740
Sequence 17, Application No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Janon Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
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Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (3).
US-10-671-242-17
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GENERAL LINGURGANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 1079-004001
CURRENT PEPLICATION NUMBER: US/09/616, 289
FRIOR PELING DATE: 2000-07-14
FRIOR PLILNG DATE: 2000-07-14
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR PELICATION NUMBER: US 60/031, 930
FRIOR FILING DATE: 1996-11-27
FRIOR PELING DATE: 1996-11-27
FRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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Publication No. US20020129388A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

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FRIOR EPPLICATION NUMBER: US 09/517,849

PRIOR PELLING DATE: 2000-07-14

PRIOR PELLING DATE: 2000-03-02

PRIOR PELLOATION NUMBER: US 09/517,849

PRIOR PELLOATION NUMBER: US 09/517,849

PRIOR PELLOATION NUMBER: US 09/517,849

PRIOR PELLING DATE: 1997-06-03

NUMBER OF PELLOATION NUMBER: US 06/031,930

PRIOR PELLING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 17

LENGTH: 4697

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                                                                                                             AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
                                                                                                                                       AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys
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                                                   723 GAAGAAGGIGIGCAGCGGGCCCCGGGAGGAGGAGGAAGCGCAAGGAGGAGCICACCICGCAC
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                    GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
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Sequence 17, Application US/10616187

Publication No. US20040013668A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCIEROSIS

FILE REFERENT APPLICATION NUMBER: US/09/616,187

CURRENT APPLICATION NUMBER: US/09/616,289

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-27

PRIOR PILING DATE: 1997-11-27

PRIOR PILING DATE: 1997-11-27

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PRIOR FILING DATE: 1997-11-27

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                                       CTGGAGGGCCTGCAGGTAAAATCCAACGGCTGGAGAAGCTGTGCCCGGGCACTGCAGACA
LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
                                                                                              GluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeu
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Best Local Similarity:
Query Match:
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US-10-616-187-17.
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                                                                                                                                                               GTGGCAAGGAATGGGGAGCCTGAACCACTCCAGTAGTCTATGGAGAAGGAACCCTCC 362
                                                                                                                                                                                                                 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 156
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                                                 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAG
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LysMetThrLysLysllvsLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp
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COMPUTER: IBM COMPATIBLE
SOFTHARE: FRASEG for Windows Versio
SOFTHARE: FRASEG for Windows Versio
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-6ep-2001
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             1563 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1592
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
STREET: 225 Franklin Street
CITY: Boscon
STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: O2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                 GlyProGlnGluProThrSerAlaArgAla
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09962055 Patent No. US20020052033A1 GENERAL INFORMATION:
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TELEFAX: 617/542-8906
N FOR SEQ ID NO: 14:
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Lees, Robert S.
Law, Simon W.
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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                                                              ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
                                                                                                                            243 GAGGATGGGGCACAGGGTGAGCCGGACCGAAGATGCAGAAAGTCCCGGACCTAT
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                            GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr
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                                                     GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu
                                                                                                                            LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
                                                                                                                                                      517 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr
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OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROPIENS AND THEIR USES
TREATING ATHEROSCLEROSIS
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| Sequence 14, Application US/09976740
| Publication No. US20020194633A1
| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M. | APPLICANT: Lees, Robert S. | APPLICANT: Lees, Romon W. | APPLICANT: Law, Simon W. | APPLICANT: Law, Simon W. | TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING; TITLE OF INVENTION: ATHEROSCLEROSIS | FILE REFERENCE: 10797-004001 | CURRENT APPLICANTION NUMBER: US/09/976,740 | CURRENT FILING DATE: 2000-10-12 | PRIOR PELING DATE: 2000-07-14
                                                                                                                             GluGluHislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAla
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   280 ThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArg
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                                                                GlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArg
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Matches:
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    PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0.
LENGTH: 4722
                                                                                                                       TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEATURE:
NAME/KEY: CDS
LOCATION: (61)...(1731)
US-09-976-740-14
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                                                                                                                                                                                     LeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln
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APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
FRIOR APPLICATION NUMBER: US/09/616,289
FRIOR APPLICATION NUMBER: US/09/616,289
FRIOR PILING DATE: 2000-07-14
FRIOR PLILNG DATE: 2000-07-14
FRIOR FILING DATE: 100-10-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-27
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Best Local Similarity:
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; LOCATION: (61)
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Sinon M.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIERCSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-01-12-17
PRIOR PELICATION NUMBER: US 60/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PLING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-10-37
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 4722
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                                                                                                                                                              Sequence 14, Application US/10023529
Publication No. US20020129389A1
GENERAL INFORMATION:
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US-10-023-529-14
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Oy 500 GlyProGluArgArgPro	Db 238 AAAACTGCTCAGCCTGGGGCGCTCTGTGATGTCTC	
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Qy 509 GlyalaGlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaPro 528	298	
Db 1618 GGGCTCAAGTACCCAACTCTCCAAGGCCACAGACGCTTCCTGCTGCTGCAGGTGCACC 1677	OY 101 GINGLYGIUPPOALEGIUPPOGIUASPALEGIULYSSETATGIUTTYTVALALEATEGASIN 1	
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RESULT 17	418	
%-10-023-523-14 ; Sequence 1. Application US/10023523 ; Publication No. US20020152485A1	OY 140 Prokeninglinglinglinglinglinglinglinglingling	LGIYASPAIGASPHISAIGAIGIO 159
; GENERAL INFORMATION: ; APPLICANT: Lees, Ann M. ; APPLICANT: Lees, Robert S. ; APPLICANT: Law, Simon W.	OY 160 GInGluLysLysLysLysGlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeu 	ulleThrLeubeumetGlnThrLeu 179
APPLICANT: Arjona, Anibal A. TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS	Oy 180 AsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeu	aLeuCysLysLysTataGluLeu 199
; FILE REFERENCE: 10797-004001 ; CURRENT APPLICATION NUMBER: US/10/023,523 ; CURRENT FILING DATE: 2001-12-17	200	sleuleuGlniysLysGlnSerGln 219
; FXIOK AFFLICATION NUMBER: US/09/elb,289 ; PRIOR FILING DATE: 2000-07-18 . DDIOR EDDITCATION NUMBER: 119 04/517 849	DD 058 CICGAGGACCGGAACICGCAGAGCAGAIGAA	
FALOR FILING DATE: 2000-03-02 PRIOR FILING DATE: 2000-03-02 PRIOR APPLICATION NUMBER: US 08/979,608		77
	OY 240 LysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGly	SASnArgSerieuLysGluGluGly 259
FORS	Qy 260 ValdinargalaargGluGluGluGluUluLysargLysGluValThrSerHisPheGlnVal	9GluValThrSerHisPheGlnVal 279
ENGTH: PE: DN PGANISN		SASNGludrgAsnSerLysLeudrg 299
; NAME/KEY: CDS ; LOCATION: (61)(1731) US-10-023-523-14	300	w -
5.07e-191 Length: 4 2552.50 Matches: 5 93.19% Conservative: 1	320	
	Oy 340 LysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLys	aGluGluArgHisGlnArgGluLys 359
US-10-023-523-44 (1-546) x US-10-023-523-14 (1-4722) Qy 1 MetLysAsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro 20	360	
61 AIGAAGAATGAAGACAAAAAGAAGGGGGTGCCAAAGAGCCGAAAAGCAGCCGG	Db 1138 GACTITCTCCTGAAGGAGGCCGTGGAGTCCCAAAGAAGAAGAAGAAAAAAAA	GATGTGCGAGCTGATGAAGCAACAG 1197 rglutwsphegluglupheglnasn 399
Oy .21 GlyGlnProGludlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40		
41 ValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlyAlaGlnAla	Oy 400 ThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThr	eLysginglumetglulysmetthr 419

US-10-023-523-44 (1-546) x US-10-616-187-14 (1-4722) Qy	21	Qy 41 ValgluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla 60 nh 181 CGAGAAGGTGCCAGGAGGCCAGGGCCGGAAGGGCCGGAGGGGGGGCTCAAGCC 237	61 ArgfhrAladinserGlyAlaLeuArgAepValSerGluGluLeuSerArgGlnLeuGlu::::	81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 1 	101	121	140	Qy 160 GlnGluLysLysLysLysLysGlyLeuGlyLysGlulleThrLeuLeuWetGlnThrLeu 179 	Qy 180 ASHThrLeuSerThrProGluGluLySLeuAlaAlaLeuCySLySLySTyrAlaGluLeu 199 	Qy 200 LeugludluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGln 219	Oy 220 LeuValGinGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSer 239	Qy 240 LysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGly 259 	Qy 260 ValGinArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnVal 279	OY 280 ThrLeuasnaspileGinLeuGlnMetGluGlnHisasnGluArgasnSerLysLeuArg 299 	Oy 300 GinGluasmMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArg 319	Oy 320 GluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAla 339	Oy 340 LysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLys 359
Oy 420 LysLyslleLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSer 439	45 14	Oy 460 LeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsn 479	Oy 480 AspieuAsniysArgValGinAspieuSerAlaGiyGiyGiyGirieuThrAspSer 499	QY 500 GlyProGluArgArgPro	Qy 509 GlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyrProGlyAlaPro 528	Oy 529 SerThrGlublaSerGlyGlnThrGlyProGlnGluProThrSerblabrgAla 546	RESULT 18 US-10-616-187-14 Sequence 14, Application US/10616187 ; Publication No. US20040013668A1	; GENERAL INFORMATION: ; APPLICANT: Lees, Ann M. ; APPLICANT: Lees, Robert S. ; APPLICANT: Law, Simon W.	; APPLICANT: Arjona, Anibal A.; TITLE OF INVENTION: OVOEL LOW DENSITY LIPOPROTEIN BINDING; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING; TITLE OF INVENTION: ATHEROSCLEROSIS	; FILE REFERENCE: 10797-004001 ; CURRENT APPLICATION WINBER: 108/10/616,187 ; CURRENT PILING DATE: 2003-07-09 ; PRIOR APPLICATION NUMBER: US/09/616,289	; PRIOR FILING DATE: 2000-07-14 ; PRIOR APPLICATION UNMER: US 09/517,849 ; PRIOR FILING DATE: 2000-03-02 ; PRIOR APPLICATION NUMBER: US 08/979,608	; PRIOR FILING DATE: 1997-11-26 ; PRIOR APPLICATION UNUBER: US 60/031,930 ; PRIOR APPLICATION DATE: 1996-11-27 ; PRIOR APPLICATION UNBER: US 60/048,547	; PRIOR FILING DATE: 1997-06-03 ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 14	LENGTH: 4 TYPE: DNA ORGANISM: FEATURE:	; NAME/KEY: CDS ; LOCATION: (61)(1731) US-10-616-187-14	Alignment Scores: 5.07e-191 Length: 4722 Pred. No.: 2552.50 Matches: 5.08 Percent Similarity: 93.19% Conservative: 12	91.04\$ Mismatches: 91.65\$ Indels: 16 Gaps:

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                    Conservative:
Mismatches:
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    Matches:
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| Publication No. US20030219743A1
| Publication No. US20030219743A1
| GENERAL INFORMATION:
| APPLICANT: Tang, Y. Tom
| APPLICANT: Liu, Chenghua
| APPLICANT: Annail, Vinod
| APPLICANT: Ben, Feiyan
| APPLICANT: Drmanac, Radoje T.
| TITLE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
| TITLE OF INVENTION: Polypeptides
| TITLE OF INVENTION: POlypeptides
| FILE REFERENCE: 792CIP2ADIV
| CURRENT APPLICATION NUMBER: US/10/115,831
| CURRENT FILING DATE: 2000-09-02
| PRIOR APPLICATION NUMBER: 09/667,298
| PRIOR APPLICATION NUMBER: 09/667,298
| PRIOR APPLICATION NUMBER: 09/667,298
| PRIOR FILING DATE: 2000-09-05-18
| WIMBER OF SEQ ID NOS: 178
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28 GluGlyAlaGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly 47		166 LySG1yLeWolyLySGJULLEINTLEONEGGININTLEWASHINTLEWERTHRYPO 185 454TTAGGAAAGGAGTTTTATTACTGATGCAGCCCTAAACACCCTTTCAACCCCCA 507 GGGGGGAGAAGGAGTTTTATTACTGATGCAGCCCTTAACACCCCTTTCAACCCCCA 186 GluGluLySLewAlaalalewCySLySLySTyrAlaGluLewLewGluGluHisArgAsn 205 508 GAGGAGAAGCTGCTGTAAAAATATGCTGATCTTCTGGAGGAGAGCAGGAGT 567 206 SerGlnLySG1nMetLySLewLewGlnLySLySG1nSerGlnLewValGlnGluLySASP 225 11	226 HisLeuargdlyGluHisGerLygalaValLeualaArgSerLysLeuGluSerLeuCys 245	346 GluMetLeuLysGluAlaGluAluGluArgHisGlnArgGluLysAspPheLeuLeuLysGlu 365 ::::::: :::
6868686	8 8 8 8 8	8 6 8 6 8	B G B	6 6 6
	Oy 447 AlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArg 466	1327 GICCTGARAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCGAACAAGGGGGTTTAGCA 490 AlaGlyGlyGlnGlySerLeuThrAspserGlyProGluArgArgProGluGly 1387 ACACCTGTGATGCAGCCCTGTACTGCCCTGGATTCTCACAGGGCTGAACACTTCCTCG 508 ProGlyAlaGlnAlaProSer-SerProArgValThrGluAlaProCysTy 1447 AAAAGAGCCTGGGAGCGCACTGGAGGCTGAGGCCTGGAAGGCGTTGCAA 524 FProGlyAlaPro 528	Db 1507 AAGCCCCGTCCA 1519 RESULT 20 US-09-960-253-172 Sequence 172, Application US/09960253 Sequence 172, Application US/09960253 Sequence 172, Application US/09960253 GENERAL INFORMATION: APPLICANT: Mohamath, Raddh APPLICANT: Mohamath, Raddh APPLICANT: Lodes, Michael J. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.556 CURRENT APPLICATION NUMBER: US/09/960,253 CURRENT PILING DATE: 2001-09-20 NUMBER OF SEQ ID NOS: 197 SOFTWARE: FastSEQ for Windows Version 4.0 SSEQ ID NO 172 LENGTH: 2045 TENGTH: 20	·· · · · · · · · · · · · · · · · · · ·

	61 ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 80	81 AspileLeuSerthrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100	11	115 rTyrvalalaArgAsnGlyGluProGluProThrProValValAsn 130	131GlyglulysGluProSerLysGlyAspProAsnThrGl 143	143 uGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGlu 161 :::	162		TGTGGAGAAGGAGGTGCAGGACTACCAGGCCCTGCTGCTTTGCATTTACAG	188 UG-ILLYSBERMAIGA-IGATGARCCYSPYSBYYANAGLIGUEGUG-IGG-IGG-IGG-IGG-IGG-IGG-IGG-IGG-IGG-	204Argasn 205 777 CCCATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA		837 TTGAAGTAGCACCTGAGTCCTTCACCTTCTCCCATCCCTTCTCTCTC	TCTGCAGCGCTCCTCTAGTAGGCAGACAGCATTCCTTGGGGATGCACAT	232 rLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArg 246 ::::::: 948 GTCTAGGCTTTGCCTAGATATGGCAAGTCTTTGCCAACTGAGGTTGTAT 1001		1002 GTTCTTAGAGGCATTGTTTTTGCCCATTCTTCCCATTTACAAGAGAATCAGGGACACAĞA 1061	247 uleuGlnargHisasnargSerLeuLysGluGluGlyValGln	ArghlaArgGl	TGCTTGCCTTCTTGGGAGCAGATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTC	265 uGluGluGluGlugluyaArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGl 285	285 nLeuGlnWetGluGlnHisAsnGluArgAsnSerLysLeuAr 299	
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GlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSer 	GluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeu 	GlulysGluthrthimetTyzargSerargTrpGluSerSerashlysAlaleuLeuGlu 	MELALIGIUGINATHANALASSELYSGIULEUGIUGIYEUGINVALLYSILEGIN 	ArgieuGluiysLeuCysArgAlaLeuGluThrGluArgAsnAspLeuAsnIysArgVal	3179691478996478990747477177799	GAAGTCCTGAAAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCGAACAGGGATTTA SerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu :::	GCAACACCTGTGATGCAGCCCTGTACTGCCCTGGATTCTCACAAGAGCTGAACACTTCC GlyproGlyalaglmalaproSer-SerproargyalThrGlualaProCy	TCGAAAAGGCCCTGGGAACGCACCTGGAGGCTGAGCCCAAGAGTCAGAGAAAGCGCTGTG	m		108260A	005560Alel full length cDNA				Length: 2194	tive:	Indels: 217 Gaps: 18	08-260A-1586 (1-2194)	MeLiysAsnGinAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSer. 	GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAla 	GGACAACCGGAAGCAGGACCCGAGGGAGCCCAGGAGCGGCCCAGCCAGGCGGC	÷-
386 GlnLeuAlaLeuTyrThrGluLy ::: 1108 CAGCTTTCTCTTTATATGGATAA				466 ArgleuGluLysleuCysArg			1468 GCAACACCTGTGATGCAGCCC 507 GlyPla	1528 TCGAAAAGAGCCCTGGGAGCG	Sigleiceigaideic 	21 18-260A-1586	; Sequence 1586, Application US/10108260A ; Publication No. US20040005560A1 ; Publication No. HILL PERSON TREATMERS ; ADDITIONERS HILL PERSON TREATMERS	GOF INVENTION: No. US200400 REFERENCE: H1-A0106 NNT ADDITIONATION MIMBER 115/1	CURRENT FILING DATE: 00/10/100/2000 NUMBER OF SEQ. 100: 4558	SEQ ID NO 1586	YPE: DNA RGANISM: Homo sapiens -108-260A-1586	Scores:	SCORE: 903.50 Percent Similarity: 47.28%	atch: 32.44%	μ̈́	1 MetLysasnGlnaspLysLys 		126 GGACAACCGGAAGCAGGACCC	
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	MOLEC'SEQUE	Alignment Scores: 1.05e-54 Length: 529 Fred. No.: 805.00 Matches: 154 Score: 100.00\$ Matches: 154 Best Local Similarity: 99.35\$ Masmatches: 0 Query Match: 128.90\$ Indens: 0 DB: 14.054 (1-546) x US-10-040-739-869 (1-529)	1 MetlysasndlnasplystysasndlyalaalalysdlnSerasnProlysSerSerPro 			Qy 81 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAla 100 [1] [Qy 121 GlyGluProGluProThrProValValAsnGlyGluLysGluProSerLysGlyAspPro 140 bb 416 GGGGAGCCTGAACCACTCCAGTAGTCAATGGAGAAGGAACCTCCAAGGGGATCCA 475 Qy 141 AsnThrGluGlulleArgGlnSerAspGluValGlyAspArgAsp 155 bb 476 AACACAGAAGAGATCCGCAGAGTGACGAGGAA 520	RESULT 23. US-09-976-740-51 ; Sequence 51, Application US/09976740 ; Publication No. US20020194633A1 ; GENERAL INFORMATION: ; APPLICANT: Lees, Ann M. ; APPLICANT: Lees, Robert S. ; APPLICANT: Law, Simon W. ; APPLICANT: Arjona, Anibal A.	
299 GGLGCATGTTGTGGTGCTACATGGGAGTCCATCATATCAGATTGAGATGGGGGCTGGG 299 GGLnGludsnWetGluLeuAla	Db 1470 AGAGGGGGACCAGCGGAGAATTTTGTGAGGCTCAGGGCTCAGGGTGGGGG 1529 Qy 361 361 Db 1530 TGGGAGGAGACAGGCTCGGCTCAGCTCATAGCCGGGTTATAGGAAAGTCTG 1589		302	1770 397 1830	QY 417 yswetThr 419 Db 1890 AGTAACT 1897 RESULT 22 INS-10-040-739-869	Seque:	Merberg, David Tracacy, Maurice Spaulding, Vikki TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS NUMBER OF SEQUENCES: 1519 CORRESPONDENCE 1519 JADDRESSEE: Genetics Institute, Inc.	ge husetts A FORM: Floppy Disk FC Compatible TEM: PC-DOS/MS-DOS entin Release #1.0, Version #1.30	\$P\$《《··································

27	<pre>Qy 56 56 Db 2760 TAAAGAAGTIAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAA 2819</pre>	Qy 56 56	Db 2820 TICTGACAGGAACTAGAITTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAA 2879	Oy 56	57	ტ	OY 58 AladinAlaArgThrAladinSerGlyAlaLeuArgAspValSerGludleuSerArg 77	78 GlnLeuGluAspileLeuSerThrTyrCysValAspAshAsnGlnGlyGlyFroGlyGlu 97	AspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrVal 117	118 AlaArdanGivelinProGluProGluProGluProGluProSvelValValAsnGlvEveGluProSevive	3179 GCAAGGAATGGGGAGCCTGAACCCAGTAGTCAATGGAGAAGGAACCCTCCAAG 32	OY 138 GlyAspProAsnThrGluGluIleArgGlnSerAspCluValGlyAspArgAspHisArg 157	Oy 158 ArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGln 177	Qy 178 ThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAla 197	Oy 198 GluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeu 213	3401 AGTCTGTTCTGCCAGGATTCAAAGGAA	Cy	4	US-10-671-242-51 ; Sequence 51, Application US/10671242 ; Publication No. US2004004049A1	TION: s, Ann M.	; APPLICANT: Lees, Robert S. ; APPLICANT: Law, Simon W. ; APPLICANT: Lariona anihal a	/ENTION: NOVEL L	OF INVENTION: ATHEROSCLEROSIS NEFERENCE: 10797-004001	NT APPLICATION NUMBER: US/10/671, NT FILING DATE: 2003-09-24	: US/09/616,28 37-14	
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS	FILE KEFEKENCE: 10/9/-004001 CURRENT APPLICATION NUMBER: US/09/976,740 CURRENT FILING DATE: 2001-112 PRIOR APPLICATION NUMBER: 00/6/616	PRIOR FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: US 08/979, 608	FILING DATE: 1997-11-26 APPLICATION NUMBER: US 60/031,93	PRIOR FILING DATE: 1996-11-27 PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR FILING DATE: 1997-06-03	; NUMBER OF SEQ ID NOS: 53 SOFTWARE: FastSEQ for Windows Version 4.0	SEQ ID NO 51 LENGTH: 22255	ORCANISM: Homo sapiens JS-09-976-740-51	<pre>Length: Matches: Conservative:</pre>	rity: 39.06% Mismatches: 26.59% Indels: 9 Gaps:	JS-10-023-523-44 (1-546) x US-09-976-740-51 (1-22255))y 1 MetLysAenGlnAspLysAsnGlyAlaAlaAlaySGlnSerAsnProLysSerSerPro 20	40	1 4 C C C E	95	b 2280 CICTGCGTTGCCACGGGCAGGGGGGAGCTGTGGGGTCGGCCTCGCTTCTGGACTTAC 2339	b 2340 AGGCCGAGGCCAGGTTGTCCGGGAGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGGC 2399		CGCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTCTAAGCACAGGAACAG	y 56	y 56 56 Y	b 2520 CAGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGT 2579	У 56 56	b 2580 TTGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTTTGTGGGGGGGAAGGAGA 2639		D 2640 IGGACTAGAAGITGCTCCGTGCCATCCCTGTGTGCTGTACCTTTACATACTTTTATGATC 2699	

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3401 AGICIGITCIGCCAGGAITCAAAGGAAAACGGIACTICICAGAGCAGC---AAGICACIC 3457
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; TITLE OF INVENTION: ATHEROSCIEROSIS FILE REFERENCE: 2011-12-17
; FILE REFERENCE: 2011-12-17
; PRIOR APPLICATION NUMBER: US 09/616,289
; PRIOR PILLING DATE: 2000-07-14
; PRIOR FILLING DATE: 2000-07-14
; PRIOR FILLING DATE: 1907-11-26
; PRIOR FILLING DATE: 1997-11-26
; PRIOR FILLING DATE: 1997-11-27
; PRIOR FILLING DATE: 1997-11-27
; PRIOR FILLING DATE: 1996-11-27
; PRIOR FILLING DATE: 1997-06-03
                               2820 ITCIGACAGGAACTAGATTIGCTGAATGATACTCCATTCTIGCTICTCAGITTCCATAAA 2879
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; Sequence 51, Application US/10023529
; Publication No. US20020129388A1
; GRNERAL INFORMATION:
; APPLICANT: Lees, Ann M.
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PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PSELSEQ for Windows Version 4.0
SCOTUD 05 51
LENGTH: 22255
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NUMBER OF SEQ ID NOS: 53 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 251 LENGTH: 22255 TYPE: DNA ORGANISM: Homo sapiens	Oy 57Gly 57 Db 2940 AACCAGGGATATAATCGTCTTCTCACTCTACCCCTCATCCTCTCTCT
9.68e-48 Length: 2 740.50 Matches: 1 40.56% Conservative: 7	78 GlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyGlu
ty: 39.06% Mismatches: 26.59% Indels: 14.9% Gaps:	Cy 98 AspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLySSerArgThrTyrVal 117
44 (1-546) x US-10-023-529-51 (1-22255) MetLysAsnGlnAspLysLysAsnGlyAlaAlaLysGlnSerAsnProLysSerSerPro 20	Oy 118 AlaargasndlyGluProGluProThrProValValasnGluGluLysGluProSerLys 137
2100 ATGAAGAACCAAGACAAAAGAACGGGGCTGCCCAAACAATCCAATCCAAAAAGCAGCCCA 2159 21 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 40 21 ACA CAAAAAACAAGAACAAGAAGAAGAAGAAGAAGAAGAAGAA	Oy 138 GlyaspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArg 157
ValGludlagluGlyProGlySerSerGlnAlaProArgLysProGlu	Oy 158 ArgProGlnGluLysLysAlalysGlyLeuGlyLysGluIleThrLeuLeuMetGln 177
99	Oy 178 ThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAla 197
2280 CTCTGCGTTGCCAGCGGGCAGGGAGGAGGAGGTGGGGGCCGCCTCGCTTCTGGACTTAC 2339	MetLysLeuLeu
AGGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGC	Db 3401 AGTCTGTTCTGCCAGGATTCAAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTC 3457 Qy 214 GlnLysLysGlnSerGln 219
56 56 2400 CGCGTCCCCCCTGCGCTCTGGCGGAGCTGCCCCCTCTAAGCACAGAAAAG 2459	Db 3458 TAGTCTAATCAAAGCCAG 3475
95 95	
, 2460 AGTTCTGGAGAGAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGT 2519	; Sequence 51, Application US/10023523 ; Publication No. US:20020152485A1 ; GENERAL INFORMATION
56 56 56 56 56 56	; APPLICANT: Lees, Ann M. ; APPLICANT: Lees, Robert S. ; APPLICANT: Law, Simon W.
99	Anibal A. NOVEL LOW DENSITY LI
2580 TIGAGGCATITCTAGAATGAICTGAATGGCAAGAAATGGGTTTTTGTGGGGGGGAAGGAGA 2639	VENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND VVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND INCE: 10797-004001
56 56 56 56 56 56 56	; CURRENT APPLICATION NUMBER: US/10/023,523 ; CURRENT FILING DATE: 2001-11-17 ; PRICR APPLICATION NUMBER: US/09/616,289
95	LING DATE: 2000-0' PLICATION NUMBER:
2700 TAACAAATATGTTCGGGTGGTAGTGAGAAATAGTTGTGTCATTTTACAAGTAAACAGACT 2759	; PRICK FILING DATE: 2000-03-02 ; PRICK APPLICATION NUMBER: US 08/979,608 · PRICK FILING DATE: 1997-11-26
99	APPLICATION NUMBER: US 60/031, FILING DATE: 1996-11-27
2760 TAAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAA 2819	; PRIOR APPLICATION NUMBER: US.60/048,547 ; PRIOR FILING DATE: 1997-06-03 ; NUMBER OF SEO ID NOS: 53
TTCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAA	RE: FastSEQ for NO 51
299	22
2880 AAAAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTTGGCTGGGCCTGAAAATCCC 2939	US-10-023-523-51

8 6 8 6 8 6 8 6 8 6 8 6 8 6 8

GCCACC	956 AGTAAACTGAAAGACCTTGCTGATCAATATAACATTACTCAGCAGAAATATGCTCACCAA 1015 327 PheLysHisLysAspLeuGlnGlnGlnLeuValaspAlaLysEeuGlnGlnalaGlnGln 346 1016 TTGAAAGAAAATGTGGAACTTGCTGATCTGAGACTTCAACAACTCAAGAG 1075 347 MetLeuLysGlualaGluGlargHisGlnarGGGLUYSASPPheLeuLuLysGluala 366 1076AAGGCTGCTCAGGAACATACAAATGCAG
3 B S	8 6 8 6 8 6 8 6 8
0y 226 HistenArgdlyGluHisSerLyghlavalteuAlaArgSerLysleuGluSerLeu-Cy 245 Db 189 GACTTGCACAGTGACATAGCACGTACAGACGACACGCACAACCTTGT 248 Cy 245 sArgGluLeuGlarDarGHisAen - ArgSerLeuLysGluGluGluGluArgdlarg 264 249 GAGGAACTTCACAGTTACACGTTACACGTTACAGACACACAC	Alignment Scores: Pred. No., Pred. No., Socre: Socr

257 143

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266 GluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAsplleGln 285
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                                                                                                  198 GCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGCCTCAAGGAATGGGAGCCTGAG
                                                                           Pro---ThrProValValAsnGlyGluLysGluProSerLysGlyAspProAsnThrGlu
                                                                                                                                                    144 GlulleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLys
                                                                                                                                                                                            318 dagarccagaccagrgargargrcgragaccgagaccaccagaggccacagganagaaa
105 AlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys
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                                                                                                                                                                                                                                      164 LysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThr 181
                                                                                                                                                                                                                                                                            378 AAAGCCAAGGCTCTGGGAAAGGANATCACC-----TGCCCCACTTAACTACC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Hyseq_Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REPERBNCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR PLING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PSSESEQ for Windows Version 3.0

SOFTWARE: PSSESEQ for Windows Version 3.0

STATEMENT OF 1999-9
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                       Sequence 18899, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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US-09-918-995-18899
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                                                                                     447 AlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArg 466
                                                                                                                                                                                                                                                 487 AspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArgFroGlu 506
              LysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Infigen Inc.
APPLICANT: Infigen Inc.
APPLICANT: EILERTSEN, KENNETH J.
APPLICANT: EILERTSEN, KENNETH J.
APPLICANT: EILERTSEN, MENTHA
APPLICANT: CHILDS, LYNETTE
APPLICANT: EISHOP, MICHAEL D.
APPLICANTON: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
TITLE OF INVENTION: CELULAR REPROGRAMMING
FILE REFERENCE: 020040-0202
CURRENT APPLICATION NUMBER: US/9/976,143
CURRENT BILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATACTGCGTGGACAACAGTCAAGGGGCCCAAGGTGAGGATGTGGCACAGGGTGAGCCT 197
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                                                  1283 AAGGAGAACGAATTTCTGAAGGGAAAATGTGAGAACTCAGATATTGCTATTGTGAAGCTC
                                                                                                                                                                     467 LeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 SerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 GCTGGAGCCCTCCGTGATGTCTCTGAGGAGTTGAGCCGCCAGCTGGAAGACATCCTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1445 GGCCCCTCCGCCAGTATTCCAGATGCCCCTTCTAGCCAAGAA 1486
                                                                                                                                                                                                                                                                                                                                GlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 520
                                                                                                                                                                                                         ctcaarcccigicaacactacagacagaaaa----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1454, Application US/09876143; Publication No. US20040081958A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1454
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OTHER INFORMATION: n is
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ORGANISM: Bovine
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RESULT 32 US-10-424-599-64592

Semiance 64592. Application US/10424599	Db 646 6AAAAGCGCAAAAGTGCAAAAG
Publication No. US200400310 GENERAL INFORMATION:	174 LeubeuMetGlnThrLeuAsnThrbeuSerThrProGluGluLysLeuAlaAlaLeuCys 19
, APPLICANT: La Rosa Thomas u APPLICANT: Kovalic David K	667
APPLICANT: Cao	eu 21 72
TILLE OF INVENTION: FIGHT BAID USES INCLEDED FOR FILE REPERRINCE: 38-21 (53223)B CURRENT APPLICATION NUMBER: US/10/424,599	214 GlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLys
CURRENT NUMBER O	GCAGAAGAGATGCA 7
5952	Oy 234 AlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg 253
) ORGAN LSM: Glycine max PEATURE:) OTHER INFORMATION: Clone ID: PAT_MRT3847_29338C.1 US-10-424-599-64592	254
Length: Matches:	Oy 274 ThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGlu 293 Db 862 TCAGCCAAGTTTCAAGATGCAATGTCAAGATGTCAGCAATAAGCTTGAGGAGGGAG
43.7/\$ CONSELVATIVE: 26.53% Mismatches: 16.41% Indels: 13 Gaps:	294 922
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Cy 1 MetLysAsnGlnAspLysLys	981
12 LysglnSerAsnProLysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGln 31	Oy 334 GINGINGUVALABPALALYSEGUSIALINIA CALINIA
Db 241 GAGAGTACTACAGAGCCTCTTGCTCCTGCAACTCCATCTCCTGAACAA 288 Qy 32 GluargProSerGlnalaAlaProAlaValGluAlaGluGlyProGly47	Qy 354 ArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCys 373
:::	374
Qy 48 Ser 48 Db 340 TCTAATGAACGATCAAATGATTTGGGAGAAAAAAAGAGTTTCAAAACAATCATGACTCA 399	1131
49 SerGlnAlaProArgiysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeu	
Db 400 GCGGAGAGTCCCTCTAGAAGCTCTATGCAGCAGAAGGGGCACAG	Qy 414 GluMetGluLysMetThrLysLysIleLysLysLeuGluLysGluThrThrMetTyrArg 433
CIGITCCCGAGICTCIGCTGICTGI	434 SerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArg
Oy 89 AspAsnAsnGlnGlyGlyProGlyGlu	H
105	TATGCCGGTCA
BluLys	Qy 474 LeuGlnThrGluArg
622	
134	US-10-425-114-6003;
	; GENERAL INFORMATION: ; APPLICANT: Liu, Jingdong ; APPLICANT: Zhou, Yihua

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112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyPro 501
    |||:::::::::::||||||||:::
760 GCTATTGTGAAGCTCATTGAAGAGCGTGAGCTAACAAAGAAGCAAATAGAAAATTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLys
                                                                                       :::|||:::
580 AACCTGCGGTTGCAACTAGCTTCTGACGGGAAAGATTTCAGCACTTTCAGGATGCCTTG
                                                                                                                                           SerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLys
                                                                                                                                                                                 640 TCAAAAAGCAATGAAGTCTTTGAAACTTACAAGCAGGAGATGGAAAAGATGATTCAGTG
                                                                                                                                                                                                                       IleLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLys
                                                                                                                                                                                                                                                            ATAAAGAATCTTAAGAAGGAGAACGAATTTCTGAAGGGAAAATGTGAGAACTCAGATATT
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                                                                HistoulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 2442 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 467, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PCOOR.
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (398)
OTHER INFORMATION: n
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                                                          APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Wacleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof fo
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION WUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Best Local Similarity:
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LENGTH: 1351
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               169 yLysGluIleThrLeuLeuMet 176
                                           375 GANGAGATCACGTTTGCTGATT 396
                                                                                              US-10-227-577-467; Sequence 467; Application US/10227577; Publication No. US20040005575A1; GENERAL INFORMATION:
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NAME/KEY: misc_feature
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135 GGGGGCCCCGGCGAGGATGGGGCACAGGGTGAGCCGGCTGAACCCCGAAGATGCAGAAGA 194
                                 SerArgThrTyrValAlaArgAsnGlyGluPro-GluProThrProValValAsn---Gl 131
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Matches:
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NAME/KEY: misc feature
LOCATION: (377)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (398)
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Sequence 467, Application US/10091504

Publication No. US20030059908A1

GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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75 AAAGAACGGGGCTGCCAACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAG 134
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SOFTWARE: PatentIn Ver. 2.0
JEANERAL INFOGRATION:

JEANERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C2

CURRENT APPLICATION NUMBER: US/10/227,577

CURRENT FILING DATE: 2002-08-26

PRIOR PILING DATE: 2002-09-76

PRIOR FILING DATE: 2001-01-7

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

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PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-07-26

PRIOR PLING DATE: 20
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Mismatches:
Indels:
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LysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 LyslleGlnArg-LeuGluLysLeuCysArgAla-LeuGlnThrGluArgAsnAspLeuA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 LeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 AAAAAACTGGAAAAAGAAACAATAATTTGGCGNACCAAANGGGAAACCAT-AATAAAGCA
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (712)..(712)
OTHER INFORMATION: n equals a,t,g, or c
  NAME/KEY: misc feature
LOCATION: (616)..(616)
OTHER INFORMATION: n equals a,t,g, or
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US-09-876-143-1445
Sequence 1445, Application US/09876143
Publication No. US20040081958A1
GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (698)..(698)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (668) (668)
OTHER INFORMATION: n equals a,t,g,
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318.00
77.05%
60.66%
                                                                         NAME/KEY: misc feature
LOCATION: (622)
OTHER INFORMATION: n equals
                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (662)..(662)
OTHER INFORMATION: n equals
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LOCATION: (705)...(705)
OTHER INFORMATION: n equals
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Best Local Similarity:
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DB:
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                                                                     150 uValGlyAspArgAspHis---ArgArgProGlnGluLysLysAlaLysGlyLeuGl 169
                  255 AGAGAAGGAACCTICCAAGGGGGATTCCAAACACAGAAGAGATTCCGGCAGAGTTGACGA 314
yGluLysGluProSerLysGlyAsp-ProAsnThrGluGluIle-ArgGlnSer-AspGl 150
                                                                                                          315 AGTICGGAGCAAGGAACCATTCGAAGGCCACAGGAGAAAAAAGCCAAGGTTTTTGGG 374
                                                                                                                                                                                                                       RESULT 37
US-10-264-049-1238

i Sequence 1238, Application US/10264049

i Publication No. US20040005579A1

i GENERAL INFORMATION:

i APPLICAT:

ITTLE OF INVENTION:

I TITLE OF INVENTION:

CURRENT APPLICATION UNDER:

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR RILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: PATENT VOICE AS 1388

LENGTH: 725
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OCATION: (226)..(226)
THER INFORMATION: n equals a,t,g,
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LOCATION: (605)..(605)
DIHER INFORMATION: n equals a,t,g,
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ON: (324)..(324)
INFORMATION: n equals a,t,g,
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OCATION: (339)...(339)
THER INFORMATION: n equals a,t,g,
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OCATION: (290)
VIHER INFORMATION: n equals a,t,g,
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OCATION: (331)...(331)
THER INFORMATION: n equals a,t,g,
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HER INFORMATION: n equals a,t,g,
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LOCATION: (384)..(384)
OTHER INFORMATION: n equals a,t,g,
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OCATION: (546)..(546)
OTHER INFORMATION: n equals a,t,g,
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THER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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DCATION: (320)..(320)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GCTGAACCCGAAGATGCANAGAAGNCCNGGACCTATNCCTCANGGANTGGGNAGCCTGAG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 Pro---ThrProValValAsnGlyGluLysGluProSerLysGlyAspProAsnThrGlu 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 TAGATCCTGTACCAGNGATGAAGTTTGAGACCGANACCACCCAAAGCCNCNGGATANTAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ACATACTGCGTGGACAACAGNNANNGGGGCCCAGGTNAGGATGTGGCANAGGGNGAGCCT 201
APPLICANT: Infigen Inc.

APPLICANT: ELLERTSEN, KENNETH J.

APPLICANT: PPISTER-GENSKOW, MARTHA

APPLICANT: CORSYTHE, TODD

APPLICANT: FORSYTHE, TODD

APPLICANT: BISHOP, MICHAEL D.

TITLE OF INVENTION: CELLULAR REPROGRAMMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGln
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                               FILE REFERENCE: 028040-0202
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/209,874
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1851, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovelic, David K.
APPLICANT: Tabaska, Jack E.
                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1). (981)
OTHER INFORMATION: n is a, c, g, or t
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1744
SOFTWARE: Patentin version 3.0
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62.88%
56.06%
11.24%
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1). (981)
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Courty Match:
DB:
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Bovine
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US-10-425-114-18551
                                                                                                                                                                                                                                                                                                                                                                                    US-09-876-143-1445
                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NO 18551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 GAAACTTACAAGCAGGAGATGGAAAAAAATGATTTTGGTGATAAAAAATCTTAAGAAGGAC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 HisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeu 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 LysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGlu 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TTGTAT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 ThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLysLeuGluLysGlu 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 LysieuCysArgAlaLeuGinThrGluArgAsnAspLeuAsnLysArgValGlnAspLeu 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 GAGCAGAGGGTTGAGTGCATTGCTCAGCTAGAAGAGAACAATATG---TTGAGAAGTAAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 SerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 CICAAAGACATIGCIGAICAGIATAACATIACICAGCAGAAAIAIGCICACCAAITGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 GAGAAAATGATGGAACTTGAGCTTGCTGATCTGAGACTTCAACAACATCAAGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 GCCGAGCAAGTTCTCAGCTTATG---ACTACTGAGAAGAACCTGCGGTTGCAACTAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-023-523-44 (1-546) x US-10-425-114-18551 (1-1035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: LIB3088-030-A1_FLI
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                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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3806 CAAGGCCAGTGCAGAGAAGCTGTGCCGACCTATGAGGATCAGCTAAGCGAGGCCAAGAT 3865
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                                                                                                                                          1371 CGAGCAGCTCTTGGGGGCCCAGATGCAGAAGAAGATCAAGGAGCTGCAGGCTCGGGCGGA 3430
                                                                                                                                                                                                                                                                                                                                                             3476 -------CGTGGAGAAGCAGCGTGCAGAGGCGGCGCGGGAGCTGGAGGA 3517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4046 GGAAAGCAAGGCCAAGAGTGCCCTGGCCCACGCCGTGCAGGCTCTGCGGCACGACTGTGA 4105
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                                                                                    113 -----SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValAsn 130
                                                                                                                                                                                                                                                                                                             131 GlyGluLysGluProSerLysGlyAsp-ProAsnThrGluGlulleArgGlnSerAspGl 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 ulyslystysalalysglyleuglylysglulleThrleuleuMetGlnThrleuAsnTh 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 rLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr------Al 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 aGlubeubeuGluGluHisArgAsnSerGlnbysGlnMetLysLeubeuGlnLysLysGl 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 uGluGluLysArgLysGluValThrSerHis---PheGlnValThrLeuAsnAspIleGl 285
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                                                                                                                                                                                                                                                                                                                                                                                                                          150 uValGlyAspArg------AspHisArgArgProGlnGl 161
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Matches:
                                                      Sequence 95, Application US/10188186
Publication No. US20040029789A1
GENERAL INFORMATION:
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; LOCATION: (87)..(5910)
US-10-188-186-95
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ID NO 95
LENGTH: 6149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                 -10-188-186-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Best Local Similarity: 22.52% Mismatches: 231 Query Match: 10.20% Indels: 185 DB: Gaps: 25 US-10-023-523-44 (1-546) x US-09-927-597-3 (1-5937)	Qy 9 GlyalaalaLysGlnSerAsnProLysSerPerGlyGlnProGlualaGlyProGlu 28	Oy 29 GlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySer 48	Qy 49 SerGlnAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAla 67 :::::	Qy 68 LeuargaspValSerGluGluLeuSerargGlnLeuGluaspileLeuSerThrTyrCys 87	Qy 88 ValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro 107	Qy 108	Qy 113 SerArgThrTyrValAlaArgAsnGlyGluBroGluBroThrProVal 128	Qy 129 ValasnGlyGluLysGluProSerLysGlyaspProasnThr 142	Qy 143 GluGlulleArgGlnSerAspGluValGly-AspArgAspHisArgArgProGlnGluLy 162 :::	Qy 162 sLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLe 182 	Qy 182 uSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGl 202	Qy 202 uHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysGlnSerGlnLeuValGl 222	Qy 222 nGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGl 242	Qy 242 uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnAr 262	Qy 262 galaarggludluglugluLysargLysGluValThrSerHisPh 277	Oy 277 edinValThrLeuAsnAspIleGinLeuGinWetGludinHisAsnGluArgAsnSerLy 297	297 sleuargGlnGluasnMetGlu	
Db 4340 GCGGCTACAGACACAGAGGATGTAACCCTGGAGCTGGAGCGGGCGACCTCAGCAGC 4399 Qy 373 sGluLeuMetLysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLy 393 110 1610 TGCTGCGCTGGACAAGAGCAGCACTTGGAACGGGCACTGGAGGAACGGGCACGCAGA 4459	Qy 393 sPheGluGluPheGlnAsnThrLeu	Qy 402	Qy 412 sGInGlumetGluLysMetThrLysLysLysLysLysLysLysLysLysGluLysGluThrThrMetTy 432	Oy 432 rArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluIysThrVa 452	Oy 452 lArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCy 471	Oy 471 sargAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaG1 491	Qy 491 yGlyGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu 506	Oy 507GlyPr 508	OY 508 0Glyalaglnala	Oy 519 rGludlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyPro 538	RESULT 41 US-09-927-597-3 ; Sequence 3, Application US/09927597	; Publication No. US20030032018Al ; GENERAL INFORMATION: ; APPLICANT: Beraud, Christophe	; APPLICANT: Freedman, Richard ; APPLICANT: Craven, Andrew ; APPLICANT: Sakowicz, Roman ; APPLICANT: Hartman, James	; TITLE OF INVENTION: Human smooth muscle myosin heavy chain ; FILE REFERENCE: CYTOPOIS ; CURRENT APPLICATION NUMBER: US/09/927,597 ; CURRENT FILING DATE: 2001-08-10	; NUMBER OF SEQ ID NOS: 17 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 5937	; TYPE: DNA ; ORGANISM: Human US-09-927-3	Alignment Scores: 1.65e-12 Length: 5937 Score: 284.00 Matches: 150 Percent Similarity: 37.69% Conservative: 101	

GENERAL INFORMATION: APPLICANT: Schlegel, Robert APPLICANT: Chen, Yan APPLICANT: Chen, Yan APPLICANT: Anoham, John APPLICANT: Monaham, John APPLICANT: Manaham, John APPLICANT: Manaham, John APPLICANT: Manaham, John APPLICANT: Manaham, Manjula APPLICANT: Manaham, Manjula APPLICANT: Manaham, Manjula APPLICANT: Glatt, Karen APPLICANT: Hoersh, Sebastian TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: OF CERVICAL CANCER TITLE OF INVENTION: OF CERVICAL CANCER FILE REPERENCE: MRI-035 CURRENT APPLICATION NUMBER: US 60/298,159 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/335,936 PRIOR SEQ ID NO 161 LENGTH: 6861 TYPE: DNA ORGANISM: Homo sapiens US-10-171-31-161	res: 1.95e-12 Length: 284.00 Matches: 37.69% Conserva milarity: 22.52% Indels: 10.20% Gaps:	US-10-023-523-44 (1-546) x US-10-171-311-161 (1-6861) QY 9 GlyAlaAlaLysGlnSerAenProLysSerSerProGlyGlnProGluAlaGlyProGlu 28	Oy 49 SerGinAlaProArgLysProGluGlyAlaGinAlaArgThrAlaGinSerGlyAla 67	Oy 88 ValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro 107	4300 CACCCAGCAGTACGAGGAGGAGGCGGCCGCTTATGATAAACTGGAAAAGACCAAGAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAACAAAGAAAGAACAAAGAAAGAACAAAGAAAA	142	Db 4420 CAACCTGGAAAAGAAGCAAGAAATTTGATCAGTTGTTAGCCGAGGAGAAAACATCTC 4479 Qy 143 GluGlulleArgGlnSerAspGluValGly-AspArgAspHiSArgArgProGlnGluLy 162
10 10 10 10 10 10 10 10	UysMetThrLysLysI)	Oy 442 aLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGl 459	Db 5499 GGAGGAGCTCGAGCAGGAGGAAACAGGCGACCACCAAGTCGCTGAAGCA 5558 Oy 482AsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp 498 Db 5559 GAAAGACAAGAAGCTGAAGGAAATCTT-GCTGCAGGTGGAGGAGGAGGAGGCAAAGTGGCCG 5617 Oy 499SerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSe 514	5618 AGCAGTACAAGGA 514 rSerProArgVal 5678 TGGAGGAGGCAGA	534 yGln	Qy 540 uProThrSerAlaArg 545 	RESULT 42 US-10-171-311-161 ; Sequence 161, Application US/10171311 ; Publication No. US20030087270A1

Qy 459 y	Qy 467 udluLysLeu	499SerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSe ::	Db 5745 TGGAGGAGGAGGAGGAGGAGCATCAACGCAACGAGAAGCTGCAACGCAAGGGG 5804 Qy 534 yGlnThrdlyPro	Oy 540 uProThrSerhlaArg 545	US-10-341-434-102 ; Sequence 102, Application US/10341434 ; Publication No. US20030215835A1 ; GENERAL INFORMATION:	; APPLICANT: OriGene Technologies ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes ; FILE REPERENCE: 9U 204 205 R . CIPDENT APPLICATION MINRED: 18470/341 434	3,16	FILING DATE: 2002-01-15 OF SEQ ID NOS: 238 EE: PatentIn version 3.1		; NAME/KEY: CDS ; LOCATION: (89)(6004) ; OTHER INFORMATION:	ignment Scores: 1.95e-12 Length:	Percent Similarity: 27.69 Generative: 101 Best Local Similarity: 22.52% Mismatches: 231 Query Match: 10.20% Indels: 185		9 GlyalaalaLysGlnSerasnProLysSerSerProGlyGlnProGlualaGlyProGlu 2	Oy 29 GlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySer 48
TTCCAAATACGCGGATGAGAGGACAGAGCTGAGGCAGAAGCCAG 4 SLySLySAlaLySGlyLeuGlyLySGlulleThrLeuLeuMetGlnThrLeuAsnThrLe 1	GGAGAAG	4582 CAAAGAGAACTCGAGGGACCAACAAATGCTCAAAGCCGAAATGGAAGACTGGTCAG 4641 222 nGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGl 242	242 uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGlyValGlnÄr 262	eGlnValThrLeuAsnAspIleGlnLeuGlnWetGluGlnHisAsnGluArgAsnSerLy 2 -::	297 sLeubzgGlnGludsnMetGlu	305 -LeualagluargLeuLysLysLeullegluGInTyrgluLeu 318	319318 318 319 318 319 319 319 319 319 319 319 319 319 319	329 -HisLysAspLeuGlnGlnLeuValAspAlaLys340	341	345 nGluMetLeuLysGlualaGluGluArgHisGlnArgGluLysAspPhele 362 	362 uLeuLysGlualaValGluSerGlnargMetCysGluLeuMetLysGlnGlnGluThrHi 382 :::	382 sLeulysGlnGlnLeualaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSe 402 ::: :::::	402 rLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIl 422 ::::: 5347 GGCCATGAGCGAC	eLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl	442 aLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGl 459

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	RESULT 4 BESULT 4 APPLICATION US/10116802 ; Sequence 14, Application US/10116802 ; Publication No. US20030065157A1 GENERAL INFORMATION: APPLICANT: Amy Lasek TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER ; PILE REFERENCE: PA-0045 US CURRENT APPLICATION NUMBER: US/10/116,802 CURRENT FILING DATE: 2002-04-04 NUMBER OF SEQ ID NOS: 519 SOFTWARE: PERL PROGRAM SOFTWARE: PROBRAM SEQ ID NO: 519 CORGANISM: Home sapiens
49 SerGInAlaProkrgivsProdluGlyAlacinAlaArgTurAlaGinSerGlyAla 67 4120 GGGGGAACAGCTGGAGAGCAGCAGAGAGAGCAGCCAGCAACACAGGGGAAACAGCAG	297 sLeuhrgGlndluAsnMetGlu

	Oy 262 galaargGluGluGluGluLysargLysGluValThrSerHisPh 277	Oy 277 eGInValThrLeuAspIleGInLeuGInMetGluGInHisAsnGluArgAsnSerLy 297	8905 CGAAAGGGATCTCCAAGCCCGGGACGAGCAGTAAGGAGAAAAGGCA	Oy 297 sLeuArgGlnGluAsnMetGlu	Oy 305 -LeualagluargleuLysLysLeullegluGlnTyrgluLeu 318	319	8734 CGACTCTGCCATCAAGGGG	Qy 329 -HisLysAspLeuGlnGlnGlnLeuValAspAlaLys340	Oy 341	Oy 345 nGluMetLeuLysGluAlaGluArgHisGluArgGluLysAspPheLe 362	362		8434	Db 8374 GGCCATGAGCACCGGGTCCGCAAAGCCACAGGGC 8336	Qy 422 eLysLysClulysCluthrThrMetTyrArgSerArgTrpGluSerSerAsnLysAl 442	Qy 442 aLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGl 459	Oy 459 Y	467 uGlulysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeu		Qy 48249nLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp 498	Qy 499SerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSe 514 ::: ::	8036	
PEATURE	NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No: 1382907.35 NAME/KEY: unsure	6438, 6453, 6780 TWATION: a, t, c, g, or other			arity: 22.52% Mismatches: 10.20% Indels: 13 Gaps:		GlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGlyProGlu 28	Glyser	GGAGGA	GCGGAACAGCCTGCAAGACCAGCTGGACGAGAGAGGGCCAAGCAGAACCTGGAGGG 9542 LeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCys 87	ccacatetecacteteaacatecagetetecaaetegaaaagagagagagagegggggggggg	CAGCACCGTGGAAGCTCTGGAAGAGGGAAGGAAGGTTCCAGAAGGAGATCGAGAACCT 9422	AGAACAG	SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProVal 128	AsnThr	nGluLy	sGlyLeuGlyLysG		userThrProGluGluLysLeuAlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluGl 	uValG1	CAAAGGAACTCGAGGGGCCAACAAATGCTCAAAGCGGAAATGGAAGACCTGGTCAG 9080 nghilwsaannislenaragiwghuhisSerlwaAlaVallenAlaArgSerlwsLeuGl	CCTGGA	uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnAr 262

Qy 534 yGlnGlnGl 540 	රු පු	143 GluGluIleArgGlnSerAspGluValGly-AspArgAspHisArgArgFroGlnGluLy 162 ::: 4413 TICCAAATACGC
Oy 540 uProThrSerAlaArg 545 Db 7856 GCAAGCTCAGGCGAGG 7841	, da	162 sLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLe 182 4458 GGAGAAG
Applicati No US200 RMATION: Malik, Fe	6 8 6	182 uSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGl 202
	G & A	
: TITLE OF INVENTION: Human smooth muscle myosin heavy chain; FILE PEFERENCE: CYTOPO18 ; CURRENT APPLICATION NUMBER: US/09/927,597 ; CURRENT FILING DATE: 2001-08-10	& g	242 uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnAr 262
- ~	<i>₹</i> 0 64	262 gAlaArgGluGluGluLySArgLySGluValThrSerHisPh 277 :
	à A	277 eGhnValThrLeuAspalleGlnLeuGlnWetGluGlnHisAsnGluArgAsnSerLy 297
1.93e-12 Length: 283.00 Matches: 38.22% Conservative:	₹ 0	297 sLeuargGlnGluAsnMetGlu
: 22.46% Mısm 10.16% Inde 10 Gaps	à a	305 -LeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeu 318
-10-023-523-44 (1-546) x US-09-927-597-1 (1-5835) 9 GlyalaalaLysGlnSerAsnProLysSerSerProGlyGlnProGlualaGlyProGlu	λό qq	319 328
3984 GGAGCTGCTTCAAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCCAGCT 29 GlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySer	λό d ·	329 -HisbysAspLeuGlnGlnGlnLeuValAspAlaLys340
4044 GGAGGAGGA 49 SerGinAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAla :::::	oy Dp.	341Leuglinglinalagi 345
4053 GCGGAACAGCCTGCAAGACCAGCTGGAACGAGGAGGAGGACCAAGCAAG	& 6 €	345 nGluWetLeuLysGluAlaGluArgHisGluArgGluLysAspPheLe 362
4113 CCACATCTCCACTCTCACATCCAGCTCTCCGACTCGAAGAAGAAGACTGCAGGACTTTGC 88 ValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro	AG GG	362 uLeuLysgluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHi 382
108	Oy Db	382 sLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSe 402
4233 CACCCAGCAGIACGAGGAGGACGCCGCIIAIGAIAAACIGGAAAAGACCAGAAAACAG 113 SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProVal :::	çy D	402 rLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysL1 422
4293 GCTTCAGCAGGAGCTGGACGACCTGGTTGTTGACAACCAGCGGCAACTCGTGTCTCTCATTTGGACAACCAGCGGCAACTCGTGTCTCTCTC	λο D D	422 eLyslysleudlulysgluthrithrMetTyrArgserArgTrpGluserSerAsnlysAl 442 ::::::
Db 4353 CAACCTGGAAAAGAAGGAAAATTGATCAGTTGTTAGCCGAGGAAAAAAACATCTC 4412	λ, , , , , , , , , , , , , , , , , , ,	442 aLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGl 459

Oy 29 GlyalaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySer 48	Db 4111 GGAGGAGGA 411	Oy 49 SerGlnAlaProArgLySProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAla 67	4120 GCGGAACAGCTGCAAGCTGGACGAGGAGAGGAGGAGGCCAAGCAGGAGCTGGAAGC	68 LeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCys	Db 4180 CCACATCTCCACTCTCAACATCTCCGACTCGAAGAGAAGAAGAGGACTGTGG 423: Ov 68 ValAspAsnAsnGlnGlvGlvProGlvGluAspGlvAlaGlnGlvGluProAlaGluPro 107	4240 CAGCACCGTGGAAGCTCTGGAAGAGGGAAGAAGAGGTTCCAGAAGGAGATCGAGAACCT	Oy 108GluAspAlaGluLys 112	Db 4300 CACCCAGCAGTACGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACCAAGAACAG 435	Oy 113 SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProVal 128	Db 4360 GCTTCAGCAGGAGCTGGACGACTGGTTGTTGATTTGGACAACCGGCAACTGTGTC 4419	Qy 129 ValAsnGlyGluLysGluProSerLysGlyAspFroAsnThr 142	::: gaagcagagaaatttgatcagttgttagccgagga	Qy 143 GluGluIleArgGlnSerAspGluValGly-AspArgAspHisArgArgProGlnGluLy 162 :::	162 SLyslysalalysGlyLeuGlyLysGluIleThrLeuLeuWetGlnThrLeuAsnThrLe	4525	Qy 182 uSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGl 202	Db 4532GABACCABGGCCCTGTCCTGGCTCGGGCCCTTGAAGGCCTTGGBAGC 4581			4642 CTCCAAGGATGACGTGGGCAAGAACGTCCATGAGCTGGAGAAGTCCAAGGGGGCCCTGGA	242 uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyVa		Oy 262 galaargGluGluGluGluLysArgLysGluValThrSerHisPh 277	277 eGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLy 297		297 sLeuargGlnGluasnWetGlu304	Db 4867 ACTGCAGAGACATCACGAGTATGAGACGGAACTGGAAGACGGGAAGCGAAAGCAACGTGC 4926	305 -LeuhlaGluhrgLeuLysLysLeulleGluGlnTyrGluLeu	4927 CCTGGCAGCTGCAACAAAAAAAGAAGCTGGAAGGGGACCTGGAAAGACCTGGAAGCTTCAGGC	319	Db 4987 CGACTCTGCCATCAAGGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCTCA 5046	
Db 5379 CCGGCAGCAGCAGCAGCAGCAGAAGAAGCTCCGGAGCAAGCTCCACGAGATGGAGGG 5438	Qy 459 y	Db 5439 GGCCGTCAAGTTCAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCT 5498	uGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeu	Db 5499 GGAGGAGCAGGTCGAGCAGGAGGCCACAGAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCA 5558	Oy 482 4snLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp 498	499SerGlyProGluArgArgProGluGlyProGluGlyBrosee	Db 5618 AGCAGTACAAGGAGGAGAGAAAAGGCAATGCCAGGGTCAAGCAGCTCAAGAGCAGGCAG	Oy 514 rSerProArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerG1 534	DD 5678 IGGAGGAGGAGGAGGAGGAGCGCATCCCAGGCAACGCCAACCGCAGGAAGCTGCAGCAGG 5737	Qy 534 y 534	Db 5738 A 5738	RESULT 46	US-10-171-311-163 ; Sequence 163; Application US/10171311 ; Publication No. US20030087270A1 ; Publication No. USP0030087270A1	; GENERAL INFORMATION; ; APPLICANT: Schlegel, Robert ; APPLICANT: Chen, Yan	; APPLICANT: Zhao, Xumei ; APPLICANT: Monahan, John	APPLICANT: Kamatkar, Shubhangi APPLICANT: Glatt, Karen	u, manjula bastian nor renne compostations vites and Maruche	TITLE OF INVENTION: OF CERVICAL CANCER; TITLE OF INVENTION: OF CERVICAL CANCER	; FILE REFERENCE: MRI-035 CURRENT APPLICATION NUMBER: US/10/171,311	CORRENT FILING DAIL: 2002-00-12 PRIOR APPLICATION UMBER: US 60/298,159 PRIOR FILING DATE: 2001-06-13	PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR FILING DATE: 2010-06-13 PRIOR APPLICATION NUMBER: 113 40.46	FILING DATE: 2001-11-14 OF SEO ID NOS: 238	RE: FastSEQ for W	~ ~	311-163	.2 Length: Matches:	ercent Similarity: 38.22% Conservative:	uery Match: 10.16%	US-10-023-523-44 (1-546) x US-10-171-311-163 (1-6900)	Oy 9 GlyAlaAlaLysGlnSerAsnProLysSerSerProGlyGlnProGluAlaGlyProGlu 28		\$P\$《《··································

PRIOR APPLICATION NUMBER: US/60/235,134 PRIOR FILING DATE: 2000-09-25 PRIOR APPLICATION NUMBER: US/60/235,637 PRIOR APPLICATION NUMBER: US/60/235,638 PRIOR APPLICATION NUMBER: US/60/235,638 PRIOR PILING DATE: 2000-09-26 PRIOR FILING DATE: 2000-09-27 PRIOR PILING DATE: 2000-09-27 PRIOR PILING DATE: 2000-09-27 PRIOR PILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/60/235,840 PRIOR PILING DATE: 2000-09-27 PRIOR PILING DATE: 2000-09-27 NUMBER OF SEQ ID NOS: 2276 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 1602 LENGTH: 3388 TYPE: DNA ONGANISM: Homo sapiens US-09-954-456-1602	Alignment Scores: Pred. No.: 279.50 Matches: Score: Score: Percent Similarity: 38.90% Conservative: 101 Best Local Similarity: 22.99% Conservative: 101 Best Local Similarity: 22.99% Courty Match: 10.04% DB: 10.023-523-44 (1-546) x US-09-954-456-1602 (1-3388) QY 19 SerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgPro 34	Db 1290 GCTCCAGGACATCCTCAAGAAGAAACCCGGCAGAAGCTCA1.	74 1452 94 1512	GAAGGCGCCCTTATGATAACTGGAAAAGACCAAGAACAGCTTCAGCAGGAGCTGGA 16 ArgasnGlyGlubroGlubroThrProvalValAsnGlyGluLysGlu 13
329 -HisLysAspLeuGlnGlnGlnLeuValAspAlaLys		 Gaccgreaagtccaagttcaagtccaccatcgcgc :: Gadgagcaggtcgaggaggccagagaaac asnlysargValGlnAspLeuSerAlaGlyG	AGCAGTACAAGGAGGAGGAGCATCAACGCCAACGCGAGGAAGCTGCAGGGGGGGG	Oy 534 y 534 Db 5805 A 5805 RESULT 47 US-09-954-456-1602 Sequence 1602, Application US/09954456 Patent No. US2020115057A1 GENERAL INFORMATION: PAPPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancy TITLE OF INVENTION: Sets TITLE REPRENCE: 689290-76 CURRENT FILING DATE: 2001-09-18 PRIOR PILICATION NUMBER: US/60/234,052 PRIOR PILICATION NUMBER: US/60/234,052 PRIOR PILING DATE: 2000-09-10 PRIOR PILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: US/60/234,052 PRIOR APPLICATION NUMBER: US/60/234,052 PRIOR APPLICATION NUMBER: US/60/234,923 PRIOR PILING DATE: 2000-09-20 PRIOR FILING DATE: 2000-09-25

us-10-023-523-44.rnpb

Page 46

Oy 486 nAspleuSerAladlyGlyGlnGlySerD. 2898 GGAAATCTT-GCTGCAGGGAGAGAGA Oy 500 yProGluArgArgProGludlyProGlyA Db 2957 CAGAGAAAGGCAATGCAAGGTCAAGCAG Oy 520 uAlaProCystyrProGlyAlaProSerT Db 3017 AGTCCCAGCGCATCAACGCAGG	RESULT 48 US-09-967-768A-245 is Genence 245, Application US/09967768A is Sequence 245, Application US/09967768A is Genence 245, Application US/09967768A is Patent No. US20020150877A1 is GENERAL INFORMATION: APPLICANT A MUGUSTUS, Meena i TITLE OF INVENTION: Cancer Gene Determinn i TITLE OF INVENTION: Cancer Gene Determinn i TITLE OF INVENTION: Cancer Gene Determinn i TITLE OF INVENTION: Cancer Gene Determinn i TITLE OF INVENTION: Cancer Gene Determinn i TITLE OF INVENTION: 2020 CURRENT FILING DATE: 2000-09-28 PRIOR PILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,034 PRIOR PILING DATE: 2000-09-28 PRIOR PILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 i MUMBER OF SEQ ID NOS: 325 i SOFTWARE: PatentIn version 3.0 i SEQ ID NO 245 i LENGTH: 3388 i TYPE: DNA CRGANISM: Homo gapiens US-09-967-768A-245	Alignment Scores: Pred. No.: Score: Score: Printly: Percent Similarity: Best Local Similarity: Cuery Match: DB:	US-10-023-523-44 (1-546) x US-09-967-768A-2v Qy	1392 1392 1452	Oy 94 GlyProGlyGluAspGlyAlaGlnGlyGlu	
1794 GGCCCTGTCCTGGTCGGCCCTTGAAGAGCCCTTGGAAGCCAAAGAGGAACTCGAGCG 1853 208 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 228 1			368 uSerClnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAl 388		GCAGAACAAGGAGCTC	母のはあります。 のは、これでは、これでは、これでは、これでは、これでは、これでは、これでは、これで
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|GAAGCTGCAGCGGGA 3059
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≿	351	aGluGluArgHisGlnArgGluLySAspPheLeuLeuLysGluAlaValGl
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ð	2499	TAGCCTGTCGGGAAGGAACGCACTCCAGGACGACGCCGCCTGGAGGCCCCGGATCGC 2558
≱.	388	aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 408
ð	2559	
<u>≯</u> ,	408	eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 428
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<u>~</u>	428	uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl 447
Д	2658	GCTGGCCACAGAGCGCGCGCGCGGAAAAAAAAGTGCCCGGCAGCAGCTCGAGCG 2717
¥	447	aGluGluLysThrValArgAspLysGluLeuGluGly
ą	2718	GCAGAACAAGGAGCTCCGAGGACTCCACGAGAGGGGGGCCGTCAAGTCCAAGTT 2777
>	460	
д	2778	CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGGAGGTCGAGCA 2837
>-	471	
а	2838	 GGAGGCCAGGAGGAAAACAGGCAGCAGCAAGTCGCTGAAGCAGAAAGACAAGAAGCTGAA 2897
>-	486	nAspLeuSerAlaGlyGlyGlyGlnGlySerLeuThrAspSerGl 500
Ω	2898	
>-	200	YProGluargArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 520
Ω	2957	CAGAGAAAGGCAATGCCAGGTCAAGCAGCTCAAGAGGCAGAGGAGGAGGAGGAGG 3016
>	520	520 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 534
Ω	3017	3017 AGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGA 3059
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279.50
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                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                   US-09-954-531-1382
NUMBER OF SEQ I
SOFTWARE: Paten
SEQ ID NO 1382
LENGTH: 3388
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Sequence 163, App
Sequence 1602, App
Sequence 245, App
Sequence 988, App
Sequence 1382, App
Sequence 85, App
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Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Lew, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
                                                               Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 46, Appl
Sequence 46, Appl
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Sequence 1
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US-09-962-055-17
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US-09-976-740-17
US-10-023-529-17
US-10-023-529-17
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US-09-976-750-71
US-09-977-597-14
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STRET: 225 Franklin Street
CITY: Boston
STATE: NA
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-MODEL-frame+p2n.model -DEV=x1h
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-Q=/Cog12_1/USTPTO_EXPO_1/USIO03523/runat_08062004_063750_29986/app_query.fasta_1.1422
-DEPUDII6hed_Applications_NA -OPYT=fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNIT$=bits -START=1 -BND=-1 -MARTRIX=biosum62
-TRANS-human-10, cdi -LIST=50 -DOCALIGN=20 -THR MCX=100
-THR MIN=0 -ALIGN=50 -MODE=LCCAL -OUTFWT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXTEN=2000000000 -USER=US10023523 GCN 1 1 810 @runat 08052004 063750_29986
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                            8, 2004, 06:37:59; Search time 943.755 Seconds (without alignments) 2561.956 Million cell updates/sec
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2702
1 KSSPGQPEAGPEGAQERPSQ......APSTEASGQTGPQEPTSARA 530
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| cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                       nucleic search, using frame_plus_p2n model
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SUMMARIES

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Query Match Length DB

Score

Result No.

2995936 seqs, 2280998010 residues

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BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext

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Title: Perfect scores. Sequence:

Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of

Searched:

Published Applications NA:*

Jatabase

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1203 AAGATGACTAAGAAGATCAAGAAGAAAGAAAAGAAACCACCATGTACCGGTCGCTGGTGG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 GIGGAIGCCAAGCICCAGCAGGCCCCAGGAGAIGCIAAAGGAGGCAGAAGAGGGGGCACAGA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1143 TTCCAGAACACACTTTCCAAAAGCAGCGAGGTATTCACCACATTCAAGCAGGAGATGGAA 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1383 GAGCGCAATGACCTGAACAAGAGGGTACAGGACCTGAGTGCTGGTGGCCGGGGCTCCCTC 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu
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CGAAGGCCACAGAGAAAAAAAGCCAAGGGTTTGGGGAAGGAGATCACGTTGCTGATG
                                      GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
                                                                                                                                          GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAG
                                                                                                                                                                                                                    603 CAGAGCCAGCTGGTGCAAGAAGGACCACCTGCGCGGTGAGGACACAGCACGTGG
                                                                                                                                                                                                                                                                   AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843 AAGCTGCGCCAAGAGAACATGGAGCTGGCTGAGAGGCTCAAGAAGCTGATTGAGCAGTAT
                                                                          CAGACATTGAATACTCTGAGTACCCCAGAGAGAAGCTGGTGCTGCTGTGCAAGAAGTAT
                                                                                                                AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
                                                                                                                                                                                        GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
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Matches:
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                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-8ep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence
LOCATION: 3...1592
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Best Local Similarity:
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Sequence 17, Application US/09976740

PUDIcation No. US2020194633A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lew Common M.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

TITLE OF INVENTION: NOTEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFRENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT PAPLICATION NUMBER: US 60/01-10-16, 289

FRIOR FILING DATE: 1997-11-26

FRIOR APPLICATION NUMBER: US 60/031,930

FRIOR APPLICATION NUMBER: US 60/031,930

FRIOR FILING DATE: 1997-11-27

FRIOR FILING DATE: 1997-11-27

FRIOR FILING DATE: 1997-11-27

FRIOR FILING DATE: 1997-10-03

SEQUENCE: FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTE
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ORGANISM: Homo
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NAME/KEY: CDS
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                             GGGGCTCAAGCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGG
                                                                                  61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
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LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
                 us-10-023-529-17
Sequence 17, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Abnn M.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW 12-17
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/616, 289
PRIOR FILING DATE: 100-07-14
PRIOR FILING DATE: 100-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
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 Length:
Matches:
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Sequence 17, Application US/10616187

Publication No. US20040013668A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lew, Simon W.

ITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCIENCES

FILE REFERENCE: 10797-004001

CURRENT PAPLICATION NUMBER: US/09/616,289

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PRIOR PLILING DATE: 1997-106-03

NUMBER OF SEQ ID NOS: 53

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; Bediacation No. US2002194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Ann M.
; APPLICANT: Law, Simon W.
; TILLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND THEIR OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TILLE OF INVENTION: ATHEROSCLEROSIS
; TILLE OF INVENTION: ATHEROSCLEROSIS
; TILLE OF INVENTION: ATHEROSCLEROSIS
; FILLE PREPERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT APPLICATION NUMBER: US/09/976,740
; PRIOR FILING DATE: 1097-11-46
; PRIOR FILING DATE: 1997-11-26
; PRIOR FILING DATE: 1997-11-26
; PRIOR FILING DATE: 1997-11-26
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; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-10-30
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.
LENGTH: 1638
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Arbibal A.
TITLE OF INVENTION: PATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION UNMER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR PILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: US/09/616,289
PRIOR FILING DATE: US/09/616,289
PRIOR FILING DATE: US/09/616,289
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Publication No. US20040040049A1
GENERAL INFORMATION:
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US-10-023-529-46
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                                                                       LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLeuIleGluGlnTyr
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                       PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer
                                    APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W
APPLICANT: Law, Simon W
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
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PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FLING DATE: 2000-07-14
PRIOR FLING DATE: 2000-07-14
PRIOR FLING DATE: 2000-03-02
PRIOR PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FLING DATE: 1997-11-27
PRIOR FLING DATE: 1996-11-27
PRIOR FLING DATE: 1996-11-27
PRIOR FLING DATE: 1996-10-37
PRIOR FLING DATE: 1996-10-37
PRIOR FLING DATE: 1997-06-03
NUMBER: OF SEQ ID NOS: 53
SEQ ID NO 46
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APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
FRIOR FILING DATE: 2001-12-17
FRIOR FILING DATE: 2000-07-14
FRIOR FILING DATE: 2000-03-02
FRIOR APPLICATION NUMBER: US 09/517,849
FRIOR PILING DATE: 1090-11-26
FRIOR PILING DATE: 1090-11-26
FRIOR PILING DATE: 1097-11-26
FRIOR PILING DATE: 1097-11-26
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ORGANISM: HOMO
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US-10-023-523-46
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Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
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                                                    GENERAL INCOMMENTATION:

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATTEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR PLING DATE: 2000-03-02

PRIOR PLING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR PLING DATE: 1997-11-26

PRIOR PLING DATE: 1997-11-26

PRIOR PLING DATE: 1997-11-26

PRIOR PLING DATE: 1997-06-03

NUMBER: OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 46

LENGTH: 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
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Conservative:
Mismatches:
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Sequence 46, Application US/10616187
Publication No. US20040013668A1
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2693.00
99.81%
99.81%
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                                              GENERAL INFORMATION:
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Best Local Similari
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, LOCATION: (1)
US-10-616-187-46
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Pred. No.:
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Qy 501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520 Db 1549 AGGCTCACAGAAGGCTTGCTACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACT 1608 Qy 521 GlyProGlnGluProThrSerAlaArgAla 530 Db 1609 GGGCCTCAAGAGGCCCACCTCGCCAGGGCC 1609 GGGCCTCAAGAGCCCACCTCGCCAGGGCC 1638	RESULT 12 US-10-276-74-784 i Sequence 784, Application US/10276774 j Sequence 784, Application US/10276774 j Publication No. US20040053245A1 j GENERAL INFORMATION: APPLICANT: Hyeaq, Inc. TILE OF INVENTION: No. US20040053245A1e1 j TILE REFERENCE: 21272-030 j CURRENT FILING DATE: 2002-11-18 j PRIOR APPLICATION NUMBER: US/10/276,774 j PRIOR APPLICATION NUMBER: 09/560,875 j PRIOR APPLICATION NUMBER: 09/560,875 j PRIOR APPLICATION NUMBER: 09/496,914 j PRIOR FILING DATE: 2000-04-20 j NUMBER: 05 SEQ 1D NOS: 2700	SOTTWARE: Custom SEQ ID NO 784 LENGTH: 25.3 TYPE: DNA ORGANISM: Homo sapiens JOS-10-276-774-784 Length: 2523 Pred. No.: 2533.00 Matches: 529 Pred. No.: 2533.00 Matches: 529 Percent Similarity: 99.81	1 LysserSerProGlyGlnProGludlyProGludlyAlaGlnGluArgProSerGln	Qy 41 GJyAlaGInAlaArgThrAlaGInSerGJyAlaLeuArgAspValSerGluGIuLeuSer 60 Land [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]		Qy 121 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 Db 527 AAGGGGATCCAAACACAGAGATCCGGCAGAGTGACGGAGGTCGGAGACCGAGACCAT 586 Qy 141 ArgArgProGlnGluLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMet 160 Db 587 CGAAGGCCACAGGAGAAAAAAAAGCCAAGGGTTTGGGGAAGGAA
AAGGGGCATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGATA A CAGATGP TO THE COLOR A CAGATGA TO THE	181 AladluLeuleudludlutisArgAsnSerdlnLysGlnMetLysLeuLeudlnLysLys 200 182 AladluLeuleudludlutisArgAsnSerdlnLysGlnMetLysLeuLeudlnLysLys 200 183 AladluLeuleudludlutisArgAsnSerdlnLysGlnMetLysLeuLeudlnLysLys 200 184 GCTGAACTGCTGGGGGGGCACCGGGATTCAAGAGCTCCTACAGAAAAG 648 201 GlnSerdlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220 1	261 PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280 829 TTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACGCACATGAGGGCAATCCC 888 281 LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 300 889 AAGCTGCGCCAAGAGAACATGGACGCTGCGCTGAGAGGCTCAATGAGCAGTAT 948 301 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeu 320 101 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeu 320 302 GluCacagGCGCGGAGGATTCGACAAGGCTGTGAGGAGTGTGAGGAGGTGTGAGGAGGTGGAGGAGGAG	ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet	381 PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 400	421 GluserSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 440	461 GluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeu 480

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NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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REGIGSTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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25
13
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                  e 14, Applic.
No. US20020052033...
No. US20020052033...
APPLICANT: Lees, Ann M.
Lew, Simon W.
Arjona, Antbal A.
Arjona, Antbal A.
Bryons, NOVEL LOW DENSITY LIF
BINDING PROTEINS ANT
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APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
                                 1727 gegeereaagaeceeaecreecaeeaeee
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Tichardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 61...1731
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 GlyProGlnGluProThrSerAlaArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding Sequence
                                                                                                       Sequence 14, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
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STRANDEDNESS: single
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2465.50
92.99%
90.77%
91.25%
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                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston STATE: MA
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                                                                        RESULT 13
US-09-962-055-14
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DB:
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                                                                                                                             GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAG
                                                                                                                                                                                         CAGAGCCACTGGTGCAAGAGAAGACACCTGCGGCGGTGAGCACAGCAAGCCGTCTG
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                                                                                             AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
                                                                                                                                                                    GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu
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                                                    PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer
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## APPLICANT: Lees, Ann M.

## APPLICANT: Lees, Robert S.

## APPLICANT: Law, Sincon M.

## TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

## TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

## TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

## TITLE OF INVENTION: APPLICANTION NUMBER: US/09/976,740

## CURRENT APPLICANTION NUMBER: US 08/979,608

## PRIOR FILING DATE: 1997-11-26

## PRIOR PILING DATE: 1997-11-26

## PRIOR PILING DATE: 1997-11-26

## PRIOR PILING DATE: 1997-11-26

## PRIOR FILING DATE: 1997-11-26

## PRIOR FILING DATE: 1997-06-03

## NUMBER OF SQ ID NOS: 53

## SOOTWARE: FRAESQ for Windows Version 4.0

## SEQ ID NO 14

## LENGTH: 44722
                                                                                      1366 TGGGAGGGGGAACAAGGCCCTGCTTGAGATGGCTGAGGAGAAAACACTCCGGGGACAAA
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400 GluLysMetThrLysLyslleLysLysLeuGluLysGluThrThrMetTyrArgSerArg
                                1306 GAAAAGATGACAAAGAAGATCAAGAAGCTGGAGAAAAGAGACCACCATGTACCGTTCCCGG
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Matches:
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Indels:
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Percent Similarity:
9
Best Local Similarity:
9
Query Match:
9
D8:
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NAME/KEY: CDS
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                                ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyGlyProGly
                                                                                                         286 CGCCAGTTGGAAGACATACTCAGTACATACTGTGTGGACAACAACCAGGGGGCCCCCGGGT
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Publication No. US20040040049A1.
GENERAL INFORMATION:
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US-10-023-523-8 (1-530) x US-09-976-740-14 (1-4722)
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REPRENCE: 10797-004001
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US/9/616,289
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1090-03-02
PRIOR FILING DATE: 1997-11-26
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PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Fastesc for Windows Version 4.0
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| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M.
| APPLICANT: Lees, Ann M.
| APPLICANT: Lees, Ann M.
| APPLICANT: Lees, Simon W. M.
| APPLICANT: Lees, Ann M. M.
| TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
| TITLE OF INVENTION: ATHEROSCLEROSIS
| FILE REFERENCE: 10797-004001
| CURRENT APPLICATION NUMBER: US/10/023,529
| CURRENT APPLICATION NUMBER: 09/616,289
| PRIOR PLING DATE: 2000-01-14
| PRIOR FILING DATE: 2000-01-14
| PRIOR FILING DATE: 2000-03-02
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Publication No. US20020152485A1
GENERAL INFORMATION
APPLICANT: Lees, Ann
APPLICANT: Lees, Robert S.
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  PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: S3
SOUTHARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 4722
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                                                                                                                               TYPE: DNA ORGANISM: Oryctolagus cuniculus
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APPLICANT: Law, Simon W. APPLICANT: Arjona, Anibal A. TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS FILE REPERENCE: 10799-1094001 CURRENT PILING DATE: 2000-12-17 CURRENT PILING DATE: 2000-12-17 PRIOR PILING DATE: 2000-07-14 PRIOR PILING DATE: 2000-07-14 PRIOR FILING DATE: 2000-03-02 PRIOR PILING DATE: 2000-03-02 PRIOR APPLICATION NUMBER: US 09/517,849 PRIOR PILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR PELLING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26	E E E " Z D \ P M	s: ity: larity:	-10-023-523-8 (1-530) x US-10-023-523-14 (1-4722) 1 LysSerSerProGlyGlnbroGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 2	Db 169 CCGCCCCCCCCCGAGAAGGTGCCAGCAGGCCCGGGAGGCCGGAG 225 Qy 41 GlyalaGlnalaArgThralaGlnSerGlyalaLeuArgAspValSerGluGluLeuSer 60 Db 226 GGGGCTCAAGCCAAAACTGCTCAGCGTGGGGGCTCTGTGATGTCTCTGAGGAGCTGAGC 285 Qy 61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyBroGly 80 C CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		120 SerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp 	Db 526 CACCGGGGGGCCACAGGAAAAGAAGGCCAAGGGICIGGGAAAGAGAGAICACGGIGGIG 585 Oy 160 MetGlnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys 179

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406 GTGGCAAGGAATGGGGAGCCGGAGCCGGGCACCCCAGTAGTCAATGGCGAGAAGGAGACC
                                                    160 MetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys
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                                     120 SerlysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp
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APPLICANT: Law, SIMON A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT PEPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
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NUMBER OF SEQ ID NOS: 53
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                                                                                                                               Sequence 14, Application US/10616187
Publication No. US20040013668A1
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92.99%
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
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Qy 91 ProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluProThr 110	Qy 111 ProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArg 130	Oy 131 GlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLys 150	Oy 151 GlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGlu 170	OY 171 GlulysleuAlaAlaLeuCysLysLyrAlaGluLeuLeuGluGluHisArgAsnSer 190	Oy 191 GlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHis 210	Oy 211 LeuargGlyGluHisSerLysRlaValLeualaArgSerLysLeuGluSerLeuCysRarg 230	Oy 231 GluLeuGlnArgHisAsnArgSerLeuLysGluGluGluGlyValGlnArgAlaArgGluGlu 250	Oy 251 GluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspileGlnLeu 270	Qy 271 GlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAla 290	Oy 291 GluargLeuiysLysLeuileGluGlnTyrGluLeuargGluGluHisIleaspLysVal 310	Qy 311 PheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGlu 330		Oy 351 ValGiuSerGlnargMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGln 370	Qy 371 LeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGlu 390	Oy 391 ValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLysLysLeuGlu 410 :::	Qy 411 LysGluThrThrMetTyrargSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet 430	Oy 431 AlaGluGluLysThrValargAspLysGluLeuGluGlyLeuGlnValLysIleGlnArg 450	Qy 451 LeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGln 470
480 LeuThrAspSerGlyProGluArgArgPro	DB 1546 GICICCGACAGCGGICCICAGGGGGGGCCGGCCCCCCCCC	509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla [1] [DB 1886 GCAGGIGCACCAGCACAGGCATCAGGCCAGGGGCCCCAGGAGCCCACCACTGCC 1725 Qy 529 Argala 530 ph 172 Argala 7331	RESULT 19 US-10-115-831-34	<pre>// Sequence 34, Application US/10115831 // Publication No. US20030219743A1 // GENERAL INFORMATION // APPLICANT: Tang, Y. Tom</pre>	Ę.	 ITILE OF INVENTION: NO. USZUGJUZIY/43A181 NUCLEIC ACIDS and TITLE OF INVENTION: POlypetides FILE REFERENCE: 792CIP2ADIV CURRENT APPLICATION NUMBER: US/10/115,831 	CORRENT FILING DATE: 2002-04-02 PRIOR FILING DATE: 2000-09-22 PRIOR FILING LOATE: 2000-09-22 PRIOR APPLICATION NUMBER: 09/577,408	FALOK FILING DATE: Z000-05-18 NUMBER OF SEQ ID NOS: 178 SOUTWARE: PL_Genes Version 2.0 SEQ ID NO 34	N R; ··	; NAME/KET: CDS ; LOCATION: (85)(1554) US-10-115-831-34	<pre>ment Scores: No.: :: int Similarity:</pre>	Similarity: 54.29% Mismacches: h: mismacches: 147.76% Indels: 16 Gaps:	-10-023-523-8 (1-530) X US-10-115-831-34 (1-2356) 13 GlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySer :::	10 GCCGCCGAAGAG	49 CGACGCAGCAGCAGAAGTTTGAAATTGGCACAATGGAAGAAGCTGGAATTTGTGGG 51 AlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyr :::	109 CIAGGGGGTGAAAGCAGATATGTTGTGAACTCTCAATCAATGATGATGATCATCAA 71 CysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGlu 71 CysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGlu 71 CysValAspAsnAsnGlnGlyGlyProGlyGlyGluAspGlyAlaGlnGlyGluBroAlaGlu	DO TO THE TOTAL THE TOTAL CALLEGE AND THE CALL

OY 130 ArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLyslySlysAla 149 Db 394 CGAACAGATCCCCTGATGGTCAGCAAGATTCAGAGTGCAACAAGGAACAAAAAACT 453 OY 150 LysGlyLeuGlyLysGlulleThrLeuLeuWetGlnThrLeuAsnThrLeuSerThrPro 169 Db 454;TTAGGAAAAGATTTATTACTGATGCAAGCCCTTATCACCCCA 507 OY 170 GluGluLysLeuAlaAlaLeuCySLysLysTyalaGluLeuLeuGluGluHisArgAsn 189 OY 17 GluGluLysCaAGAGTCTCTGTAAAAACCTCATACACACA 507 OY 190 SerGlnLysGluMetLysLeuLeuGlnLysLysGlnSerGlnCeuValGlnGluLysAsp 209	568 GTTCAGAAGCAAATGAAGATCCTGCAGAAGAAGCAAGCCCAGATTGTGAAAGAAA	28 30 32 34 34 36 36	1048 GCGACAGAATACGAACAATGAAACGAAACGAAACTAAAAAAC
	508 rProdlyAlapro 512 1507 AAGCCCCGTCA 1519 SULT 20 -09-960-253-172 Sequence 172, Application US/09960253 SEREAL INFORMATION: APPLICANT: Mohamath, Raodoh APPLICANT: Lodes, Michael J. TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210121.56 CURRENT APPLICATION NUMBER: US/09/960,253 CURRENT FILING DATE: 2001-09-20 NUMBER OF SEQ ID NOS: 187 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 172 ENGTH: 2045 TENGTH: 2045 TYPE: DNA ORGANISM: Homo sapiens US-09-960-253-172 Alignment Scores: 4.2e-95 Dred. No.: 1285.00 Pred. No.: 1285.00 Ratches: 284 Percent Similarity: 53.99\$ Mismatches: 39 Owery Match: 47.56\$ Gabs: 8	US-10-023-523-8 (1-530) x US-09-960-253-172 (1-2045) Oy 12 GluGlyAlaGinGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly 31

473 SerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu 490		
::: 1468 GCAACACCTGTGAGCCCTGGATTCTCACAAGAGCTGAACACTTCC 1527	ପ୍ପ	TTCAAGAATCTGAATACCCCCGGTTTTCTCTCCCCGCCAAGGAAAAAAGGA
491 GlyProGlyAlaGlnAlaProSer-SerProArgValThrGluAlaProCy 507	λο O	155 ulleThrLeubeuMetGlnThrLeubsnThrLe 166 ::::
sTyrProGlyAlaPro 512	දු දු	166 uSerThrProGluGlubysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGl 186
DD 1588 CAAAGCCCCCGTCCA 1603 RESULT 21	8	186 uHis
	3 & 	VIOLETTE CONTRACTOR CO
	qa	825 ITGAITITACCTITGAAGIAGCACCTGAGTCCTTCACCTTCTCTCCATCCCTTCTCTCT 884
ER: US/10/108,260A	දු පු	192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212
NUMBER OF SEQ ID NOS: 5458 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1586 LENGTH: 2194	, & A	SerLysL : GATA
PE: DNA GGANISM: Homo sapiens 108-260A-1586	ò	
	q	990 CTAGGCTGTTATGTTCTTAGAGGCATTGTTTTTGCCCATTCTCCCATTTACAAGAGAAT 1049
Pred. No.: 2.68e-57 Length: 2194 Score: 820.50 Matches: 241 Percent Similarity: 45.89% Conservative: 38	ζζ	231GluLeuGlnArgHisAsnArgSerLeuLysGluGlyValGln 245
<pre>y: 39.64% Mismatches: 30.37% Indels:</pre>	ò	245 245
Gaps: -108-260A-1586 (1-2194)	α Ω	1110 GAGTGTGTTTATTGCTTGCCTTCTTGGGAGCAGATTCCATCCA
LysserSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln	& વ	246 -ArgalaArgGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLe 265
	& 4 6	265 uAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAs 279 ::: ::: ::: ::: ::: ::: ::: ::: ::: :
174 GCGGCTCCTGCAGTAGAAGCAGGAGGTCCCGGCAGCCAGGCTCCTCGGAAGCCGGAG 233 41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60	λ _ο α	279 nSerLysLeuArgGlnGluAsnMetGluLeuAla
234 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGC 293 61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80	% da	292 gLeulysLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLy 312
294 CGCCAACTGGAAGACATACTGAGCACATACTGTGAGACAATAACCAGGGGGGCCCGGGC 353 81 GluaspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu 95	y d	312 SHishysAspLeuGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLe 332
354 GAGGATGGGGGCACAGGGGGGGGGGGGGGGGGGGGGGGG	ñ	ulysollulacilollollollollollollollollollollollollol
coaaagraargaargaargaagaaccraagaagagagacccccaaaccaacc	q _Q	
113 1TyrGlyGluLysGluProSerLysGlyAs 123 	À A	1518 TIGGGGGGGGGGGGGAGAGACAGGCTGGGCTCTGGCTCAGCTCATAGCCGGGTTATAT 1577
pProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHrsArgArgPr	8	
	<u>a</u> à	15/8 GGGAGAAGICIGGCCAGACCAGGCACAGAIICCIIGAGIACCAGICIGAGAGCAGGAAGC 183/ 345
143 oGlnGlu		

Page 24

Db 14273 GGCTCAGCTCATAGCCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTT 14332 Qy 345	Cy 346Leuleulys 348 Db 14393 CATAGCCCTGGGGGCTTCTGACAGGATCTGGGGTTCTGGAAATAGCTCCTGAAA 14452	Oy 349 GluhlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLys 368	Oy 369 Gln 369	Qy 369 369 Db 14573 CCTGGGGGTAGTGAAATGGGACCCTCATTCTAGGACTGGCTGTGTCCTGGCTGTGCTATGAC 1463:	Qy 369 369 Db 14633 GCCTTGGTTGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCT 1469:	Oy 369 369 Db 14693 TITGAGGAGGTAGGAACAGAAGAGTITGAAAATCAACATAAAGGCAAAATAAAAGTCACC 14752	Qy 369 369 bh 14762 Charachermerchaldermanachamminganmanachermerchaldanahananacher 14812	369	Db 14813 TGCTTTGTTTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACG 14872	OY 369 369 DD 14873 GGTCTGAGTGTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCT 14932	Oy 370GinleuAlaleuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer 386 Db 14933 TTCTCCCCACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCC 14992	Oy 387 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLys 401	401	15052 GGCCAGGCATGGCTGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCT	Dy 15112 GRAAGTECCAACTGGGGGGGGGGCAGGGCTGTTAGGAAGGTCACCAGCCTTTCC 15171	401	15	401 15232 TCTTTTCTGTTTGTTTTTTTTTTTGGGGGGTTTGTTGTTG	Qy 401 401 b 15292 TGTTTGAGATGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTC 15351	401	Db 15352 ATTGCAGCCTTTGCCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCTGACTAGCTG 15411
Db	357 ysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrTh 		Oy 397 InGluMetGluLysMetThr 403 	RESULT 22 US-09-976-740-51 ; Sequence 51, Application US/09976740	Publication No. US20020194633A1 GENERAL INFORMATION: APPLICANT: Lees, Ann M. APPLICANT: Lees, Robert S.	Law, Simo Arjona, P ENTION: N	FENTION: ATHEROSCLEROSIS ICE: 10797-004001 ICATION NUMBER: US/09/976,740	FILING DATE: ZOUT-ICPLICATION NUMBER: 09/ LING DATE: 2000-07-14	PLICATION NUMBER: US 08/979,60 LING DATE: 1997-11-26	96-1: 96-1: 9ER: 97-0:	NUMBER OF SEQ ID NOS: 53 SOFTWARE: FactSEQ for Windows Version 4.0 LENGTH: 22255	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-976-740-51	ment Scores: No.:	50 Matches: 8% Conservative: 8% Mismatches:	26.70% Indels: 9 Gaps:	US-10-023-523-8 (1-530) x US-09-976-740-51 (1-22255)	Oy 305 GluhisileAspLysValPheLysHisLysAspLeuGlnGlnGlnCeuValAspAlaLys 324 :::	Oy 325 LeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAsp 344	345 Phe	14213 TTTGTGAGGCTCAGGCCCCAGGGTTGGGGGGTGTGGGGAGACAGGCAGG	

	Qy 485 ProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504 bb 16792 CCTGGAGGGCCAGGGGCTGAGGCTCAAGCACCCAGGTCCCCAGGGTCCAAGAA 16851 Qy 505 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlnGlnThrGlyProGlnGlu 524 bb 16852 GCGCTTGCTACCAGGAGCACCAGAAGCATCAGGCCAGACTGGGCCTCAAGAG 16911 Qy 525 ProThrSerAlaArgAla 530 pb 16912 CCCACCTCGGCCAGGGCC ccCACCTCCGCCAGGGCC 16929	RESULT 23 US-10-671-242-51 US-10-671-242-51 Sequence 51, Application US/10671242 Publication No. US20040040049A1 GENERAL INFORMATION: APPLICANT: Lees, Robert S. APPLICANT: Lees, Robert S. APPLICANT: Lees, Robert S. TILLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS TITLE OF INVENTION: ATHEROSCIEROSIS USAGANA APPLICATION NUMBER: US/10/671.242	CURRENT FILING DATE: 2003-09-24 PRIOR APPLICATION NUMBER: US/09/616,289 PRIOR APPLICATION NUMBER: US/09/616,289 PRIOR APPLICATION NUMBER: US 09/517,849 PRIOR FILING DATE: 2000-03-02 PRIOR PILING DATE: 1997-11-26 PRIOR PILING DATE: 1997-11-26 PRIOR APPLICATION NUMBER: US 60/031,930 PRIOR PILING DATE: 1997-11-27 PRIOR APPLICATION NUMBER: US 60/031,930 PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR PILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 28 NUMBER OF SEQ ID NOS: 28 NUMBER OF SEQ ID NOS: 28	Frances 101 minows version 1 22255 Wi Homo sapiens 4.71e-48 Len 721.50 Mat 721.50 Con 11arity: 23.68* Mis 5: 13.70* Gap 13.70* Gap 13.70* Gap Gap 13.70* Gap Gap Gap 13.70* Gap Gap Gap Gap 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
401	TTGGAGACACAGGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGGGCCAGCTCTGA 1 CCATTTCCTTCTGTCTGTCACATAACCTAGATGCTAAGAAGAAGAAGAGAGAG	432 Gludlu	CCAGTGGTAGGTCTCCAGTGGAGTGAAGGGAGCAAATGGAAGAAAAAAAA	16252 GACCTTGCTGAAAGTTTTTTGGGTTTTTTTGCTGCTGAATGTTTTTAGGTA 16311 433

LeuGInGInaliacilowierLeuLysGlualiacilocilakrohisGlualyshsp
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Db 14873 GGTCT	PRIOR FILING DATE: 1997-06-03
Qy 369	; FKIOK FILING DATE: 1996-11-27 ; PRIOR FILING DATE: 1996-11-27 . DETOR EDELITARION NUMBER: 115 60/048 547
Db 14813 TGCTT	AFFLICATION NUMBER: US U8/9/9/9/ FILING DATE: 1997-11-26 ADDITCATION NUMBER: US 60/031
69E	FILING DATE: 2000-03
Db 14753 CTAAG	; PRIOR FILING 2000-07-14 ; DRIOR FILING 2000-07-14 • DRIOR ADDITION NIMBER 113 00/517 840
369	•
Db 14693 TTTGA	; FILE REFERENCE: 10797-017070-0170 CHODENNY ADDITONATION WINDED: 110/10/003 500
369	USE IN DIA
Db 14633 GCCTT	APPLICANT: And January Associated A. Trophometry binners.
369 ·	A APPLICANT Lees, Robert S. ADDITCANT Lees, The Common Manual Common Man
Db 14573 CCTGG	; GULICALIO NO: OSCOZOLEGOSOL. ; GENERAL INFORMATION:
Oy 369	; Selence 51, Application US/10023529
Db 14513 CAACA	RESULT 24
Oy 369 Gln	Db 16912 CCCACCTCCGCCAGGGC 16929
Db 14453 GAGGC	Oy 525 ProThrSerAlaArgAla 530
Oy 349 Glual	Db 16852 GCGCTTGCTACCCAGGGCACCAGAGCATCAGGCCAGACTGGGCCTCAAGAG 16911
Db 14393 CATAG	Oy 505 AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 524
Oy 346	Db 16792 CCTGAGAGGAGGGGCCCTGGGGCCTCAACCACCCAGCCTCCCCCAGGGTCACAGAA 16851
Db 14333 GAGTA	Qy 485 ProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504
Qy 345	Db . 16732 CTGAACAAGAGGGTACAGGACCTGAGTGCTGGTGGCTGGC
Db 14273 GGCTC	Oy 465 LeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlyGlnGlySerLeuThrAspSerGly 484
Qy 34'5	Db 16672 CAGGTAAAAHTCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACAGA
Db 14213 TTTGT	Oy 445 GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp 464
Qy 345 Phe	Db 16612 CACTGAAGGTCTCATTTCTTTCCCTAGAAACAGTCGGGGTAAAAGAACTGGAGGGCCTG 16671
Db 14153 CTCCA	Oy 434
Oy 325 LeuGl	Db 16552 GCCTTGTTAAAGTGTTTGCCGCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGCACGG 16611
Db 14093 CAGCA	Qy 433 433
Oy 305 GluHi	Db 16492 CAIGGCTTCAACTAGGACIGTTTCCTAAAGGGGGCCAGCTTTGGACTCGGTCTGCTCTCA 16551
US-10-023-523-8 (1-	Qy 433 433
Query Macch: DB:	Db 16432 TACGTTATCTCCAAGCCGTGCCCCTTTTCTGCACCATGCTGCCCCACCTGACAGCCTAGT 16491
Best Local Similari	Qy 433 433
Score:	Db 16372 ATGAGACAGGCTCAAAAGTCCATTGCCAAGGTCACGTGGTAGATAAATGGAGGAA 16431
Alignment Scores:	Qy 433 433
US-10-023-529-51	Db 16312 CGTTGTTCATTGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAG 16371
TYPE: DNA	Oy 433 433
SEQ ID NO 51	Db 16252 GACCTTGCTGAAAGTTTTTGGGTTTTTTTTTTTTTTGCTGCTGAATGTTTTTAGGTA 16311
NUMBER OF SEQ ID	Qy 433 433

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isileaspiysvalphelyshisiysaspieuglnglnglnleuvalaspalaiys 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITGAGGCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGGAGACAGGCTGGGCTCT 14272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCTCATAGCCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTT 14332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAGTCTGAGAGCCAGGAAGCCTCAGTGGGTCTGGTGCTTGTGGCTAAAAACCAAA 14392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTGAGAGCATATAACCTGACCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCAT 14572
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                                                                                                                                                                                                                                                   Length: 22255
Matches: 224
Conservative: 1
Mismatches: 1
Indels: 721
Gaps: 4
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Page 28

у 369 369 В 14693 ТТТСАНСАНСАНСАНСАНТНОВАВНОСНАВАНТАВАНТАВАВТОНС 14752	 b 14753 CTAAGTCTCCTACTTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTT 14812	у 369 369	Db 14813 TGCTTTGTTTTAAGGAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACG 14872	14873 GGTCTGAGTGTGTTGACCAGAGTGCCTCCCAGAGAACCCAGTCTTATCTGTGGGCTGCT	370	14933 TTCTCCCCACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCC	y 387 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLys 401	Db 14993 AAAAGCAGCGAGGTATTCACCACTTCAAGCAGAGGAGATGGA-AAAGGTAACTGTGGTCCA 15051	у 401 401	Db 15052 GGCCAGGCATGGCTGCTGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCT	у 401	b 15112 GGAAGCTCCCATCTGGGGTGTCTCAAGGGCTGTTAGGAAGGTTCACAGCCTTTCC 15171	У 401 401	Db 15172 CCTCTTGAGGCAGTATCAGTGTATGTATACACTCCAGGTTGTCCCAGGGAATGGGGCAG 15231	γ 401 401	Db 15232 TCTTTTCTGTTTGGTTTTTTTGGGGGGTTTGTTGTTGTTG		b 15292 IGTITGAGAIGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTC 15351	у 401 401	Db 15352 ATTGCAGCCTTTGCCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCGTGACTAGCTG 15411	у 401 401	Db 15412 GAATTACAGGGGGGGGCCACCATGCCTGGGTAATTTTTTTT	у 401 401	b 15472 TIAGIAGAGGGGTITCACCAIGITGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGT 15531	γ	Db 15532 GATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGG 15591	у 401 401	b 15592 CCCCTTACCATTCCTTATTGGTGGACACCTCTGACTTCCTGGTGGTGAGGTGGC 15651	γ 401 401	b 15652 ACAGAGGGCATTGACTGCATCCTGTAATGCCTTGCGCCTTGGGATCAATCA	у 401	b 15712 TTGGAGACACAGGTGCAGGTCCCCACCTTGGAGACACAGACCTTGGAGAGGCCAGCTCTGA 15771
TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS FILE REFERENCE: 10797-004001	OR APPLICATION NUMBER: US/09/616,289 PER FILING DATE: 2000-07-14 OB ADDITAMINA WINDED: 116 06/617 040	OR FILINGIALOW NUMBER: 2000 - 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	PRIOR FILING DATE: 1997-11-26 PRIOR APPLICATION WANDER: US 60/031,930 PRIOR ETIMO DATE: 1006-11-27		NUMBER OF SEQ 1D NOS: 53 SOFTWARE: FastSEQ for Windows Version 4.0		ORGANISM: Homo sapiens Qy		B Length:	3.78% Conservative: 1	26.70% Indels:	14 Gaps:	-8 (1-530) x US-10-023-523-51 (1-22255)	324		C	Phe	 ptigigaggecocorgagitagggiaggaggigaggagagagagaga	101000000000000000000000000000000000000	GGCTCAGCTCATAGCCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTT 14332		Can an and an analysis of the contract of the	8/110/110/1			349 GIUALAVAIGHUSETCINATGMETCYSGIULEUMETLYSGIAGINGINGINGINGINGINGINGINGINGINGINGINGING			CAACAGGIGAGAGCAIAIAACCIIGACCIIICAAGIIICCCIICACIGGGCCCCCAI		UCTGGGGGTAGTGGAATGGGACUCTCATTUTAGGAUTGGCTGTGTCUTGGUTGCTATGAU	369369

GCCTTGGTAGGAGGATTTGAGAGGATTTTGTAGAGCAAAAAAAA	DD 15532 GATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACTGCCTGG 15591 401
TGCTTTG GGTCTGA TTCTCCC	433
387 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLys	16072 CCAGTGGTAGGTCTCCAGTGGGAGTGAAGGAGCAAATGGAAGAAAGGAATAAAAGGCA 433
15112 GGAAGCTCCCATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCC 15171 401	433
401 401 15292 TGTTTGAGATGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTC 15351	QY 433
ATTGCAGCCTTTGCCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCGACTAGCTG GAATTACAGGCGGGGCCACCATGCCTGGCTAATTTTTTTT	16432 TACGTTATCTCCAAGCCGTGCCCCTTTTCTGCACCATGCTGCCCCACCTGACCAGCCTAGT 433
401 401 15472 TTAGTAGAGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGT 15531	Db 16552 GCCTTGTTAAAGTGTTTGCCGCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGCACGG 16611 Qy 434

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Sequence 1333, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT PEPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                            ValalaargasnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer 120
                                                                                                                                                                                                                                                                                          164 GCGGCTCCTGCAGTAGAAGCAGAAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 AAGGGGGATCCAAACACAGAAGAGATCCGGCAGAGGTGACGAGGAGGAGGAGAGAAAAA 520
                                                                                                                                                                                        1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
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                                       Conservative:
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Matches:
Conservative:
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                                                                                                                                           US-10-023-523-8 (1-530) x US-10-040-739-869 (1-529)
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Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1333
LENGTH: 614
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US-09-833-381-1333
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652.50
83.66%
71.29%
                 713.00
99.28%
98.56%
26.39%
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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DB:
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                                                                                                                                                  LeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGly
                   16612 CACTGAAGGTCTCATTTCTTTCCCTAGAAACAGTCCGGGATAAAGAACTGGAGGCCCTG
                                                                                                                                                                                                                                  ProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu
                                                                GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp
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Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
NUMBER OF SEQUENCES: 1119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: -CURNOWn>
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 869:
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    APPLICATION UNDRER: 09/036,520
    FILING DATE: 03-UNV-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 869, Application US/10040739
Publication No. USZ0020173635A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                          16912 CCCACCTCCGCCAGGGCC 16929
                                                                                                                                                                                                                                                                                                                                                                                                      525 ProThrSerAlaArgAla 530
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TYPE: nucleic acid
STRANDEDNESS: double
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LaVallie, Edward
Racie, Lisa
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INFORMATION FOR SEQ ID NO: 869
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ZIP: 02140
COMPUTER READABLE FORM:
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150 LysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrPro 169

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	90	Qy 170 GluGluLysLeuAlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsn 189	Db 69 CACCACAANCTGGCAGCTCTCTGTAAGAATATGCTGATCTTCTGGAGGAGCAGGAGT 128	Qy 190 SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAsp 209	DD 129 GTTCAGAAGCAAATGAAGATCCTGCAGAAGAAGCAAGCCCCAGATGTGTGAAAGAAGTT 188	Oy 210 HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu-Cy 229	189 CACTIGCAGAGTGAACATAGCAAGGCTATCTTGGCAAGAAGCAAGC	229 sardlilenGlnArdHisAsnArdSerLeilvsGluGlvValGlnArd	S.Z.S. PALE GENERAL STREET, S. S. S. S. S. S. S. S. S. S. S. S. S.	CAGAGAACTTCAGCGTCACAATTAAGACCGTTAAAGGAGGAAAATA1GCAGCAAAAA	Qy 249 GluGluGluGluUu-LysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspI1 268	Db 309 GAGGAAGAACAACGTAAAGAACCAACTGCACATTTCCAGATTACCTTAAATGAAAT 368	Oy 268 eGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGl 288	Db 369 TCAAGCCCAGCTGGAGCAGCATGACATCCACAAAGCTCCGACAGGAAAACATTGA 428	Ov 288 uLeuklaGlukraLeuLvsLvsLeulleGluGlnTvrGluLeukrgGluGluHisIleAs 308	429 GCTGGGGGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAGAGC	308		327	549	RESULT 29	US-10-425-114-32431 ; Sequence 32431, Application US/10425114		APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua	, APPLICANT: Kovalic, David K. , APPLICANT: Screen, Steven E	APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei		FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114		; SEQ ID NO 32431 ; LENGTH: 1955	, TYPE: DNA , ORGANISM: Zea mays		US-10-425-114-32431	2.22e-31 Length:	501.00 Matches: milarity: 46.30% Conservat	rity: 28.60% Mismatches: 18.54% Indels:	13 Gaps:	US-10-023-523-8 (1-530) x US-10-425-114-32431 (1-1955)	

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334 CACTIGCAGAGTGAACAIAGCAAGGCTATCTIGGCAAGAAGCAAGCIAGAAICTCTIIGC 275
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                                                                                                                                                                       69 ThrTyrCysValAspAsnAsnGlnGlyGlyBroGlyGluAspGlyAlaGlnGlyGluPro
                                                                                                                                                                                                           138 ACATACTGCGTGGACAACAACAGTGAGGGGCCCCAGGTGAGGATGTGGCCACAGGGTGAGCCT
                                                                                                                                                                                                                                                                                                                         198 GCTGAACCCGGAAGATGCAGAGAAGTCCCGGACCTATGCCTCAAGGAATGGGGAGCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                           Pro---ThrProvalvalTyrGlyGluLysGluProSerLysGlyAspProAsnThrGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 GAGATCCGGACCAGTGATGAAGTCGTAGACCGAGACCACCGAAGGCCACAGGANAAGAAA
                                                                                                             78 GCTGGAGCCCTCCGTGATGTCTCTGAGGAGTTGAGCCGCCAGCTGGAAGACATCCTCAGT
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 334
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18899, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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91.89%
78.38%
17.17%
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Best Local Similarity:
Query-Match:
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Pred. No.:
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ValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLlysLeuGlu 410
                                                                                  LeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGlu 390
                                                                                                                                                                                                                                                                                                                   411 LysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet 430
                                                                                                                                                                                                                                                                                                                                                                                                                                431 AlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArg 450
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APPLICANT: Infigen Inc.
APPLICANT: BILBERGEN, KENNETH J.
APPLICANT: PFISTER-GENSKOW, MARTHA
APPLICANT: CHILDS, LYNETTE
APPLICANT: CHILDS, LYNETTE
APPLICANT: EISHOP, MICHEL D.
APPLICANT: BISHOP, MICHEL D.
APPLICANT: BISHOP, MICHEL D.
APPLICANT: DENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
TITLE OF INVENTION: CELULAR REPROGRAMMING
FILE REFERENCE: 028040-0202
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/209,874
PRIOR APPLICATION DATE: 2001-06-06
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LOCATION: (1)...(937)

OTHER INDERMATION: n is a, c, g, or t

US-09-876-143-1454
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Publication No. US20040081958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1744
SOFTWARE: Patentin version 3.0
SEQ ID NO 1454
LENGTH: 937
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ORGANISM: Bovine
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rGluLeuArgGluGluHisIleAspLys 3	131 GlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysAlaLys 1
Db 94 GGGGAGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAGCACATTGATAAG 35	GABAAGGGCAAAAGTGCAAAAG
Oy 310 ValPheLysHisLysAspLeuGlnGlnGlnHeu 320	Qy 151 GlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGlu 170 Dh. 667GGTACTTTAATGA.
54 GIGILCACACATANGGACCIGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	171 GluLysLeuAlaAlaLeuCysLysLysTyr
10-4 eque	Db 685 AAGGAGCTTTTAGAATTTACACTGAAGTACCAACAAGTGTTG726
; Publication No. US20040031072A1 ; GENERAL INFORMATION:	Qy 191 GlnLysClnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHis 210
; APPLICANT: La Rosa Thomas J ; APPLICANT: Kovalic David K	Db 726 726
# APFILCANT: Investment Cao Vinite Applicant Cao Vinite Compared Fig. 11TLE OF INVESTMENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVESTMENTION: Soy Nucleic Acid Molecules and Other Tenomography.	Oy 211 LeudrgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArg 230
	231 GluLeuGlrArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAla
CURRENT FILING DATE: 2003-04-28 UNDMBER OF SEQ ID NOS: 285684	Db 781 GAGTTACAACGCCAAAATAAAATGCTGATGGAAGAATGCAAAACGTGTATCAACTGAGGGG 840
; SEQ ID NO 64592 ; LENGTH: 1696	
ileb: DNA ; OPENISM: Glycine max	AT 90
; FEALUNE: ; OTHER INFORMATION: Clone ID: PAT_MRT3847_29338C.1 US-10-424-599-64592	Qy 271 GlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAla 290 :::::
7 Length: Matches:	291 GluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHislleAspLysVal
ercent Similarity: 44.66% Conservative:	
16.82% Indels: 13 Gaps:	Qy 311 PhelysHisLysAspLeuGlnGlnGlnClnLeuValAspAlaLysLeuGlnGlnAlaGlnGlu 330
US-10-023-523-8 (1-530) x US-10-424-599-64592 (1-1696)	331 MetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAla
9 AlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGlu 28	1080
268 GCAACTCCATCTCCTGAACAAGAAACCCCTGAATAGTTACAAGGATGAT	Qy 351 ValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGln 370
Oy 29 GlyProGly	-TTACGGTTGCAA 1
32	Qy 371 LeualaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGlu 390
4,	391 ValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLysLeuGlu
46 ThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAsp	DD- 1227 ATTTTGAAACATTCAAACAAGAGATGAGAAGATGGCAAAATCAATC
4 d 8 1	411 LysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet
481 TCTCTGCTGTCGAGGTAAATGAGGAACAAGAAGAAGAAGGCAAAGTTCA	1287
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Qy 111 ProvalValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArg 130	OY 465 LetAshLySArgyalcin 4/0
Db 645 645	
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326 GlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPhe 345
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                                                                                                       ----TIGTATGCTGAACAAGTTTCTCAGCTTATG---ACTACTGAGAAG
                                                                                                                                                                      874 ------CAAGGCCCTCCGCCAGTATTCCAGATGCCCCTTCTAGCCAAGAA 918
                                                                              LeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThr
                                                                                                                                                  366 HisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu
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GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869; CURRENT APPLICATION NUMBER: US/09/764,869; CURRENT APPLICATION ADDICATION OF THE PROOF SEQ ID NOS: 2442; NUMBER OF SEQ ID NOS: 2442; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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ORGANISM: Homo
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LOCATION: (377)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 SerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGlu 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 CAATACCACAAAGTGGTTGCAGAAAGGGATCAAGCCATTGCAGTCAAAGATAGACTAGAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 SerleuCysArgGluLeuGlnArgHisAsnArgSerleuLysGluGluGlyValGlnArg 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGlu 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 TCTCTTTGTAGGGAATTTCAGCGTCAAACAAAATGCTAAAGGAAGAGGAGGCCAAAGGGTA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsn 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AsplieGinLeuGinMet---GluGinHisAsnGluArgAsnSerLysLeuArgGlnGlu 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HislleAspLysValPheLysHisLysAspLeuGlnGlnLeuValAspAlaLysLeu 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AAATATGCTCACCAATTGAAAGAGAAATGCTGGAACTTGAACTTGCTGATCTGAGACTT 492
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: 700550751_FLI
JS-10-425-114-6003
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50.13%
31.40%
16.45%
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ORGANISM: Zea mays
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Best Local Similarity:
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                                                                                                                                                                                                                                                                   SEQ ID NO 6003
LENGTH: 1351
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	Oy 134 uValGlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGl 153	Oy 153 yLysGluIleThrLeuLeuMet 160 Db 375 GANGAGATCACGTTTGCTGATT 396	RESULT 36 US-10-227-577-467 ; Sequence 467, Application US/10227577 ; Publication No. US20040005575A1 ; Publication No. US20040005575A1	; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies ; FILE REFERENCE: PCO07C2 ; FILE APPLICANT ANAMADD 1001000	CURRENT APPLICATION NUMBER: US/10/22/,5// ; CURRENT FILING DATE: 2002-08-26 ; PRIOR APPLICATION NUMBER: 10/091,504 ; PRIOR FILING DATE: 2002-03-07 ; DRIOR PILING NUMBER: 00/074,804	PRIOR AFFLING DATE: 2001-01-17 PRIOR PLING DATE: 2001-01-17 PRIOR APPLICATION NUMBER: 60/179,065 PRIOR FILING DATE: 2000-01-31 PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04,886 PRIOR PILING DATE: 2000-06-28	; PRIOR APPLICATION NUMBER: 60/217,487 ; PRIOR FILING DATE: 2000-07-11 ; PRIOR PILING DATE: 2000-08-14 ; PRIOR FILING DATE: 2000-08-14 ; PRIOR APPLICATION NUMBER: 60/220,963		מבפ נוופ אושלהפי סו) FEATURE: NAME/KEY: misc feature LOCATION: (377) DOTHER INFORMATION: n equals a,t,g, or c LOCATION: (398) LOCATION: (398) COTHER INFORMATION: n equals a,t,g, or c US-10-227-577-467	Alignment Scores: 6.48e-20 Length: 405 Pred. No.: 350.00 Matches: 83 Score: 79.03\$ Conservative: 4 Best Local Similarity: 75.45\$ Mismatches: 17 Query Match: 12.95\$ Indels: 6 DB: 16 Gaps: 2 US-10-023-523-8 (1-530) x US-10-227-577-467 (1-405)	Oy 57 GludluLeuSerArgGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGln 76
Qy 57 GludluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln 76 :::	77 GlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLys	97 SerArgThrTyzValAlaArgAsnGlyGluPro-GluProThrProValValTyrGl 	115 yGluLysGluProSerLysGlyAsp-ProAsnThrGluGluIle-ArgGlnSer-AspGl 	Oy 134 uValGlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGl 153	Qy 153 yLysGluIleThrLeuLeuWet 160 Db 375 GANGAGATCACGTTTGCTGATT 396	RESULT 35 US-10-091-504-467 ; Sequence 467, Application US/10091504 ; Publication No. US20030059908A1 ; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; APPLICANT: Rosen et al.	091,504 le Wrapper or Palm	; SEC IN NO 467 ; LENGTH: 405 ; TYPE: DNA ; ORGANISM: Homo sapiens	FEATU NAME/ LOCAT OTHER NAME/ LOCAT	US-10-091-504-467 Alignment Scores: 6.48e-20 Length: 405 Fred. No.: 350.00 Matches: 83 Forcent Similarity: 79.09\$ Conservative: 4 Best Local Similarity: 75.45\$ Mismatches: 17 Ouery Match: 12.95\$ Indels: 6 DB: 25\$	US-10-023-523-8 (1-530) x US-10-091-504-467 (1-405) QY 57 GluGluLeuSerArgGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGln 76 :::	Oy 97 SerArgThrTyrValAlaArgAsnGlyGluPro-GluProThrProValValTyrGl 115

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367 LeuLysGinGinLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 LyslysleuGlulysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 LeulysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGluThrHis 366
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Matches:
Conservative:
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LOCATION: (698)..(698)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
 LOCATION: (553)..(553)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (712)..(712)
CTHER INFORMATION: n equals a,t,g,
US-10-264-049-1238
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LOCATION: (616)..(616)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (668). (668)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (662)..(662)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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NAME/KEY: misc feature
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LOCATION: (705)..(705)
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Best Local Similarity:
Query Match:
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                                               97 SerArgThrTyrValalaArgAsnGlyGluPro-GluProThrProVal---ValTyrGl 115
GGGGGCCCCGGCGAGGATGGGGCACAGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAG 194
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                                                                                                                                                                                                       315 AGTICGGAGCAAGGGAACCATICGAAGGCCACAGGAGAAGAAAAAAGGCCAAGGITTITIGGG 374
                                                                                                                                           255 AGAGAAGGAACCCTCCAAGGGGGATTCCAAACACAGAAGAAGATTCCGGCAGAGTTGACGA 314
                                                                    TCCCGGACCTATGTGGCAAGGAATGGGGGAGCCTTGAACCAACTTCCAKTAGTTCAATTGG
                                                                                                                115 yGluLysGluProSerLysGlyAsp-ProAsnThrGluGluIle-ArgGlnSer-AspGl
                                                                                                                                                                             134 uValGlyAspArgAspHis---ArgArgProGlnGluLysLysLysAlaLysGlyLeuGl
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LOCATION: (546)..(546)
THER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
FEATURE:
NAME/KX: misc feature
LOCATION: (226)..(226)
OTHER INFORMATION: n equals a,t,g, or
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OCATION: (290)...(290)
THER INFORMATION: n equals a,t,g,
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LOCATION: (324)..(324).
NTHER INFORMATION: n equals a,t,g,
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LOCATION: (384). (384)
OTHER INFORMATION: n equals a,t,g,
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AAME/KEY: misc_feature
ACATTON: (120).. (320)
OTHER INFORMATION: n equals a,t,g,
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THER INFORMATION: n equals a,t,g,
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OCATION: (339).
THER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Muleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-425-114-18551
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55.75%
34.51%
11.27%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 TAGATCCTGTACCAGNGATGAAGTTTGAGACCGANACCACCCAAAGCCNCNGGATANTAA 381
                                                                                                           APPLICANT: Infiger inc.
APPLICANT: Infiger inc.
APPLICANT: ELERTSEN, KENNETH J.
APPLICANT: ELLERTSEN, KENNETH J.
APPLICANT: CHILDS, LYNETTE
APPLICANT: CHILDS, LYNETTE
APPLICANT: RORSYTHE, TODD
APPLICANT: BISHOP, MICHAEL D.
APPLICANT: RORSYTHE, TODD
APPLICANT: BISHOP, MICHAEL D.
APPLICANT: CHILDS, LYNET BISHOP, TITLE OF INVENTION: CELLULAR REPROGRAMMING
FILE REPRESENCE: CS05040-020.
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT FILING DATE: 2001-06-06
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; Sequence 18551, Application US/10425114
; Publication No. US20040034888A1
                                              Sequence 1445, Application US/09876143
Publication No. US20040081958A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/209,874
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 1744
SOFTWARE: Patentin version 3.0
SEQ ID NO 1445
LENGTH: 981
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LOCATION: (1). (981)
OTHER INFORMATION: n is a,
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Best Local Similarity:
Query Match:
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ORGANISM: Bovine
                                -09-876-143-1445
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372 275 392 335 432

452 515 551

Db 4425 GGATGAGAGGACAGAGCTGAGGCAGAAGCCAGGGAGAAG 4464	Oy 152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172 Db 4465GAAACCAA 4472	Oy 172 sLeuhlaAlaLeuCysLysTyrAlaGluLeuCleuGluGluHisArgAsnSerGlnLy 192 11.	232 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGl 232 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGl 232 uGlnArgHisAsnArgGaAgaGrGaAGGGGAGAGGGGGGGGGGGGGGGGGGGG	Db 4758 TCTCCAAGCCCGGGACGAGAAGAAGAAGAAGAGAGACGACTGCAACTGAAGACAACTTCA 4817 Qy 287 tGlu		Qy 325	Qy 352 uSerGlnArgMetCysGluLeuMetLysGlnGlnThrHisLeuLysGlnGlnLeuAl 372	Qy 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysCl 412 Db 5293	Oy 431 aGluGluLysThrValArgAepLysGluLeuGluGly
Db 552GGCCGCTCCGCCAGTATTCCAGACGCCCCTTCTAGCCAAGAAGACATGCCA 602	Oy 493 GlyalaGlnalaProSer 498	64465	### PFPLICANT: Haterman, James TITLE OF INVENTION: Human smooth muscle myosin heavy chain FILE REFERENCE: CYTOP018 FILE REFERENCE: CYTOP018 CURRENT APPLICATION WURBER: US/09/927,597 CURRENT FILING DATE: 2001-08-10 NUMBER OF SEQ ID NOS: 17 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: PASTSEQ for Windows Version 4.0 SOFTWARE: DATE: DATE: USASTS CORPORATION: Human US-09-227-597-3	Alignment Scores: 4.85e-13 Length: 5937 Pred. No.: 282.50 Marches: 153 Score: 38.48\$ Conservative: 101 Best Local Similarity: 23.18\$ Mismatches: 229 Query Match: 10.46\$ Indels: 27 DB:	-10-023-523-8 (1-530) x US-09-927-597-3 (1-5937) 3 SerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgPro :::	4026 TACGAAGCTGCCCAGCTGGAGGAGGAGGGGAGAGCGGAAGAGAGGGGAGGAGGAGGA	4131 78 4191 92	103 Argash	Db 4371 GAGGAAATFTGATCAGTTGTTAGCCGAGGAGAAAACATCTCTTCCAAATACGC 4424 Qy 133 ASpGluValGly-AspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe 152

. 1	୍ ପୁପ	TACGAAGCTGCGCCAGCTGGAGGAGGAGGAGCGGAACAGCCTGCAAGA
CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCA	ò	ProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu
455CysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGl 470 	e &	4138 CCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTGGAGCGCCACATCTCCACTCTCAA 4197 58 GlutenSerArdGlutenGlutenGlutenGlutenGlutenSerThrTvrcVsValAspAspAspAspGlutenGlv 77
nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGl	੍ਹੇ ਰੂ	CATCCAGCTCTCCGACTCGAAGAAGCTGCAGGACTTTGCCAGCACCGTGGAAGCTCT
	ò	78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro91
yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl	୍ପ (GGAAGAGGAAGAAGAGGTTCCAGA
503.0 CAGARGARANGGCARIGCCAGGGICARGCICARGCAGGCAGGCAGGCAGGCAGGCAGGGGGGGGGG	à a	4318 GAAGGCGCCGCTTATGATAAACTGGAAAAGACCAAGAACAGGCTTCAGCAGGAGCTGGA 4377
GATGAGGCCACGG	õ	103 ArgAsnGlydluProGluProThrProValValTyrGlydluLysGlu 118
520ThrGlyProGlnGluProThrSerAlaArg 529	셤	4378 CGACCTGGTTGTTGGACAACCAGCGGCAACTCGTGTCCAACCTGGAAAAGGA 4437
5756 AGAGCAACGAGGCCATGGGCGAGGTGAACGCACTCAAAAGCAAGC	8 8	ProSerLysGlyAapProAsnThrGluGluIleArgGlnSer
	8 &	4438 GAGGAAATTTGATCAGTTGTTAGCCGAGGAAAAAACATCTTTCCAAATACGC 4451 133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe 152
Publication No. US20030087270A1 GENERAL INFORMATION:	qa	
	<i>&</i> :	uGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172
APPLICANT: Monahan, John APPLICANT: Kamatkar, Shubhangi	q Q	GAAACCAA
APPLICANT: Glatt, Karen APPLICANT: Gannavarapu, Manjula APPLICANT: Hoersh, Sebastian	ያ	172 SLeualaalaLeuCySLySLySTyralaGluLeuLeuGluGluHisArgAsnSerGlnLy 192
OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF INVENTION: OF CERVICAL CANCER	ठे ह	192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212
FILE KEFEKENCE: MALOUSS CURRENT APPLICATION NUMBER: US/10/171,311 CURRENT FILE 2002-06-12	8 8	gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232
AFFLICATION NUMBER: 0.0 00/230,153 FILING DATE: 2001-06-13 APPLICATION NUMBER: US 60/298,155	ପ୍ଧ	4660 CAAGAACGICCAIGAGGAGAAGICCAAGGGGGCCCIGGAGACCCAGAIGGAGGAAT 4719
FILING DATE: 2001-06-13 APPLICATION NUMBER: US FILING DATE: 2001-11-14	දු පු	232 uGlnargHisAsnArgSerLeuLysGluGlyValGlnArgAlaArgGluGluGluGl 252 ::::
NUMBER OF SEQ ID NOS: 238 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 161. IRNGTH: 6861	\$ 6	252 uLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAs 267 :
	8 6	
res: 5.75e-13 Length: 282.50 Matches:	3 & 1	tGlu
Local Similarity: 23.18% Mismatches: 229 Local Similarity: 10.46% Indels: 178 15 Gaps: 27	3 & f	SLysLeulleGluGlnTyrGluLeu
US-10-023-523-8 (1-530) x US-10-171-311-161 (1-6861)	<u>a</u> .	GAAGAAGCIGGAAGGGGACCIGAAAGACCIGGAGCIICAGGCCGACILIGCCATCAAGGG
SerProGlyGlnProGluAlaGlyProGluGlyAlaGluArgPro	중 : 점	505 AGGGAGGAGGAGGAGCTACGAGCTACGAACTGCAGGCTCAGATGAAGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
4036 GCTCCAGGACACCCAGGAGCTGCTTCAAGAAACCCGGCAGAAGCTCAACGTGTC 4092 19 SerGlnalaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 38	8	318 nGlnLeuValAspAlaLys 324

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BAGCTGCTTCAAGAAGCCCGGCAGAAGCTCAA---CGTGTC 4092
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|TIGGACAACCAGCGCAACTCGTGTCCAACCTGGAAAAGAAGCA 4437
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:GGGCCCTTGAAGAGGCCTTGGAAGCCAAAGAGGAACTCGAGCG 4599
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rcgaagaagctgcagactttgccagcaccgtggaagctct 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTTCCAGAAGGAGATCGAGAACCTCACCCAGCAGTACGAGGA 4317
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AGGGACAGAGCTGAGGCAGAAGCCAGGGAAGAAG----- 4531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GluAspAlaGluLysSerArgThrTyrValAla 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GlyGluProGluProThrProValValTyrGlyGluLysGlu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgasphisargargProGlnGluLysLysLysAlaLysGlyLe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seuleuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yslysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192
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                                                                                                                                                                                                                                                                          aValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 38
                                                                                                                                                                                                                                                                                                                                                           nAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                               eugluAspileLeuSerThrTyrCysValAspAsnAsnGlnGly 77
                                                                                                                                                                                         luala------GlyProGluGlyAlaGlnGluArgPro 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yAlaGlnGlyGluProAlaGluPro------
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Db 5823 AGAGCAACGAGGCCATGGGCCGAGGTGAACGCACTCAAGAGCAAGCTCAGGCGAGG 5880	RESULT 43 US-10-116-802-14/c ; Sequence 14, Application US/10116802 ; Publication No. US20030065157A1 ; GENERAL INFORMATION: ; APPLICANT: Amy Lasek ; TILLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER ; FILE REFERENCE: PA-0045 US ; CURRENT APPLICATION NUMBER: US/10/116,802 ; CURRENT APPLICATION NUMBER: US/10/116,802	PRIOR FILING DAME: 60/281,593 PRIOR FILING DAME: 60/281,593 NUMBER OF SEQ ID NOS: 519 SOFTWARE: PERL Program SOFTWARE: PERL Program ILENGTH: 11665 PERGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No: 1382907,35	FORMATIC 2-14 ores: ores: imilarity: imilarit	US-10-023-523-8 (1-530) x US-10-116-802-14 (1-11065)	39 ProGludlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu	Oy 78 GIAPTOGIVOLUARSPGIYALAGINGIYGIUPTOALAGIUPTO	Db 9343 CGACCTGGTTGTTGGACAGCGGCAACTCGTCTCAACCTGGAAAAGAACCA 9284 Oy 119 ProSerLysGlyAspProAsnThrGluGluIleArgGlnSer 132 Db 9283 GAGGAAATTTGATCATTTAGCCGAGGAAAAAACATCTTCTACCAAATACCC 9230 Oy 133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysLysLysRalaLysGlyLe 152
252 uLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAs 267 	piledinieudinMetdiudinHisasngluargasnSerLysLeuargdinGluasnMe 2	4945 GARGAGGGGACCTGAAAGACCTGAAGGCTCTGGGCGACTCTGCGATCAAGGG 5004 303 -ArgGluGluHistleAspLysValPheLysHisLysAspLeuGlnGl 318	5125 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTATGÀAĠĠĠACCTGCGCGCCGC 5184 335 aGluGluhrgHisGlnArgGluLysAspPheLeuLeuLysGluhlaValGl 352	5305 CCAGCTGGAGGAGGAGGAGGAGGCCAACATGGAGGCCATGAGGACCAC 5359 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 412 5360		CysargalaLeuGlnThrGluargasnaspLeuAsnLysargValGl GGAGGCCAGAGAGAAAACAGGCGCCACCAAGTCGCTGAAGCAGAAAGACAAGAAGCTGAA nAspLeuSerAlaGlyGlyGlyGlyGlySerLeuThraspSerGl ::::::	484 yProGluArgArgProGluGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504

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152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuAsrThrProGluGluIly 172			372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerILysSerSerGluValPh 392

Oy 352 uSerdlnArgMetCysGluLeuMetLysGlnGlnDrHisLeuLysGlnGlnLeuAl 372		Qy 444	5577 GGAAATCTT-GCTGCAGGACGAGCGCAGAGATGGCCGAGCAGTACAGGAGGCAGG 484 yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 5636 CAGAGAAAGGCAATGCCAGGTCAAGCAGCTCAAGAGGCAGCAGGAGGCAGGAGGCAGGAGGCAGAGGCAGGCAGGCAGAGGCAGGCAGAGGCAGGCAGAGGAG		APPLICANT: Zhao, Xumei APPLICANT: Zhao, Xumei APPLICANT: Kamatkar, Shubhangi APPLICANT: Kamatkar, Shubhangi APPLICANT: Glatt, Karen APPLICANT: Glatt,	CURRENT APPLICATION NUMBER: US/10/171,311 CURRENT FILING DATE: 2002-06-12 PRIOR APPLICATION NUMBER: US 60/298,159 PRIOR PILING DATE: 2001-06-13 PRIOR PILING DATE: 2001-06-13 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR APPLICATION NUMBER: US 60/395,936 PRIOR APPLICATION NUMBER: US 60/335,936 PRIOR PILING DATE: 2001-11-14 NUMBER OF SEQ ID NOS: 238 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 163 LENGTH: 6900 TYPE: DNA CORDANISM: Homo sapiens US-10-171-311-163
GlýProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro	3 ASpGluValG1y-Sapargasplateroglubroflings and a spGluValG1y-SG1y-SG1y-SG1y-SG1y-SG1y-SG1y-SG1y-S	4425	192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212 1533 GACCAACAAAAATGCTCAAAGCCGAAATGGAAGACCTGGTCAAGGTCCAAGGATGACGTGGG 4592 212 gGlyGluHisSerLysAlaValLeuArgSerLysLeuGluSerLeuCysArgGluLe 232 1593 CAAGAACGTCCATGAGAGTCCAAGCGGCCCTGGAGACCAAGAGAT 4652 232 uGlnAvGHisAsanArgSerLeutysGluGluGlyValGlnArgAlaArgGluGluGl	GAAGACGCAGCAGAAAGGCTGGAAGACGCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGCCAGAAGCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCCAAAGGCCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCCAAAAGGCCAAAAGGCCAAAAGGCCAAAAGGCCAAAAGGCCAAAAGGCAAAAAGGCCAAAAAA	4758 TCTCCAAGCCCGGGACGACAATGAGAAAGGAGGGAGCAACTGCAGAGACACTTCA 4817 287 tGlu	303 -ArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGl 318 4938 GAGGAGGAGCATACGCAAACTGCAGGCTCAGATGAAGGACTTCAAAG 4997 318 nGlnLeuValAspAlaLys

8 6 8 6 8 6 8 6 8 6 8 6 8 6

1	318 nGlnLeuValAspAlaLys	5185 TGAGAGGCTCGCAAACAAGGAACCTCGAGAAGGAGGAAACTGGCAGAGGAACTGGCAGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	392 eThrThrPheLysGlnGluMecGluLysMetThrLyssysllebustyLyslebustuLysGl 4 3360CGGGTCCGCAAAGCCACACAGGCCGAGCAGCAGCAGCACACAA 5 412 uThrThrMetTyrArgSerArgTrpGluSerSerAshLysAlaLeuLeuGluMetAl 4 5404 GCTGGCCACAGAGCGCACACGCCCAGAAGAATGAGAGTGCCCGGCAGCAGCAGCGG 5 431 aGluGluLysThrValArgAspLysGluLeuGluGly		0y 484 yProGluhrgArgProGluGlyProGlyAlaGinAlabroSerSerProArgValThrGl 504
Jansent Scores: 6.99e-13 Length: 6900	4036 GCTCCAGGACCCCAGGAGCTGCTTCAAGAAGAAACCCGGCCAGAAAGATCAAGATOLU 4092 19 SerGINAlaAlaProAlaValGluAlaGluGlyProGlySerSerGINAlaProArgLy8 38 19 SerGINAlaAlaProAlaValGluAlaGluGlyProGlySerSerGINAlaProArgLy8 38 10 SerGINAlaAlaProAlaGluAlaGAGGAGGAGGAACAGGCTGCAAGA 4137 39 ProGluGlyAlaGluAlaArgThrAlaGluSerGlyAlaLeuArgAspValserGlu 57 11	22 77 27	103 ArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGlu 118	152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172 4532GAAACCAA 4539 172 sLeuAlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192 172 sLeuAlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192 1840 GGCCCTGTCCCTGGCTCGGGCCTTGAAGAGCCTTGGAAGCGAACAGAGCGAGGG 4599 192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212 185 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212 186 GACCAAAAAACCCTAAAAGCGGAAAACGAGCTCGCTCGAGGAGAGCGTGGG 4659	212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232 232 uGlnArgHisAsnArgSerLeuLysGluGluGluGlyValGlnArgAlaArgGluGluGluGluGl 252 332 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluGl 252 332 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgArgCCCCGAGGCCCCAA 4773 4720 GAAGACGCAGCAGGAGGACGAGSerHisPheGlnValThrLeuAsnAs 267 252 uLysArgLysGluValThr

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133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe 152
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                                                                                  152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy
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                                          ------GGATGAGAGGGACAGAGCTGAGGCAGAAGCCAGGGAGAG--
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GCTCCAGGACACCCAGGAGTTGCTTCAAGAAGAAACCCGGGCAGAAGCTCAA---CGTGTC 1346
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Matches:
                               CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PLING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PELING DATE: 2000-09-26
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ORGANISM: Homo sapiens
US-09-954-456-1602
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Best Local Similarity:
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78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro	1746GATGAGGACAGAGCTGAGGAGAGGGAGAAGCAGGGAGAAGCAGGGAGAAGCAGAGGAAGAA	192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr	1974 GAAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCGGAGGACGCCAA 2027 252 uLysArgLysGluValThr	287 2139 294 2199	303 2259 318	2319 AGAGCTGGAAGATGCCCGTGCCTCCAGAGATGAGATCTTTGCCACAGACCAAAGAAATGA 325
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	504 3017 SULT 47 -09-967-768 Sequence 245 Patent No. 1	TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu; TITLE OF INVENTION: Sets; TITLE OF INVENTION: Sets; CREENT APPLICATION NUMBER: US/09/967,768A; CREENT FILING DATE: 2001-09-28; PRIOR APPLICATION NUMBER: US/60/236,109; PRIOR FILING DATE: 2000-09-28;	FALOR FILING DATE: 2000-09-28 NUMBER OF SEQ ID NOS: 325 SOFTWARE: Patentin version 3.0 SEQ ID NO 245 LENGTH: 3388 TYPE: DATE: YPPE: DATE: Patentin version 3.0 CRANISM: Homo sapiens US-09-967-768A-245 US-09-9	res: 5.26e-13 Length: 278.50 Matches: arity: 38.90% Conservative mlarity: 22.99% Mismatches: 10.31% Gaps: Gaps: 22.99% Mismatches: 10.31% Gaps: Arity: 22.99% Mismatches: Arity: 23.99% Mismatches: Arit	US-10-023-523-8 (1-530) x US-09-967-768A-245 (1-3388) Qy	

Best Local Similarity: 22.99\$ Mismatches: 225 Query Match: 10.31\$ Indels: 164 DB: 9 Gaps: 25	US-10-023-523-8 (1-530) x US-09-954-531-988 (1-3388)	Qy 3 SerProGlyGlnProGluAlaGlyProGluGlyAlaGluGluArgPro 18.	Db 1290 GCTCCAGGACACCCAGGAGTTGCTTCAAGAAAGAAACCCGGCAGAAGCTCAACGTGTC 1346	SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys	1347 TACGAAGCTGCGCCAGCTGGAGGAGGAGGAGCGGAACAGCCTGCAAGA	Sy Floction ()	58 GluLeuSerArgGlnLeuGluAspileLeuSerThrTyrCyşValAspAsnAsnGlnGly 77	Db 1452 CATCCAGCTCTCCAACTCAAAGAAGAAGCTGCAGCACCTTTGCCAGCACCTCT 1511	Qy 76 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro 91	Db 1512 GGAAGAGGAAGAAGAGGTTCCAGAAGAGAGATCGAGAACTTCACCCAGCAGTACGAGA 1571	Oy 92GluaspalaGluLysSerArgThrTyrValAla 102	Db 1572 GAAGGGGCGCTTATGATAAAACTGGAAAAGACCAAGAACAGGCTTCAGCAAGAGCTGGA 1631 Ov 103 ArgashGlvGluFroGluFroThrProValValTvrGluGluGvsGlu 118		Oy 119 ProSerLysGlyAspProAsnThrGluGluIleArgGlnSer 132	Db 1692 GAGGAAATTTGATCAGTTGTTAGCCGAGGAGAAAAACATCTCTTCCAAATACGC 1745	Qy 133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLe 152	Db 1746GdATGAGAGGAGAGCTGAGGCAGAAGCCAGGAAAAG 1785	152 uGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy	Db 1786GAAACCAA 1793 Oy 172 sheuAlaAlaLeuCySLysLysTyTAlaGluLeuLeuGluGluHisArqAsnSerGlnLy 192	1794	Oy 192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212	Db 1854 GACCAACAAATGCTCAAAGCCGAAATGGAAGACCTGGTCAGCTCCCAAGGATGAGGTGGG 1913	Cy 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232	1914 CAACAACCATCCATCCATCGATCAAGAAGTCCACCCCCTCGAAGAACCATCCAT	OY 25Z MOIDARGHISABRARGSSETJEULASKALUGIJUGIJVALGIRARGALAGATGAGALGGAGALUGIJUGI 25Z 11:1:1	Oy 252 ulysArgLysGluValThrSerHisPheGlnValThrLeuAsnAs 267	Db 2028 ACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCCAGTTCGAAAGGGA 2078	267 piledinLeuGlinMetGluGlnHisAsnGluArgAsnSexIysLeuArgGlinGluAsnMe 287	6707	d 	
Cy 352 uSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAl 372	Oy 372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392	Db 2559 ccagcregadadeargeadeageadeageadeargeagecargadeargeagecargadeargeage	Oy 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 412	Db 2614CGGGTCCGCAAAGCCACACAGGCGGGCGAGCAGCTCAGCAACGA 2657	uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl	431	2718 GCAGAACAAGGTCCGGAGCAAGCTCCAGAAGTGAAGGGGGGGG	Oy 444 454	Db 2778 CAAGTCCACCATCGCGGCGTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCA 2837	Oy 455CysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGl 470	Db 2838 GGGGCCAGAGAGAAAAAAGGCGACCAAGTCGCTGAAGCAGAAAGACAAAAGTGAA 2897	Oy 470 nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGl 484 :::::::::	484 yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl		Oy 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 518	Db 3017 AGTCCCAGCGCATCAACGCCAAGGAAGCTGCAGGGA 3059	RESULT 48 US-09-954-531-988	; Sequence 988, Application US/09954531 ; Patent No. US20020165180A1	O	TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77		PRIC	PRIOR FILING DATE: 2000-09-20 PRIOR PELING TOWNER: US/60/234,034	PRIC	PRIOR FILING DATE: 2000 PRIOR APPLICATION NUMBER PRIOR FILING DATE: 2000	SOFTW	TENCETT NO YES TO THE TENCETT OF THE TENCET	ORGANI 3-09-954-	Scores:	Fred. No.: 5.2be.13 Length: 5388 Score: 278.50 Matches: 146 Percent Similarity: 38.90% Conservative: 101	* * * * * * * * * * * * * * * * * * *

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1290 GCTCCAGGACACCCCAGGAGTTGCTTCAAGAAGAAACCCCGGCAGAAGCTCAA---CGTGTC 1346
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1572 GAAGGCGGCCGCTTATGATAAACTGGAAAAGAACAAGAACAGGCTTCAGCAGGAGCTGGA 1631
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| GGAAGAGGGGAAGAAGAAGGAGTICCAGAAGGAGATCGAGAACCTCACCCAGCAGTACGAGGA 1571
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Matches:
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                  2319 AGAGCTGGAAGATGCCCGGGCCTCCAGAGATGAGATCTTTGCCACAGCCAAAGAGAATGA 2378
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                                                                                                         303 -ArgGluGluHisIleAspLysValPheLys------HisLysAspLeuGlnGl
                                                                                                                                                                                                                                                                        2379 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTCATGCAGCTACAAGAGGACCTCGCCGCCGC
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                             ----GlnTyrGluLeu-
                        sLysbeulleGlu-----
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1854 GACCAACAAAATGCTCAAAGCCGAAATGGAAGACCTGGTCAGGTCCAAGGATGACGTGGG 1913	212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232 ::::::: 1914 CAAGAACGTCCATGAGAGAGTCCAAGGGGCCCTGGAGACACCCAGAGAGAT 1973	252	1974 GAAGACGCAGCTGGAAGACTGGAGGACGACGAGGCTGCAAGCCTCGGAGGACGCCAA 2027	252 uLysarglysgluvalthrSerHisPheglnValthrLeuAsnAs 267	267 pileGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGinGluAsnMe 287	tGluLeuAlaGluArgluArgluArgluArgluArgleuLy		294 sLysLeulleGluGlnTyrGluLeu	303 -ArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGl 318	2259 GAGGGAGGAAAGCCATCAAGCTACGCAAACTGCAGGCTCAGATGAAGGACTTTCAAAG 2318	nGlnLeuValAspAlaLys	AGAGCTGGAAGATGCCCGTGCCTCCAGAGATGAGATCTTTGCCACAGCCAAAGAGAATGA	325	aglugubraHisglubraGlufwsbsrbhsfaufaufwsglublaValgl	TGAGAGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGGAGGAGCTGGCCAG 2498	372	2499 TAGCCTGTCGGGAAGGAACGCACTCCAGGACGAGGAGGCCCGCCTGGAGGCCCGGATCGC 2558	372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392	412	2614	412 uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl 431 5.: :: ::	agluglutvsThrValArdAsptvsGlufeuGluglv443	GCAGAACAAGGAGCTCCCGGAGCTCCCACGAGATGGAGGGGCCGTCAAGTT 2777	454	2778 CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGGAGGTCGAGGA 2837	455CysargalaLeuGlnThrGluArgAsnAspLeuAsnLysargValG1 470	2897	nAspLeuSerAladlyGlyGlyGlnGlySerLeuThrAspSerGl 484	2898 GGAAATCTT-GCTGCAGGTGGAGGAGGGGCAAGATGGCGGAGGAGTACAAGGAGCAGG 2956
DP DP	S S S	ò	Db	Oy Db	yo da	3 &	연	λ Q Q	à	QQ	۲۵ :	ΩÞ	à é	à à	연	<i>λ</i> ο	qq	S S S	ò	ପ୍ର	ر ك بر	3 8	40 10 10 10 10 10 10 10 10 10 10 10 10 10	δ	QQ	δ.	QQ	& 1	a a

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APPLICANT: Young, Paul
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Bodgess, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Carter. Reinhard
APPLICANT: Carter. Reneth
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION WIMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR PLLING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PLLING DATE: 2000-09-29
PRIOR PLLING DATE: 2000-01-01
PRIOR FILING DATE: 2000-01-01
PRIOR FILING DATE: 2000-01-01
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NUMBER OF SEQ ID NOS: 1067
SEQ ID NO 85
LEAGTH: 3388
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LEAGTH: MANAGER: DATE: DATE
LEAGTH: BASE
                                1290 GCTCCAGGACACCCAGGAGTTGCTTCAAGAAACCCGGCAGAAGCTCAA---CGTGTC 1346
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1452 CAICCAGCTCTCGAAGAAGAAGCTGCAGGACTTTGCCAGCACCGTGGAAGCTCT 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1392 ccagcricaccagangarganganaccaaaccagagaccaccarcricacricicaa 1451
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484 yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 ProGluGly---AlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SerproGlyGlnPro-----GluAlaGlyProGluGlyAlaGlnGluArgPro 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro--------
                                                                                                                                                  3017 AGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGA 3059
                                                                                                 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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09-873-367C-85
equence 85, Application US/09873367C
bblication No. US20030165839A1
ENERAL INFORMATION:
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22.99%
10.31%
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ORGANISM: Homo sapiens
)9-873-367C-85
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: Local Similarity:
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Argasn	1786	303 - ArgGludluHisTleAspLysvalPheLysHisLysAspLeudAnd1 2259 GAGGGAGAHACTCAGCAAACTGCAAACTGAAAGAGCTCAAAGAACTGCAAACTGCAGGCTCAGATGAAGAACTGAAAGAACTGAAAGAACTGAAAGAACTGAAAGAACTGAAAGAACTGAAAGAACTTCAAAGA 318 nGlnLeuValaspalaLys	372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh

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&	392	392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 412
qa	2614	
òy	412	uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl 431
Ор	2658	2658 GCTGGCCACAGAGGGCGCACGGCCCAGAAGAATGAGAGTGCCCGGCAGCAGCTCGAGGG 2717
ζŏ	431	431 aGluGluLysThrValArgAspLysGluLeuGluGly
ДQ	2718	GCAGAACAAGGAGCTCCGGAGCAGCTCCACGAGATGGAGGGGGCCGTCAAGTCCAAGTT 2777
ολ	444	
qq	2778	2778 CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGGTGGAGGAGGAGGAGGGTCGAGCA 2837
δλ	455	CysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValG1 470
Db	2838	2838 GGAGGCCACAGAGAAACAGGCAGCACCAAGTCGCTGAAGCAGAAAGAA
ŏ	470	470 nAspLeuSerAlaGlyGlyGlyGlnGlySerLeuThrAspSerGl 484
Ωp	2898	GGAAATCTT-GCTGCAGGTGGAGGACGAGCGAAGATGGCCGAGCAGTACAAGGAGCAGG 2956
ò	484	484 yProGluArgArgProGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504
qq	2957	CAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAGAGGCAGCTGGAGGAGGCAGAGGAGGAGG 3016
~	504	504 uAlabroCysTyrProGlyAlaProSerThrGluAlaSerGly 518
Db	3017	3017 AGTCCCAGCGCATCAACGCCAAGGAAGCTGCAGCGGGA 3059

Search completed: June 8, 2004, 13:13:40 Job time : 1129.75 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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8, 2004, 06:37:58 ; Search time 3868.11 Seconds - nucleic search, using frame_plus_p2n model June OM protein Run on:

(without alignments) 4091.647 Million cell updates/sec US-10-023-523-8 2702 1 KSSPGQPEAGPEGAQERPSQ......APSTEASGQTGPQEPTSARA 530 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect scored Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

em_esthum:*
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em_estmu:*
em_estov:* em_estpl:, em_estro.; em_htc:* gb_estl:* gb_est2:; gb_est3:* gb_est4:* gb_est5:* em_estba:* em_estom: gss

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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t)		3	1413	3010	2853	2842	3520	271	2088	5250	1799	1454	1195	5991	9580	5123	3463	3590	2709	1421	7018	2800	3346	3102	2413	144	160	559	7771	1960	1848	5534)288	CD578468	1388	083	ממי	0000	7070	0000	, v	7007	200	2000	100	2007	440/	9330	4717	100	0
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Result No.	1,111	· -	7	·	4	U	9	7	80	ο 0																								33									4. 4		r L					4, r	

ALIGNMENTS

RESULT 1 AK031783 LOCUS DEFINITION

AK031783

Mus musculus 11 days embryo head cDNA, RIKEN full-length enriched library, clone:6230424F16 product:hypothetical protein, full insert seguence

GI:26327606 AKO31783 AKO31783.1

ACCESSION VERSION

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KVEVLKEQVSIKAADGDLVSPATQPCAVLDSFKETSRTLGWHLBARAKSVGEKSAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MATRLEEVTRGRGGGTEEASEGGRGGRRRSPPQKFEIGTMEEAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 LysserArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGly 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 GlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 rereadecaaargararrerreaacareaacaceceaarreregegegegeaaaaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 GTTTTATTACTGATGCAAGCGCTAAACACCCTTTCAACCCCCAGAGGAGAAGCTGGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysVal---AspAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 GAAGAAATTCCTGGACGAGAAGCTCGAACAGGTCCTCCTGATGGCCAGCAAGATTCAGAG
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                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                         29. _1603
/note="unnamed protein product; hypothetical
(evidence: rsCDS, ProCreat, decoder, NCBI CDS
Predictor, Longest-ORF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2797
260
68
62
4
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Matches:
Conservative:
Mismatches:
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/db_xref="taxon:10090"
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29. .1603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /proteIn_id="BAC27547.1"
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                                                                                                                                                                             clone="6230424F16"
                                                mol_type="mRNA"
strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation of Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of Chases I to 2797)

In ature 420, 563-573 (2002)

Redachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kasukawa,T., Katoh,H., Kawai,J., Shili,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Konno,H., Konno,H., Kowai,M., Ohasu, Ohasto,N., Nakai,K., Nomura,K., Numazaki,A., Ohno,M., Ohasto,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sakai,C., Sakai,C., Sakai,K., Saitoh,H., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sagab,Y., Tangami,M., Tagawa,A., Shiraki,T., Sakazume,N., Takakaku,A., Shiraki,T., Takaku,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y., Towaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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High-efficiency full-length cDNA cloning
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Analysis of the mouse transcriptome based on functional annotation
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Nature 420, 563-573 (2002)
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                           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
176 LeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLys 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                     236 AsnArgSerLeuLysGluGluGluGlyValGlnArgAlaArgGluGluGluLysArgLys 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            683 АНТААGACCTTAAAGGAGGAGAATATGCAGCAGGCACGAGAGGAGGAAGAACGACGTAAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHis 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeulleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAsp 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 LeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAla 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 GluGluArgHisGlnArgGluLysAspPheleuLeuLysGluAlaValGluSerGlnArg 355
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                                       1343 AGGGCTCTTCAGACAGAGAGAAATGAGCTCAACGAGAAGGTCGAAGTCCTG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 ArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGlnAspLeu 472
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Mus musculus
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AK044130

ACCESSION VERSION

KEYWORDS

DEFINITION

RESULT 2 AK044130

SOURCE ORGANISM

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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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KKADLLEESRNVQKQMKLLOKKQACVTKEKYLLOSBHSKALTLARSKLESLCRELQRH
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/dev_stage="10 days neonate"
64. .1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 TCTCAAGCAAATGATATTCTTCAACATCAAGACCCCAGTTGTGGTGGCACAACTAAGAAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 CATTCACTGGAAGGGGATGAAGGC----AGT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GACTTTATTACAAAGAAACAGAAATTTGGTGAGCTCAGTATTCTGTACACAGGAGAAAGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 GAAGAAATTĆĆTGGÅCGAGAAGCTCGAACAĞĞTCCTĆĆTGATGGCCAGCAAĞAİTCAĞAĞ 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 LysSerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGly 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 GluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluVal 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AACAAAGAGAGAGACTIAGGAAAAGAAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLygLeuAlaAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 GTTTTAŤTAČTGAŤGČČÁÁGCGČŤÁŘAČÁČČČŤŤTČÁŘČČČČÁGÁGÁGÁGÁGÁGÁGÁGÍT 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysVal---AspAsnAsn 75
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                             /protein id="BAC31791,1"
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/db_xref="MGI:2409425"
/db_xref="taxon:10090"
/clone="A830093C13"
                                                                                                                                                                            (evidence: rsCDS, ProCr
Predictor, Longest-ORF)
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958 TIGCAACAACAGCTIGIGGAIGCCAAACTICAGCAAACAACACAGGTGAIAAAAGAAGCT 1017
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library, clone:4932441K18 product:hypothetical protein, full insert
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                                                                           216 SerlysAlaValLeuAlaArgSerlysLeuGluSerLeuCysArgGluLeuGlnArgHis 235
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ATTOTIGOAGAAGAAGAGCCCAGATTGTGAAAGAGAAGTTCACCTTCAGAGTGAACAC 657
                                                                                                                                                                                                                                                                                256 GluValThrSerHisPheGlnValThrLeuAspAspIleGlnLeuGlnMetGluGlnHis 275
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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KKYADLLEBSRNVQKOMKI LÖKKQAQI VKEKVHLOSEHSKA İLARSKLESLCRELQRH NKTLKÜENMOQAREBERRKEATAHPQI TLNB IQAQLEQHDI HNAKLIKQEN ELGEKL KKLI EQYALIREBHIDKVYRKELQQOLYDAKLQOQI TOLI KBADEKHQREREFILLEAT ESHRKYEQKYQLYQLIKQDLSL YMDKPEREPOTTMAKSINEL FITTRQBMEKMTKKI KKL EKETI I WRTYKMENNNKALLQMAEEKTVRDKEVKAPQI KLERLEKLCRALQTERNELNE KVEVLKEQVS I KAADGDLVSPATQPCAVLDS PKETSRRTLGMILEARAKSVCEKSAAQ
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ICGLGVKADMVCNSQANDILQHQDPSCGGTTKKHSLEGDEGSDFITKNRNLVSSVFCT
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                                                                                                                                                                                                                                                                                                                                                                                          <u>QEKREEIPGREARTGPPDGQQDSECSRNKEKTLGKEVLLLMQALNTLSTPEEKLAALC</u>
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                                                                                              /note="unnamed protein product; hypothetical protein (evidence: rsCDS, Procrest, decoder, NCBI CDS
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Mismatches:
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/db_xref="G1:26326083"
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                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, X., Itoh, M., Xomo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Korbo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashizo, H., Itoh, M., Sumi, N., Ishii, Y., Nakamua, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yajiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SCS), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Stanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length obNas
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="MGI:2392716"
/db_xref="taxon:10090"
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strain="C57BL/6J"
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6 (bases 1 to 3810)
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/drawe_vpre="mintor bill."
// Lab host="mintor bill."
// Site 2: Not 1; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1966. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EooR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGACACG. This library was created for the University
low Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIWH), Hemin Chin, Ph.D.,
  Clone Distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole brain"
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/clone="IMAGE:6825755"
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                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6"
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1279.00
98.86$
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LeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAla 335
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Azrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                              GluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHis 275
                                                                                                                                                                                                                                                                                                       276 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys 295
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 798)
NHP-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone="IMAGE:30547339"
/tissue_type="whole eye"
/tesue_type="whole eye"
/dev_srage="embryo 12.5,13.5,14.5 dpc"
/lab_host="NHIOB (TI phage resistant)"
/clone_lib="NHI-BMAP_HB0"
/clone_lib="NHI-BMAP_HB0"
/note="Organ: Eye' Vector: pxx- Asc; Site_1: EcoR I;
/site_2: Not I: The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, iligated
with EcoR I adaptor, digested with NotI and then cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  775 bp mRNA linear EST 09-OCT-2003
UI-M-HBO-ckk-j-20-0-UI.rl NIH BMAP_HBO Mus musculus cDNA clone
IMAGE:30547339 5', mRNA sequence.
CP728426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BWAP)
                                                                                                                                                                                                                                                                                      699
                                                                                             549
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                                                                                                                                           TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 319
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 775)
                                                                                                                                                                                                                                                                       CTAGTGGACGCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAGGAGCAAAGGACGGCAC
                                                                                                                                                                         TACGAGCTTCGTGAGGAGCATATCGACAAAGTCTTCAAACATAAGGACCTGCAGCAGCAG
CACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAGCATAACGAGCGAAAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Mus musculus"
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/strain="C57BL/6"
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directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAAGT. This library was created for the University Iowa Brain Anatomy Project (ARPP): 'Gene Discovery in the Developing Mouse Nerrous System', supported by National Institute of Mental Health (NIMH)."
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similari
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CF735205
LOCUS
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BG827157 11H_MGC_17 Homo sapiens cDNA clone IMAGE:4903690 5',
        GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGlu 226
                                                                                                                                                                                                             AlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsn 266
                                                                                                                                                                                                                                                             eccercargadeagaagaagaageaagaagaagaagacrrcacacrrcaagrgacacreaar 361
                                                                                                                                                                                                                                                                                                                AsplieGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGlnGluAsn 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeu 346
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Genomics, Inc.

CDNA Education: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

http://image.llnl.gov

Plate: LLCM1802 row: f column: 11

High quality sequence start: 6

High quality sequence start: 6

High quality sequence stop: 775.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 932)
                                                                                                                                        SerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                  MetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHis
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Homo sapiens
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BG827157
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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BG827157
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/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole or in page resistant)"
/clone lib="Null BMAP HBO"
/clone lib="Null BMAP HBO"
/note="Organ: Bye; Vector: pXx- Asc; Site l: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                                                                                             Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 LysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeu 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTACCCCAGAGGAGAAGCTGGCTGCACTGTGCAAGAAGTATGCTGAGCTGCTGGAAGAG 121
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UI-M-HBO-ckc-1-18-0-UI.rI NIH_BMAP_HBO Mus musculus cDNA clone
IMAGE:30615737 5', mRNA sequence.
CF735205
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/db_xref="taxon:10090"
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Location/Qualifiers
                                                                                  CF735205.1 GI:37631541
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Best Local Similarity:
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VERSION
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ORGANISM
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CA320886
UI-M-FW0-ccb-h-16-0-UI.rl NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6817313 5', mRNA sequence.
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of Iowa
                                                                                    842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Mus musculus (house mouse)

Mus musculus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musculus

(bases 1 to 806)

I (bases 1 to 806)

INH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs:r@mail.inh.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Libra at:

Mitp://minge.lini.gov

Mitp://mail.inh.gov

Mitp://mail.inh.gov

Mitp://mail.inh.gov

Mitp://mail.inh.gov

Mitp://mail.inh.gov
                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                       SerProArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly
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Conservative:
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Location/Qualifiers
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CA320886.1 GI:24538984
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AUTHORS
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CA320886
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                                                    /dlone lib="NIH MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: NAOI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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172
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/clone="IMAGE:4903690"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/-lone_lib="NIH MGC 17"
                                                                                                                                                                                                                                                           Length:
Matches:
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REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES	ORIGIN Alignment Sopred. Pred. No.: Score: Percent Similest Local & Query Match	US-10-023-523 QY Db QY 122 QY Db R41 QY Db QY 142 Db CY Db Db 793	6 6 6 6 6 6 6 6 6 6 7 6 6 6 6 8 6 6 6 6 8 6 6 6 6 8 6 6 6 6 9 7 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 10 8 6 6 6 6 10 8 6 6 6 6 6 10 8 6 6 6 6 6 6 10 8 6 6 6 6 6 6 10 8 6 6 6 6 6 6 6 10 8
14 Gaps: 1 1 1 1 1 1 1 1 1 1	GlutisargasnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuVal GaGCATCGGAACTCGCACAAGCAGAACAACCACCACAAGAACAAGAACCAAGAACCACAGAACCACACAGAACCACAGAACCAAGAACCAAGAACCAAGAACCAAGAACCAAGAACCAAGAACCAAGAACAAAGAACAAAAAA	543 AATATGGAGCTAGCCGAGAGGCTTCAAGAAGTTGATCGAGCAATACGAGCTTCGTGAGGG 602 306 HislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeu 325 603 CATATCGACAAAGTCTTCAAACATAAGGACCTGCAGCAGCAGCAGCCCAAGCTC 662 326 GlnGlnAlaGlnGluMetLeuLysGluAlaGluAlaGluArgHisGlnArgGluLysAspPhe 345 603 CATATCGACAAGGAGGAGGAGAGAGAGAGCAGCAGCAGCAGCAGAGAGAGAGTTT 722 326 GlnGlnAlaValGluSerGluAlaGluArgMetCysGluLeuMetLysGlnGlnGluThr 723 61 CACCAGGAGAGCGAGAGCCAAAAGAGAGAGAGAGAGAGA	RESULT 9 BX752507 BX7525

/clone_lib= /note="Organ Site_2: Not Bonaldo, Le 1996, Denat gel.First s primer cont size select with ECOR I directional sequence lo	Down Brain Down Brain Developing Institute of program cocon and	Dercent Similarity: 97.31% Best Local Similarity: 96.54% Query Match: 14 DB: 16.023-523-8 (1-530) x CB2479 QY 103 ArgAenGlyGluProGlu Db: 1 ArgAenGryGluProGlu	122		Db 481 CAGGTGACACTGAATGAC Oy 282 LeuargGlnGluasDMet Db 541 CTGCGCCAGGAATATC Oy 302 LeuargGluGluHisTle Db 601 CTTCGTGAGGACATATC Oy 322 ASDAlatvstenGluGluGluGl
493 GAAGGAGTACAGAGGCTCGTGAGGAGAAGAAACGCAAAGAAGAACTAACCTCCCATTTC 434 262 GINVAIThTEGUAShASDIleGInLeuGInMetGluGInHisASAGINACCTCCCCATTTC 434 433 CAAGTGACGCTCAATGACATCCAGTCACATGAGCACAATGAACGTAATGAATG	CTANGRAGAGGCACATTGACAAGTTTTCAAACGTAAGGGTCTTCAAGGCAACTGGTG ASPAIALYSLEUGINGINAIAGTGTTTTCAAACGTAAGGGTCTTCAAGGAACTGGTG ASPAIALYSLEUGINGINAIAGTGTGTGTGTAAGGTAATTGTTTTTTTTTTT	193 GAMANGGARITICIGITGAANGAGGACACICGAGGGAGGGAGGAGGAGAGGAGAGAGAAA 134 362 GINGINGINTHRHISTEALVSGINGINCHEUNIALEENTYTHYGIULYSPHEGIUGUPHE 381 133 CAGCAAGAGACCCACACAACAACAATAAGACACTGAAACAGAAAATAGAGAGTTT 74 382 GINAERTHYLEUSETLYSSEYSEAGAGTAAGACACTGAATAACAGAGAAATAGAGAGTTT 74 382 GINAERTHYLEUSETLYSSEYSEAGAGTAAGACACTGAATAAAAAAAAAAAAAAAAAAAA 15 73 CAAAACACCTTGATCTAAAAAACAGTGAGGAGATTTTAA-CAAGAAATGGAAAAA 15	402 MetThrLysLys 405 14 AAAAAAAAAA 3		(BMAP) Seq primer: pYX-5. Location/Qualifiers 1.779 Notganism="Mus musculus" /mol_type="mRNA" /strain="C57Bif6" /db_xref="taxon:10090" /clone="iYAGE:6837167" /tissue_type="whole brain" /dev_stage="embryo 12.5dpc" /lab_host="mPH'0B [71 phage resistant)"
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	40 00 00 00 00 00 00 00 00 00 00 00 00 0	07	S S	RESULT 10 CEL47992 LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUFCE

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lib="NIH BNAP FIO"

"Organ: Brain; Vactor: pYX- Asc; Site_1: EcoR I;

Not 1; The library was constructed according

Not 1; The library was constructed according

Denatured RNA was size fractionated on a 1% agarose

rst strand cDNA synthesis was primed with oligo-dr

containing a Not I site. Double strand cDNA was
elected according to mRNA size fraction, ligated

containing a Not I site not and then cloned

contain into pix-Asc vector. The library tag

ce located between the Not I site and the polyA tail

CCACGAC. This library was created for the University

rain Anatomy Project (BMAP): 'Gene Discovery in the

ping Mouse Nervous System', supported by National

m coordinator."
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725 bp mRNA linear EST 15-JUL-2003
IMAGE:E697868 5', mRNA sequence.
                                                                                                                        142 ArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGln 161
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       103 ArgAsnGlyGluProGlu---ProThrProValValTyrGlyGluLysGluProSerLys 121
                                                                                           122 GlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArg 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741 GATGCAAAGCTTCAGCAAGCACAAAAAATGTTGAAAGAAGTGGAAGAGCGTCACCAGCGG 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 GlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPhe 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 LeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuVal 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 GluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLys 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 AGAAGCAAGCTCGAAAGTTTGTGCAGAGAGCTACAGAGACACCGTACACTAAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 GluGlyValGlnArgAlaArgGluGluGluLysArgLysGluValThrSerHisPhe
                                             93 AAAAATGGTGATACTGAACTAGTAGTCCAAGAGGTTAATGGTGAGAAGGAGGAAATGCGG
                                                                                                                                                                                                                                                                                                                    261 ACTOTGAACACACTCAGCACCCCAGAGGAAAGCTGACTGCCCTGTGTAAGAAGTATGCA
                                                                                                                                                                                                                                                                                                                                                                  GlubeuleuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 SerGinLeuValGinGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GAAGGAGTACAGAGGCTCGTGAGGAGGAAGAAACGCAAAGAAGTAACCTCCCATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 GlnAsnThrLeuSerLysSerSer 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921 CAAAACACCTTGTCTAAAAGCAAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU701958.1 GI:23626281
                                                                                                                                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                        AL961454 Innear EST 04-DEC-2003
AL961454 XGC-gastrula Silurana tropicalis cDNA clone TGas127p15 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is from a Xenopus Gene Collection (XCC) library constructed by Aaron M. Zorn.

Constructed by Aaron M. Zorn.

Constructed by Aaron M. Zorn.

Gastrulae. Bross. The construction of poly A+ RNA from stages 10-13

gastrulae. EcoRI-NotI cut CDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site. I: EcoRI; Site. 2: NotI

Host: Escherichia coli. Location/Qualifiers
342 GlulysAspPheleuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLys 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 GlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAla 102
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 945)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Nov 27, 2002 this sequence version replaced gi:25785049.
Contact: Taylor R
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Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TGAS127pl5.plkSP6
Sequencing primer: 5P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                            AL961454.2 GI:38703803
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1225.00
84.76%
77.13%
45.34%
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                                                                                                                                                                                                                                              mRNA sequence.
AL961454
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Best Local Similarity:
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TITLE
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BQ769910 135 bp mRNA linear BST 26-JUL-2002 UI-W-FIO-byt-i-21-0-UI.rl NIH BMAP_FIO Mus musculus cDNA clone IMAGE:5702108 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin. University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLN; at:
                                                                                                                                                                                                                                                                                                                                                   315
                                      301 AACCGGICCCTGAAGGAAGAAGGCGTGCAGCGAGCCCGTGAGGAGGAGGAGGAAGAAGCGCAAA 360
                                                                                                                                                                         361 GAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAGCAT 420
                                                                                                                                                                                                                                   276 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys 295
                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                            481 TTGATCGAGCAATACGAGCTTCGTGAGGAGCATATCGACAAAGTCTTCAAACATAAGGAC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 LeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGlnMetLeuLysGluAla 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 GluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArg 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 735)
   236 AsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLys 255
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/clone="IMAGE:5702108"
/tissue_type="whole brain"
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/lab_host="mhi0B (TI phage resistant)"
/clone_lib="NIH_BMAP_FI0"
/nore="Topan: Brain; Vector: pXX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according
                                                                                                                      GluvalThrSerHisPheGlnvalThrLeuAsnAspIleGlnLeuGlnMetGluGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 MetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThr
                                                                                                                                                                                                                                                                                               421 AACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                         296 LeuileGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/strain="C57BL/6"
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Mus musculus
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BQ769910.1 GI:21978384
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/tissue type="whole brain"
/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="whole brain"
/clone lib="While MAP Fro"
/clone lib="While MAP Fro"
/clone lib="While MAP Fro"
/clone lib="While MAP Fro"
/clone lib="While MAP Fro"
/clone lib="whole brain Vector: pXx Asc, Site_l: ECOR I;
Site_l: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:191-866,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with ECOR I adaptor, digested with NotI and then cloned
directionally inco pXx Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
lowa Brain Anatomy Project (MAMP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                         Email: cgapbs:r@mail.nib.gov
Tissue Procurement: Dr. Jim Lin, gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
                                                                                                                                                                                                                                                                                                                                            This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 GlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAla 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerlysAlaValLeuAlaArgSerlysLeuGluSerLeuCysArgGluLeuGlnArgHis 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 crerecaagaagrarecreaecrecregaagagcarcegaacreecagaagcargaag 180
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Indels:
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Matches:
                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6"
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1209.00
100.00%
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Best Local Similarity:
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                               TITLE
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   AUTHORS
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Similarity:
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1956. Denatured RNA was size fractionated on a 1% agarcee gel. First strand CDNA synthesis was primed with Oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Bcor I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCACAGAC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIME), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AAGCTCCTGCAGAAGAAGCAGAGCCAGCTCGTGCAGGAGAACGACCATCTGCGAGGGGAA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 GlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAla 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 GAGATCACTCTGCTGATGCAGACACTGAACACGCTGAGTACCCCCAGAGGAGGAGGTGGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 GCACTGTGCAAGAAGTATGCTGAGCTGCAAGAAGAGCATCGGAAACTCGCAGAAGCAGATG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 CACAACCGGTCCCTGAAGGAAGAAGCGTGCAGCGAGCACCCGTGAGGAGGAGGAGGAGGAGGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 LysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGlu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 HisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArg 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 CACAGCAAGGCTGTCCTGGCCCGAAGCAAGCTTGAGAGTCTGTGCCGGGAGCTGCAACGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 LysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGln 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLys 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 CATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGTCAAG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLys 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 GACCTGCAGCAGCAGCTAGTGCACGCCAAGCTCCAGGGCCCAGGAGATGCTGAAGGAG 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ATTGGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAGAAGAAGAAGGAGGTCTAGGGAAG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 AAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAG
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Matches:
Conservative:
Mismatches:
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/lab host="DH10B TOTA"
/lab host="DH10B TOTA"
/lab host="DH10B TOTA"
/lab host="DH10B TOTA"
/loce="Organ: mIxed; Vector: pVX-Asc; Site_1: EccRI;
/note="Organ: mIxed; Vector: pVX-Asc; Site_1: EccRI;
/note="Organ: mIxed; Vector: pVX-Asc; Site_1: EccRionally
cloned Denatured RNA was size fractional and all agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according tomRNA size fraction, ligated with
EcoR I adaptor, dispested with Not I and then cloned
directionally into pXX-Asc vector. Average insert size
4-5KD Adaptors 5'(AATTGGCAGGAG3) and 5'd
(CCTGTGCGC3): 3' Linker sequence - GCGGCCCTGAGAGC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
(ATTATACGACTAAAGGAG3): 1. binker sequence primer 5'd
(TATATACGACTAAAGGGG3): . binker sequence primer 5'd
(TATATACGACTAAAGGGG3): 1. binker sequence primer 5'd
(TATATACGACTAAAGGGG3): 1. binker sequence primer 5'd
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(TATATACGACTAAAGGGG3): 1. binker sequence primer 5'd
        EST 25-NOV-2003
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Contact: Dariels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg :3! RMIONO' Betheada, MD 20892
Email: cgapbs-ramininingov
Email: cgapbs-ramininingov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Prayad by: The I.M. A.G.E. Consortium (Libr.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
thtp://mage.llni.gov m. column: 18
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
1 (bases 1 to 759)
NIH-Moc http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
        p mRNA linear EST
Homo sapiens cDNA clone
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Conservative:
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CF995807
AGENCOURT 16109164 NIH MGC 221 Hoi
IMAGE:30708497 5', mRNÀ sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30708497"
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Location/Qualifiers
1. 759
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1205.00
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 817)
                                              AAGGACCACCTGCGCGGGTGAGCACACAAGGCCGTCCTGGCCCGCGCAGCAAGCTTGAGAGC
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LysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSer
                                                                                                                                                         LeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAla
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                          AKO84639 MLS misculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330024K18 product:MUSCLE-DERIVED PROTEIN MDP77 VARIANT 1, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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/db xref="Laxon:10090"
/clone="D33024K18"
/tissue type="heart"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/ske vage="13 days embryo"
                                                                                                                                        Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokchama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
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Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

iocation/Qualifiers
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136 ValArgAspLysGlu :::				Koya,S., Kurihara, Nakamura,M., Nishi Nakazaki,Y., Saito, Sano,H., Sasaki,D. Sogabe,Y., Tagami, Takeda,Y., Tanaka, Muramatsu,M. and
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toh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., yama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., i.Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Matsumoto, H., Sakaguohi, S., Ikegami, T., Kashiwagi, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watchiki, M., hikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., ted sequence analysis (ERS) system-384-format peline with 384 multicapillary sequencer
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I. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
d. subtraction of cap-trapper-selected CDNAs to
gth cDNA libraries for rapid discovery of new genes
10), 1617-1630 (2000)
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                                 ortium and the RIKEN Genome Exploration Research
III Team.
Transcriptome based on functional annotation
ength CDNAs
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LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCys 455
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AUTHORS TITLE JOURNAL

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BQ714219
BQ714219
SQROUNT_8291711 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6308909
S, mRNA Sequence.
N S, mRNA Sequence.
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BQ714219.1 GI:21853118
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Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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/clone lib="Mhy BMAP FYO"
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Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcage
gel: First strand cDNA synthesis was primed with oligo-dry
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Erain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                 linear EST 09-JUL-2003 musculus cDNA clone
1569 CTGAAAATGAAGAGGTGGACGCAGAGGAAGCCAACAGTTTTCAAAAAGCTGTGGAAAACC 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Trisue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 750)
                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                              bp mRNA
I_BMAP_FY0 Mus
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Location/Qualifiers
1. 750
/organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                           CA327097
UI-M-FYO-ccy-g-01-0-UI.rl NIH_BMJ
IMAGE:6826106 5', mRNA sequence.
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FEATURES

1

ArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 64

Percent Similarity: Best Local Similarity:

Query Match: DB:

Scores:

Pred. No.:

Score:

Alignment

ORIGIN

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us-10-023-523-8.rst

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LeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg-SerLe
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/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
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87.59%
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/db xaref="taxon:10090"
/db xaref="taxon:10090"
/dlone="IMAGE:5702161"
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/dew stage="whole brain"
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/clone_lib="NIH BMAP_FIT phage resistant)"
/clone_lib="NIH BMAP_FIT phage resistant)"
/clone_lib="NIH BMAP_FIT phage resistant con a lib agarose
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1966. Denatured RNA was size fractionated on a lib agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pVX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
lows Brain Anatomy Project (BMAP): 'dene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ770181
UI-M-FIO-byt-1-02-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:5702161 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
This.clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                              rHisPheGlnValThrLeuAsnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAs 279
760 chdaccccaádcaádchhdadadhchdráccdadadchaccaddadcdanchcch 819
                                                                                                   ulysglugluglyvalglnArgAlaArgGluGluGluGluLysArglysGluValThrSe 259
                                                                                                                                                                                                                                                                                                                                                  880 ACC-TTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAGCATAACGAGCGAAA 938
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                           820 GAAGGAAGAAACCGTGCAGCGAGCCCTGAGGGAGAAGAAAAAAGAGGAGACTTC
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/db xref="taxon:10090"
/Libe_taxon:10090"
/Libe_tax
                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
DNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
Seq primer: pyx-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CTGCAGATGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCCAGGAGAATATGGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValPhelysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCCGAGGCTCAAGAAGTTGATCGAGCAATACGAGCTTCGTGAGGAGCATATCGACAAA
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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COMMENT
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Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSer 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHis 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArg 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGlu 250
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Musinaes 1 to 716)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                         111 ProvalvalTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArg
                                                                                                                                                                                                                                                                                                                                         131 GlnserAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLys
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                       Length:
Matches:
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                                                                                                                                          Gaps:
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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AUTHORS
TITLE
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CF728006
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VERSION AK031023.1 GI:2608210 KEYWORDS .HTC; CAP trapper.	Alignment Scores: 2.46e-65 Length: 819
LOCUS AK031023 DEFINITION Mus musculus adult mal library, clone:5830498	O, A, E
RESULT 23 AK031023	pCMV_SPORT6; Site_1:
Db 781 GAGCAG 786	/clone="IMAGE:4239513" /lab_host="DH10B (Tl_phage-resistant)"
317 GlnGln 318	/strain="FVB/N" /db_xref="taxon:10090"
722 ATCGAGO	/organism="Mus musculus" /mol_type="mRNA"
797 TEGIN	FEATURES Location/Qualitiers source 1. 819
7 0	
	http://image.llnl.gov
Qy 278 ArgAsn-SerLysLeuArgG	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:
DD 602 ACTICACACTICCAGGIGAC	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Qy 258 ThrSerHisPheGlnValT	Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc.
	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Oy 238 SerLeuLysGluGluGlyVa	TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)
Db 482 GCTGTCCTGGCCCGAAGCAA	I (Dases I to 819) NIH-MGC http://mgc.nci.nih.gov/.
Oy 218 AlaValLeuAlaArgSerLy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoni; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Qy 198 GlnLysLysGlnSerGlnL	
Db 362 AAGAAGTATGCTGAGCTGCT	BF783468
Oy 178 LysLysTyrAlaGluLeuLe	DECUS BE/83468 819 Dp mRNA linear EST 12-JAN-2001 DEFINITION 602111238F1 NCI CGAP Kidl4 Mus musculus cDNA clone IMAGE:4239513
DD 302 CTGCTGATGCAGACACTGAA	
Qy 158 LeuLeuMetGlnThrLeuAs	/12 GAG
Db 242 CGAGACCATCGGAGGCCAC	OY 490 GIU 490
Qy 138 ArgAspHisArgArgProGl	OOT CAGGACCIGACIGGGGGGCAICACIGACAIIGGCICIGAGCGGAGGGCA
Db 182 GAGACCTCTAAGGGAGAGG	OY 4/O GINASDIEUSEYIAGIYGIYGIYGIYGELEGUINASDSEEGIYATOGIUATGAAGIYO 489
Qy 118 GlubroserLysGlyAspP	OUL CGGCIGGANGANGCIGIGCCGAGCACIGCAGAGCGCGCAAIGACGGGAAA
	450 ArgLeuGluIysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgval
Qy 99 ThrTyrValAlaArgAsnGl	Db 541 ATGGCTGAAGAAAACCGTCCGGGACAAAGAGCTGGAGGGCCTGCAGGTGAAATCCAG 600
Db 62 CCGGCTGAGGAGGACACA	430 MetalagluGluLysThrValArgAspLysGluLeuGluGluGluValLysIleGln
	Db 481 GAGAAAGAAACCACCATGTATCGATCCCGGTGGGAAAGCAGCAACAAGGCTCTGCTGGAG 540
Oy 59 LeuSerArgdinLeuGillAs 	Oy 410 GluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGlu 429
-10-023-523-8 (1-530)	
10	Qy 390 GluvalpheThrThrPheLysGlnGluMetGluLysMetThrLysLysLieLysLysLeu 409
Query Match: 42.21%	Db 361 CAGCTCGCCCTGTACACGGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAGT 420

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4452 bp mRNA linear HTC 18-SEP-2003
ale thymus cDNA, RIKEN full-length enriched
98L23 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                            31nGluLysLysLysAlaLysGlyLeuGlyLysGluIleThr 157
                                                                                                                                                                                                                                                                                      ThreedanaspileglaleeuGlametGluGlahisAsnGlu 277
                                                                                                                                                                           31yGlubroGlubro---ThrProValValTyrGlyGluLys 117
                                                                                                                                                                                                                                    ProAsnThrGluGluIleArgGlnSerAspGluValGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                      AsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCys 177
                                                                                                                                                                                                                                                                                                                                                                                                       JeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JenvalGlnGluLysAspHisLeuArgGlyGluHisSerLys 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alGlnArgAlaArgGluGluGluGluLysArgLysGluVal 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGCAGCGAGCCCGAGAGGAGGAGAAGCGCAAAGAAGTG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnGluAsnMetGluLeuAlaGlu-ArgLeu-LysLysLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGAGAATATGGAGCTAGCCGAGGAGGCTCAAAGAAGTTG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rrgGluGluHisIleAspLysValPheLysHisLysAspLeu 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3lnGlyGluProAlaGluProGluAspAlaGluLysSerArg 98
128
Conservative:
Mismatches:
Indels:
Gaps:
                                                                    58 (1-819)
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1. 4452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                958 TCTCAAGCAAATGATATTCTTCAACATCAAGACCCCAGTTGTGGTGGCACAACTAAGAAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045 GACTITATTACAAGAACAGAAATTTGGTGAGCTCAGTATTCTGTACACAGGAGAAAAGA 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 LysserArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGly 115
                                                                                                                                                                                                                                                                     /note="hypothetical protein (evidence:
rsCDS, ProCrest, decoder, NCBI CDS Predictor, Longest-ORF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGluArgHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysVal---AspAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 GlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLyGglu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuleuglnLysLysglnSerglnLeuValGlnGluLysAspHisLeuArgGlyGluHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu
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260
260
67
351
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Mismatches:
Indels:
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                            3.55e-64
1136.50
43.97%
34.85%
42.06%
                                                                                                                                                      sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                   misc feature
                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,700 kull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4452)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itch,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itch,M., Yamai, J., Shii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwaqi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matahiki,M., Yoneda,Y., Ishikawa,T., Oaxaa,K., Taranka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsi,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format gequencing pipeline with 384 milticapillary sequencer sequencer loss of 11, 1757-1771 (2000)
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                            Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FANTOM Consortium. Functional amouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                  Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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                               Chordata;
Rodentia;
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Mammalia; Eutheria;
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 2581 TATGTTCCTATTTGTAATTGCTATTAGTACTTTTGCAAGGATGTTTCTATTTTTTAGTTA 2640	347 LeulysGlualaValGluSerGlnargMetCysGluLeuMetLysGlnGlnGluThrHis 366 	367 LeulysginginleualaleuTyrThrGluLysPheGluGluPheGlnAsnThrLeuser 386	LysSerSerGluValBheThrThrPheLysGlnGluMetGluLysMetThrLysLysIle ::: :::	407 LysLysLeuGluiysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla 426 	427 LeuleuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnVal 446 281	Lys I leglnargLeugluLysLeuCysargalaLeuglnThrGluargasnaspLeuasn	2941 AAACTGGAACGGTTAGAGAAGCTGTGCAGGGCTCTTCAGACAGA	%5/ bysalgvalolimbpueu 4/2 ::::: ::: 3001 GAGAAGGTCGAAGTCCTG 3018		CA324134 UI-M-FY0-cco-f-03-	IMAGE:6822244 5', mRNA sequence. CA324134	CA324134.1 G1:24542232 EST. Mis miscrilis (house mouse)	ייים ביים אלים ביים אלים ביים ביים ביים ביים ביים ביים ביים ב	buralýous, merazos, choluara; transaraj verteblaraj bureleoscomi, Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (hacas 1 to 778)	NIH-WGC http://mgc.nci.nih.gov/. NATional Institutes of Health. Mammalian Gene Collection (MGC)	Unpublished (1999) Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin University of Towa	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	ו		This clone was contributed by the Brain Molecular Anatomy Project	ime.		/organism="musmusmusmusmusmusmusmusmusmusmusmusmusm	/stran="C>/bu/b" /db xref="taxon:10090"	/clone="IMAGE:682244" /tissue_type="whole brain" /acceded:10000000000000000000000000000000000	dev stagge="emoryo 13.5,14.5,16.5,17.7.oupc". Jab hoot="hD100 (11 phage resistant)"	/crous_lib= Nin bran_riv /note="Organ: Brain; Vector: pXX- Asc, Site_1: EcoR I; Site_2: NAT I: The library was constructed according	Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
qq	o o	OY Dp		2 Dp 93	6 ov			3	RESULT 24 CA324134	LOCUS	ACCESSION	VERSION KEYWORDS SOIRCE	ORGANISM		AUTHORS	JOURNAL						0000	SOUICE						
7	1501 GAAGCAACACTTTCCAGATAACTCTAAATGAAATCCAAGCTCAGTTGGAACAACAT 1560 276 AsnGluargAsnSerLysLeuargGlnGluasnMetGluLeualaGluargLeuLysLys 295 :::	296 LeuileGludintyrGluLeukrgGluGluHisīleAspiysValPhelySHisīysAsp 315 6 LeuileGludintyrGluLeukrgGluGluHisīleAspiysValPhelySHisīysAsp 315 621 CTTATTTGAGGATATGGAGTAAAGGAAAAGGAATATTGATAAAGTATTCAAAAGAA 168	316 LeuglnGlnGlnLeuValAspalaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAla 335	336 GlugluargHisGlnArgGluLygAspPhe	345	1801 AGGTATTGCCAGTATTTTAACTAATTCCATGTCACTCCTGAGGTATGATAGAAAAGCCCT 1860 345	1861 GGAAGGCTTCTGGCTACTTATTCTATTCAGAGAICCACATGCCTGCTTGAGTGCTAGGA 1920	345	345	1981 GGGAAATGATTTTCATTGGGGAAATTTTAATTTTATTGAGTCATATTCTCCCCTTTATTT 2040	345 345	2041 TIGITGAGICAGGGICICAIATIGIAGCICIGGGGGGAIGACCTIGAACTACTIGAA 2100	345 345	2101 GCACCATCCCAAATTTAGGAAGTCCTGGGGATTAAACCCTGGGCTTTCTACTTACATATA 2160	345 345	2161 AAGCAAGCACATCTCCAGTCTCACACCCATTTTGTTTTG	345 345	2221 CCTCCATAGCCTTTCGCCCCATCTTCTCTTGTTCCTTAGGTAGAAGGTTTCTCAG 2280	345 345	2281 TCATGTAGGAGGTACTTAGCCATGTTTTCTGCTAATATCAGACATGTGATTATTTTCACC 2340	345 345	2341 IGAAACCACCCAAACACCATCTTTAAAACCTCAACTTTGTAAATTGTTTTAGGCCTCCAC 2400	345 345	2401 TATACCTTTCTACTTAAGCAGTAAAATAATATAAGTATTCAAACATTTCTACTTCCTAA 2460	345 345	2461 TGATGGAAGGTATTTGTAAATGGTAACTGGTGGAAATAAGGTGTTCCATTTTGGAGGGTA 2520	345 345	2521 GTCATTCTTGCTAAAATAGTGAGGTGAAGGATGTGGAGTAACTATGGTACTTGACATAAT 2580	346

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Bonaldo, lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nnb.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

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Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
                                                                                                                                                                                                                                                                                                                          BST.
Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                     GGAGAAGCGCAAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCA
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UI-M-FYO-Cdq-i-09-0-UI.rl NIH_BMAP_FYO Mus musculus CDNA clone IMAGE:6833074 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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AUTHORS
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1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PXT-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University lowa Brain Anatomy Project (BMAP), Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.
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Best Local Similarity:
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/ciosue type="whole brain"
/dev stage="embryo 12.5dpc"
/lab.host="hubtle (Ti phage resistant)"
/dov stage="embryo 12.5dpc"
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/clone lib="NIH BMAP F10"
/site_2: Not I: The library was constructed according
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1996. Denatured RNA was size fractionated on a 1% agarose
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGlu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TT-GGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAGAAGAAGGCAAGGGTCTAGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMet 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCTICCTGCAGAAGAAGCAGAGCCAGCTCGTGCAGGAAGGACCATCTGCGAGGGGGAA 299
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:10090"
'clone="IMAGE:5721214"
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                                                                                                                                                                              Seq primer: pYX-5.
Location/Qualifiers
1. .699
                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6"
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Best Local Similarity:
Query Match:
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UI-M-FI0-byp-e-23-0-UI.rl NIH BMAP_FI0 Mus musculus cDNA clone
IMAGE:5721214 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 699)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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                                                                                                                                                                                                                                                                              126 GAAGTTGGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAGAAAGCCAAGGGTCTAGGG 185
                                                                                                                                                                                                                                                                                                                                                            AAGAGAGATCACTCTGCTGATGCAGACACTGAACACGCTGAGTACCCCAGAGGAGAAGCTG 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLe 293
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                             GluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro---ThrProValVal
                                                                                                                           114 TyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAsp
                                                                                                                                                                   GCTGCACTGTGCAAGAAGTATGCTGAGCTGCTGGAAGAAGCATCGGAAACTCGCAGAAGCAG
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                                                        GAGAAGTCCCGAACCTATGCAGCCAGGAATGGGGAGCCTGAACCAGGCATTCCAGTCGTC
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AUTHORS
TITLE
JOURNAL
COMMENT
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154

239 214 234

Matches:

27

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US-10-023-523-8 (1-530) x BX855901
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AL637771.2 GI:38216372
        1099.00
92.25%
83.33%
40.67%
        Score:
Percent Similarity:
Best Local Similarity:
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      274
                                                                    294
                                                                                                                        LysteullegludinTyrgluLeuArgGlugluHislleAspLysValPheLysHisLyg 314
                                                                                                                                                                                                        AspleuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGlu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="AGENAE Rainbow trout multi-tissues subtracted
library (tcay)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Scrinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
(bases 1 to 780)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pT7T3D-pac, Rainbow trout multi-tissues -
normalized + 1 subtraction (tcay); Clone distribution :
AGENAE Resource centre. Francois PIUM,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (IREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE"
LysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGln
                          420 AAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAG
                                                            HisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLys
                                                                                                                                            CATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAG
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/db xref="taxon:802"
/clone="taxon:802"
/clone="taxon:805b;i.o."
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intest
kidney, liver, muscle, ovary, pituitary, testis"
/day_stage="from embryos to adults"
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Construction and primary characterization of normalized ilbraries in rainbow trout, Oncorhynchus mykiss
Contact: Guiguen Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                   AlaGluGluArgHisGlnArgGluLysAspPheleuLeu
                                                                                                                                                                                                                                                                       660 GCAGAGGAGCGGCACCAGCGAGAAGAAGAATTTCTCCTG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oncorhynchus mykiss"
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Oncorhynchus mykiss
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Seq primer: M13R,
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1. .780
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TITLE
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Alignment Scores:

Pred. No.:

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AL637771 ACC-neurula Silurana tropicalis cDNA clone TNeu020c17 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota, Metazoca; Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                         154 LysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeu
                                                                                                                                                                                                                                                           Met LysbeuleuglnLysLysGlnSerGlnLeuvalGlnGluLysAspHisLeuArgGly
                                                                                                                                                                                                                                                                                GAGGAGATCACCCTGCTGATGCAGACCCTGAATACTCTGAGTACTCCAGAGGATAACTG
                                                                                                                                                                                          174 AlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln
                                                                                                                                                                                                                                                                                                                          214 GludisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 LysLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHis
                                                                                                                                                                                                                                                                                                                                               234 ArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluLys
                                                                                                                                                                                                                                                                                                                                                                                                             246 AGACACAACGCACACTCAAGGATGACGGGATGCAGCGTGCACGTGTGGAGGAGGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 LysAspleuGinGinLeuValAspAlaLysleuGinGinAlaGinGluMetLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 AAGAAACTCATCCAACAGTACGAAGTACGAGAGGAGGAGCACATTGACAAGGTGTTCAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 GluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 TyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPheThr
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23
23
0
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            Conservative:
Mismatches:
Indels:
                                                                                             (1-780)
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KEYWORDS
SOURCE
ORGANISM
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199

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                                                                                                                                                                                                                                   33 LysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGlu 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nii.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
CONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linn at:
http://image.llnl.gov
Plate: LLCM2830 row: I column: 10
High quality sequence stop: 566.
                                                                                                                                                                                                                                                                                                                                                            SerGlnArgMetCysGluLeuMetLysGlnGluThrHisLeuLysGlnGlnLeuAla
                                   313 HisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeu
                                                                                                                                                                542 AAAGAAGTGGAAGAGCGTCACCAGCGGAAAAGGAGTTTCTGTTGAAAGAGGCCAGTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   602 TCCCAGCGCATGTGTGAACTAATGAAACAGCAAGAGACCCACCTCAAACAACAGTTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 799)
NIH+MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
HUB49604
AGENCOURT_10437001 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:6598234 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 CIGTATACAGAGAAGTTTGAGGAGTTTCAAAACACCTTG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 LeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu 385
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU849604.1 GI:24034567
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1078.00
96.14%
95.28%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                            Hinkton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
ECGRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: ECORI, Site_2: NotI
Host: Escherichia coli DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notes "Vector: pCS107; Site 1: EcoR1, Site 2: Not1; cDNA was olige dT primed from 5ug of poly A+ RNA from neurula. EcoR1-Not1 cut cDNA was then ligated into pCS107 with EcoR1 at the 5' end and Not1 at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GlyLysGluileThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 LeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CTGACTGCCCTGTGTAAGAAGTATGCAGAACTGTTGGAGGAGCACAGGACATCTCAGAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AATGAGCACAGGCATCCTGGCAAGAGCAAGCTCGAAAGTTTGTGCAGAGAGCTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GlnArgHisAsnArgSerLeuLysGluGlyValGlnArgAlaArgGluGluGluGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 CAGAGACACACCGTACACTPAAGGAGAAGGAGTACAGAGGCTCGTGAGGAGGAAGAAGAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 LysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMet 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 GluglnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArg 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AAACGCAAAGAAGTAACCTCCCATTTCCAAGTGACGCTCAATGACATCCAGTCACAGATG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 LeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLys 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
1 (bases 1 to 702)
CroningM.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGAAAGGAGATCACATTATTAATGGCAGACTCTGACACACTCAGCACCCCAGAGGAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 GlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArg
                                                                                                                                On Nov 7, 2001 this sequence version replaced gi:16789750.
Contact: Huckle E
Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage≈"neurula"
/lab_host="Escherichia coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TNeu020c17.plkSP6
Sequencing primer: SP6.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="XGC-neurula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-023-523-8 (1-530) x AL637771 (1-702)
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1081.00
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL185e05"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 ATTGACAAAGTTTTCAAACATAAGGATCTTCAACAACAGCTAGTGGACGCCAAGCTTCAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 GinAlaGinGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeu 346
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The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerbeuCysArgGlubeuGlnArgHisAsnArgSerbeuLysGluGluGluGlyValGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 GCTCGTGAGGAGGAAGAAACGCAAGGAAGTAACCTCTCATTTCCAAGTGACACTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 AAAAGCAATGAGGTTTTCACCACTTTTAAACAAGAATGGAAAAGATGACAAAGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                              1. .698
/organism="Xenopus laevis"
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                                                                                     http://xenopus.nibb.ac.jp.
Location/Qualifiers
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1070.00
96.89%
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    Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 160
                                                                  89 AAAAGCAGCCCAGGACAACCGGAAGCAGGACCCGAGGAGCCCAGGAGCGAGGCGCCCAGCCAG
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                                                                                                                                                                                                                                                        209 GGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                    GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnSerGlnLeuValGlnGluLygAspHisLeu---ArgGlyGluHisSerLygAla-Va 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747
                                                                                                                       21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLySProGlu 40
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Kenopus laevis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                       1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
                                                                                                                                                                                                                                                                                                                          629 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAG
                                                                                                                                                                     61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                             329 gadgargoggcacagggrogacoggcroaaccogaagargcagagagagrocoggaccrar
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                                                                                                                                                                                                              GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer
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1 (bases 1 to 698)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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US-10-023-523-8 (1-530) x BU849604 (1-799)
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TITLE

	Db 248 GAGGAGAAGCGCAAGGTGACCTCGCACGTCCAGGTGACACTGAATGACATTCAGCTG 307	Oy 271 GlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAla 290	Oy 291 GluArgLeuLysLysLeuIleGluGluTyrGluLeuArgGluGluHisIleAspLysVal 310	311 PhelysHistysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlagInGln	331 MetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAla 	351 ValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlnGluThrHisLeuLysGlnGln	371 LeuhlaLeufyrThrGluLysPheGluGluPheGluAsnThrLeuSerLysSerSerGlu 	ValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGlu 	Qy 411 LysGluThrThrMetTyrArgSerArg-TrpGluSerSer-AsnLysAlaLeuLeuGluM 430 		Qy 448 IleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsn 463	Оу 463 463	863 GACCTTGGCACCCAAAAAAGGGGTTCTCCAGA	Qy 464	Qy 469 46	983	Oy 470 GlnAspLeuSerAlaGlyGlnGlySerLeuThrAspSerGlyPro 485 Db 1043 CAAACGGGGGGGGGGGAAAAACAGGTTAAGGGGAGGGGCCAAATTCTCCCTGA 110	roArgValThr 50	1103 GCGAAC	Qy 504 GlualaProCysTyrProGlyalaProSerThrGluala 516	Qy 517 SerGlyGlnThrGlyProGlnGluProThrSeralaArgAla 530 :::	
682 TTGCTTGTCARGGCA 696		BM455349 LOCUS BM455349 LOCUS DEFINITION AGENCOURT_6406997 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5500322 5', mRNA sequence.		_	REFERENCE 1 (bases 1 to 1318) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: capabs-romail.nh.gov Tissue Procurement: Lou Staudt cDNA Library Preparation: Life Technologies, Inc.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	http://mage.llnl.gov Plate: LLAM12135 row: b column: 03 High quality sequence start: 90 High quality sequence stop: 669.	rce	/done="naxon:9e06" /clone="nakon:9e06" /tissue_type="lymphoma, cell line" /lab_host="DH10B (phage-resistant)"		Note: this is a NIH_MGC Library."	Scores:	Score: NO:: 2.05e-bU Length: 1318 Score: 1069.50 Matches: 256 Percent Similarity: 63.07% Conservative: 19 Rest Local Similarity: 68.72% Mismatches: 69	39.58% Indels: 12 Gaps:	9 (1-1	LysLysTyrAlaGluLeuCluGluHisArgAsnSer	8 AAALGGGGGGGGGATCTCGTACCACCGTAACGAAGGGGGGGGGG	AAAACCGTCGACCCACGCGTCCCCACAGAGCCACTGCTGCAAGAAGAACGACAC	211 LeuargGlyGluHisSerLysAlaValLeuAlaargSerLysLeuGysArg 230 		

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CD578468 647 bp mRNA linear EST 09-JUL-2003
UI-M-FYO-cfs-n-14-0-UI.rl NIH BMAP_FYO Mus musculus cDNA clone
IMAGE:6855471 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lih., University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/incousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole brain"
/dev stage="embryo" 13.5,14.5,16.5,17.5dpc"
/lab_host="blub" 11 hage resistant)"
/clone_lib="NIH_BMAP_FYO"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                          427 uLeuGluMetAlaGluLuLysThrValArgAspLysGluLeuGluGlyLeuGlnValLy
                                                                                                                                                                                                                                                        422 GCTGGAGATGGCTGAAGAGAAAACGTCCGGGACAAAAAGAGCTGGAGGCCTGCAGGTGAA
                                                                                                                                                                                                                                                                                                                   sileGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLy
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                                                                          sLysleuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLe
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/organism="Mus musculus"
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861 bp mRNA linear EST 26-JUN-2001
602888485F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5043572
5', mRNA sequence.
BI102887
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Site_2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. |"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/strain="FVB/N"
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High quality sequence stop: 738.
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                                                                                                                                                                                                                     Mus musculus (house mouse)
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1061.00
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Seq primer: pYX-5.
Location/Qualifiers
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UI-M-EWO-cba-p-12-0-UI 5', mRNA sequence.
BU613886.1 GI:23280101
with EcoR I adaptor, digested with NotI and then cloned with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCCAGACAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequenoding by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae, Mus.
1 (bases 1 to 653)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                    4.34e-59
1044.50
93.48%
90.87%
38.66%
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Best Local Similarity:
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DB:
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University of lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M31 REVENSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAS10893 722 bp mRNA linear EST 15-NOV-2002 UI-R-FJO-cpv-o-09-0-UI.rl UI-R-FJO Rattus norvegicus cDNA clone UI-R-FJO-cpv-o-09-0-UI 5', mRNA sequence.
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-FJO"
                                                                                               362
                                                                                                                            271
                                                                                                                                           482
                                                                                                                                                                                                                                                      311
                                                                                                                                                                                                                                                                                    542
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                                                                                                                                                                                      nMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGl 291
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
wArgLeuLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPh
                                                                                                                                                                                                                   GATGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGA
                                                                                                                                                                                                                                                                                GAGGCTCAAGAAGTTGATCGAGCAATACGAGCTTCGTGAGGAGCATATCGACAAAGTCTT
                                                                                                                                                                                                                                                                                                              eLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMe
                                                                                                                         uGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGl
                                                              uLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/db_rxef="taxon:10116"
/clone="UJ-R-FOO-cpv-o-09-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
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Genome Res. 6 (9), 791-806 (1996)
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EST.
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DEFINITION
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CA510893
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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PUBMED
COMMENT
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/note="Vector: pXX-Asc, Site 1: EcoR 1; Site 2: Not I, UI-R-FJO is a cDNA library containing the following tissue (s): rat embryo. The library was constructed according to Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated con ECOR I adaptor, digested with Not I, and cloned directionally into pTT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)" 119 139 HisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeu 159 239 182 242 179 219 422 482 259 542 62 101 ValAlaArgAsnGlyGluProGluPro---ThrProValValTyrGlyGluLysGluPro GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr GCAGCCAGGAATGGGGAGCCTGAACCGGGCATTCCAGTCGTCAATGGCGAGAAGAGACC SerlysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp MetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys 123 TCTAAGGGGGAGCCTGGCACAGAAGAGATCCGAGCAAGTAGACGAGGTTGGAGACCGAGAC TyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLys LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal LeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeu 423 chdecceaaghaagchreagacchereceaagcheaacagcacaaccancera LysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSer 183 AAGGAAGAAGGTGTGCAGCGAGCCCGTGAGGAGGAGGAGAAGCGCAAAGAGGCGTGACTTCA Length:
Matches:
Conservative:
Mismatches:
Indels:

279 602

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Eukaryota; Buteleostomi; Eukaryota; Butheria; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 735)

3. Ilased Chtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

3. Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENA linear EST 18-MAR-2002
JI-M-EQO-bwn-b-08-0-UI.rl NIH_BMAP_EQO Mus musculus cDNA clone
WRAGE:5698471 5', mRNA sequence.
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                                                                                                                                                                                                                                                                MetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGlu 291
LeuLysGluhlaGluGluArgHisGluhArgGluLysAspPheLeuLeuLysGluhlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 CGACTTAAGAAGCTTATCGAGCAATATGAGCTAAGAGAAGAGAGCACATTGACAAAGTTTTC
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                                                                                                                                                                                                                                                                                              301 gagaaacecaaagaaaraaacreccarrrecaagreacacreaareacarecaacae
                                                                                                                                                                                                                                                                                                                                                                       292 ArgiculysiysLeuileGluGlnTyrGluLeuArgGluGluHisileAspLysValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 LysHisLysAspLeuGlnGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMet
                                                    LeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGlu
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/clone_lib="NIH_BMAP_EQ0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .735
/organism="Mus musculus"
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/clone="IMAGE:5698471"
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Location/Qualifiers
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/strain="C57BL/6"
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Mus musculus
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EcoRI at the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: trop@sanger.ac. uk
Sanger Xenopus tropicalis EST project 2001
TropIcALIS SEQUENCE ID: TEGG080008.plkSP6
Sequencing primer: SF6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
constructed by Aaron M. Zorn.
constructed by Aaron M. Sorn.
constructed by Aaron
                                                                                                                                                                                                                                                                                                       Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                 I (bases 1 to 665)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 16, 2002 this sequence version replaced gi:22938408.
Contact: Taylor R
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                   TACGAGCTTCGTGAGGAGCAGTTTTTGAAA 692
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/clone="TEgg080c08"
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/note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed_according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on al agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (EMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 782)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Ticklel, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                   BU231392 782 bp mRNA linear EST 26-NOV-2002 603947670F1 CSEQCHN23 Gallus gallus cDNA clone ChEST902117 5', mRNA
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University of Manchester Institute of Science and Technology
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Mismatches:
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/strain="White Leghorn, Hisex"
/db xref="taxon:9031"
/clone="ChEST902117"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Simon. Hubbard@umist.ac.uk.
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Gallus gallus
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RESULT 38
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862 bp mRNA linear EST 04-DEC-2002

AGENCOURT 11044319 NICHD XGC Emb1 Xenopus laevis cDNA clone
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
LeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluGluLysArgLysGluValThr
                                                  SerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArg
                                                                                                                   GlnTyrGlubeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGln
                                                                                                                                                                        GinLeuValAspAlaLysLeuGinGinAlaGinGluMetLeuLysGluAlaGluArg
                  AsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGlu
                                                                                                                                                                                                                          365 CAACTGGTGGATGCCAAACTCCAGCAACTACCAACTTAATAAAGAAGCAGAGAAAA
                                                                                                                                                                                                                                                                         439 LysgluLeuGluGlyLeuGlnValLysIleGlnArgleuGluLysLeuCysArgAla 457
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1 (bases 1 to 862)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM14488 row: a column: 20
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Xenopus laevis
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CA793605.1 GI:26042492
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Unpublished (1997)
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CA793605
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/organism="Xenopus laevis"
/mol type="mRNA"
/db Xref="taxon:8355"
/dlone="ImAGB:665533"
/tissue type="embryo (stage 10)"
/tissue type="embryo (stage 10)"
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/lab_bost="NH10B (phage-resistant)"
/lab_nost="Necror: pGMV-8PoRn6; Site 1: NotI; Site 2: SalI;
/note="Vecror: pGMV-8PoRn6; Site 1: NotI; Site 2: SalI;
/lab unidirectionally. Primer: Oligo df. Average insert
size 1:55 kb. Constructed by Life Technologies. Note: This
is a Kenopus Gene Collection (XGC) libzary."
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422 CAGCAAACCACTCAGCTTATGAAGBAAGCCGAAGAGAGAGACATCAGCGGGAAAAGAGAGTTT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 ITGTTGAATGAGGCAACTGAAAGGCAAAAGTTTGAAGAATTAAAACAACAAGAAAGC
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Matches:
Conservative:
Mismatches:
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High quality sequence stop: 687
Location/Qualifiers
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88.85%
71.22%
38.38%
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AGENCOURT 8752844 NIH_MGC_130 bp mRNA linear EST 21-AUG-2002
S', mRNA sequence.
BQ950691
                                                                                                                                                               279 AsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGlu 298
                                                                                                                                                                                        243 AATGCTAAACTGCGTCAAGAGAATGTTGAGCTTGCTGATCGACTTAAGAAGCTTATCGAG 302
                                                                                                                                                                                                                                                               299 GinTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGln 318
                                                                                                                                                                                                                                                                                                          303 CAATATGAGCTAAGAGAAGAGACATTGACAAAGTTTTCAAAGATAAAGGATCTTCAACAG 362
                                                                                                                                                                                                                                                                                                                                                           319 GlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluArg 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 CACCAGGGGAAAAGAGTTTCTGTTGAAAGAGGCGCAGTCGAATCCCAGCGCATGTGTGAA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 GluGluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGlu 398
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NIH-WGC http://mgc.nci.nih.gov/.
259 SerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArg 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 LeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPhe 378
                                                                                                                                                                                                                                                                                                                                                                                                      363 CAACTGGTGGATGCGAAGCTTCAGCAAGCACAAGAAATGCTGAAAGAAGAAGAAGAGCGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (phage-resistant)"
/clone lib="WHH MGC 130"
/hote="organ: ofcrysts; Vector: pCMV-SPORT6.1; Site_1:
/note="organ: ofcrysts; Vector: pCMV-SPORT6.1; Site_1:
ScoRV; Site_2: NotI; Cloned unidirectionally. Primer:
                                                                                                                    183 recentriceaagreacereareacarecagreacagageaceacacarearearea
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

Plate: LLANL3798 row: h column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 MetGluLysMetThrLysLyslleLysLysLeuGluLysGluThrThrMet 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 АТGGAAAAGATGACAAAGAAGATTAAGAAGCTGGAAAAAAGAGACAACCATG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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/db xref="taxon:10090"
/clone="IMAGE:6335682"
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Location/Qualifiers
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Mus musculus
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AUTHORS
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JOURNAL
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CDNA Library Preparation:

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llni.gov

Plate: LLAM11780 row: E column: 11
                                                                                                                                                                                                                                 654 bp mRNA linear BST 22-MAY-2002 CC. CC. MAY-2002 MAY-2002 MAGE:238018 5', mRNA sequence. BQ389733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="gastrula"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NCH0B XGC_Embs"
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Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.0 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
                                                NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
Mational Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
                      AlakeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGln 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S ATCCTGGCAAGAAGCAAGCTCGAAAGTTTGTGCAGAGAGCTACAGAGACACAACCGTACA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AAAAAACAGACCCAGCTTATTCAAGAAAGGATCTACTTCGTAATGAGGAAGGCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                 446 ValLys1leGlnArgleuGluLysLeuCysArgAlaLeuGlnThrGluArgAsn 463
                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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Silurana tropicalis
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/db_xref="taxon:8364"
/clone="IMAGE:5308018"
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                                                                                                                                                                                                                                                                                                                                                     BQ389733.1 GI:21077420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae, Silurana.
1 (bases 1 to 654)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                   393 GCAGCCAGGAATGGGGAGCCTGAACCAGCATTCCAGTCGTCAACGGCGAGAAGGAGACC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                         512
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 b. Constructed by a NIH_MGC Library
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                                                                                                                                                                                                                                                                                 61 ArgGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
                                                                                                                                                                                           21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu
                                                                                                                                                                                                          96 AAGGGCAGCCCGGGGCAACGGAAGCAGGACCGGAGGAGCCCATGGACGACCCAGACAG
                                                                                                                                                                                                                                      GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer
                                                                                                                                                                                                                                                                                                                                               GAGGAGGAGCACAGGAGAGCCCACTGAGCCGGAAGACACGGAGAAGTCCCGAACCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                              HisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGCCCCGAGCAAGCTTGAGAGTCTGTGCCGGGGAGCTGCCACGGGACCACCGGGATCCC
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Oligo dT. Average insert size 1.95 kb.
ResGen, Invitrogen Corp. Note: this is a
                                                     930
218
9
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7
                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                             x BQ950691 (1-930)
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                                                 1.13e-57
1025.00
84.70%
81.34%
37.93%
                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                             US-10-023-523-8 (1-530)
                                          Alignment Scores:
Pred. No.:
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EST 03-SEP-2002

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BU151934

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AGENCOURT 8753209 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6394355
5', mRNA Sequence.
BU151934
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/clone lib="NIH MGC_130"
/clone lib="NIH MGC_130"
/note="Corgan: oFocysts; Vector: pCMV-SPORT6.1; Site_1:
ECGRV; Site_2: NGT Cloned unidirectionally. Primer:
oligo dT. Average insert size 1.95 kb. Constructed by
ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                    Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostor
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; I
1 (bases 1 to 954)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freemar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GACCTGCAGCAGCAGCTAGTGGACGCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                            Ph.D. comb Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://mrage.lnl.gov
Plate: LLAM13897 row: e column: 12
High quality sequence stop: 512.
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:6394355"
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                                                                            BU151934.1 GI:22665466
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85.71%
37.55%
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775 CAGGCCGACGGGCCTACGAGCCACTCCGCCAGGCCTACAACCTGAGGCGCGAGGGAAGCG
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Mismatches:
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Matches:
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DB:
                                     Alignment 9
Pred. No.:
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602258906F1 NIH_MGC_85 Homo sapiens cDNA clone INAGE:4342392 5',
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/tissue_type="lymphoma, cell line"
/lab_host="DH10B [phage-resistant)"
/clone_lib="NHH MGC 85"
/note="Organ: lymph; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                MetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLys
                                                                                                      ACGTC-CGGGACAA-GAGCTGGAGGGCCTGCAGATC-CAGCGGCTGAAGCTG
  PhelysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGluThrThr
                         GlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu-----
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/db_xref="taxon:9606"
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF796069
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RESULT 44

us-10-023-523-8.rst

280 SerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGln 299 361 ATGAAGCTCTGTCACGAGAACACACAGAGAAGCTTGCAAAAGCTTCATCGATCAC 420 300 TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 319 421 TATGAGCTCAGAGAGGACATCTGGACAAATATTTAAACAGAACTGCAGAGAGGAGAGAGA	Db 601 CTGAAGAGACACACTCCTGCAGGCTCACTCTTTTTTTTTAAA 660 Qy 380 GluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet 399 601 GAATTCCAGACACACTAACTAAAAGCAACGAGGTGTTTGCCACGTTCAAACAGGAATG 720 Qy 400 GluLysMetThrLysLysIleLysLysLeuGluLysGluThrThrMetTyrAxgSerArg 419 721 GACAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	420 TrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAGGGGCTGAA 440 GluLeuGluGlyLeuGlnValLysSIGIAArgLeuGluLysLeuCysArgAlaLeuGln 1	Db 901 GAAGAGAACGAACTCCACAAAAAATCAGAGAAATATCTGAAAAGGATGAC 960 Qy 480 LeuThrAspSerGlyProGluArgArgProGluGly	Oy 492 500 1141 AGTTCTCAGGAGGTGCTGACGCCGCTCTCAAGGAGCCACCCCTCTGATCCT 1200 Oy 501	RESULT 45 AW412004 LOCUS LOCUS DEFINITION u055109.y1 NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:2646473 5' similar to SW:IL14_HUMAN P40222 INTERLEUKIN-14 PRECURSOR; mRNA ACCESSION AW412004 VERSION AW412004 KEYWORDS EST.
AY405165 AY405165 DEFINITION Homo sapiens HCM2133 gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION VERSION AY405165 AY40516 AY40511 AY40516 AY40516 AY40511 AY40516	JOURNAL Science 302 (5652), 1960-1963 (2003) REFERENCE 14671302 REFERENCE 2 (bases 1 to 1611) AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive.	Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and them based on alignment. Location/Qualifiers 1. 1611 /mol_type="genomic DNA" /db_xref="taxon:9606" /locus_tag="HCM2133"	Alignment Scores: Pred. No.: S. 99e-55 Length: 1611 Pred. No.: Score: Pred. No.: 988.00 Matches: Conservative: 56 Best Local Similarity: 48.02* Mismatches: 107 Query Match: 29.57* Indels: 60 Bs: US-10-023-523-8 (1-530) x AY405165 (1-1611) Qy 160 MetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys 179	180 TyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLys [240 LysGluGluGluValGlnArgAlaArgGluGluGluGluGluGluCysArgLysGluValThrSer [1

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/db_xref="taxon:9606"
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/cell lib="HeLA"
/clone lib="HeLA"
/clone lib="than sapiens HELA CELLS COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was primer was not and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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BX370444 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDM A clone CSODKO06YO23 5-PRIME, mRNA sequence.

BX370444.1 GI:30437782
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Libhrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 880.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?see_ECSOBAG046ZA04 CSO4345_1&cluster=880.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fullhength.invitrogen.com/ Invitrogen Corporation 1600
http://fullhength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG046ZA04_CSO4345_1.
                                                                                                                                                                                                                  332
                                                                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                                                                                                                                                                 333 LysgludladludludrgHisgludysAspPheLeuLeuLysGludlaValGlu 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600
                                                                                                                    420
                                                                                                                                                                            293 LeuLysLysLeulleGluGlnTyrGluLeuArgGluGluHislleAspLysValPheLys 312
301 AAGCGCAAAGAAGTGACTTCACACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 970)

1.i., W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length, cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                         481 CATAAGGACCTGCAGCAGCAGCTAGTGGACGCCAAGCTCCAGGAGGCGCGAAGAGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 AATGAGGCAGATGAGCGGCACCAGCGAGAGAAGGAGTTTCTCCATGAAGAAGAGTGTGTGGAG
                                                                                                                                                                                                                                                                                                313 HislysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeu
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                                                                                                                    361 GAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGG
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Indels:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeu 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2646473"
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/note="Organ: lugy, Vector: pCMV-SPORT6; Site_1: Sall;
/tipe="organ: lugy, Vector: pCMV-SPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | LeualaalaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae; Murinae; Mus
                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (basea to 620)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong strand Seq primer: -40RP from Gibco High quality sequence stop: 431.

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                         musculus (house mouse)
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985.00
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95.63%
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DB:
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/dev_grage="150011/"
/dev_grage="150011/"
/dev_grage="150011/"
/clone_lib="CSEQCHN71"
/note="0rgen: hearts; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., pNAS
(1994) 91: 9228-9323 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysSerArgThrTyrValAlaArgAsnGlyGluProGluPro---ThrProValValTyr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||||:::
67 AAGIGICGCAGIGAGICCCCGAGGAACGGAGATCAGGAGTCAGGCAGGCCCCGAGAIGAAI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLys 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluileThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAla 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GCACTGTGCAAGAAATACGCTGAGCTGCTGGAAGAGCACCGTAACTCCCCAGAAACAGGATG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGlu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GinGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 GAAATCACTTTGTTGATGCAGACCCTGAACACCCTGAGGCACTCCAGAGGAGAAACTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 AAGATTTTGCAGAAGAAGAGAGACACACACTGGTGCAAGAGAAGGACCACCTGCAGAGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 HisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArg
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116
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6
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Matches:
Conservative:
Mismatches:
Indels:
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/clone="ChEST366f17"
                         Location/Qualifiers
1. .720
/organism="Gallus gallus"
      Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-023-523-8 (1-530) x BU359309 (1-720)
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977.00
88.848
82.23%
36.16%
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Best Local Similari
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Phasianinee; Gallus.

Loases 1 to 720)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                              GATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCATCGAAGG
                                    103 ArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSerLysGly
                                                             LeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGlu
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University of Manchester Institute of Science and Technology
(UMIST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, Tel: 01612008930
Fax: 01612360409
US-10-023-523-8 (1-530) x BX370444 (1-970)
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Gallus gallus
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Mus musculus

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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                                                                                                           ArgAlaArgGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeu
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LeuserThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGlu
                                                                                       GluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuVal
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7827164 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:6014257
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/lab_host="DH10B (phage-resistant)."
/clone_lib="NUH WGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 2:8 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SESTACABAGAAAACTTTAGAAAAGAAGTTTTATTACTGATGCCCTAAACAC 77
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NIH-MGC http://mgc.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                         SLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLys-ValPheLysHisL
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                                       nHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLy
           Lys-GluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Bmail: capaber-Gmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can blound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM13208 row: h column: 02
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6014257"
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BQ421247.1 GI:21116562
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89.15%
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5', mRNA sequence.
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KEYWORDS
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DEFINITION
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MetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys
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/strain="NMRI"
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83.61%
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BG975353
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  Brain Molecular Anatomy Project
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                             dev_stage="embryo 12.5dpc"
lab_host="DH10B (T1 phage :
                                                                                                                                                                                                                                                                 tissue_type="whole brain"
This clone was contributed by the (BMAP)
                                                                                                                                    'organism="Mus musculus"
                                                                                                                                                                                                              db_xref="taxon:10090"
clone="IMAGE:6837021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-023-523-8 (1-530) x CB247697 (1-784)
                                                Seq primer: pYX-5.
Location/Qualifiers
                                                                                                                                                           mol_type="mRNA"
strain="C57BL/6"
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/db xref="maxon:10090"
/clone="IMAGE:4978775"
/tissue_type="tumor, gross tissue"
/dev stage="tumor, gross tissue"
/dev stage="5 months"
/lab_host="DH10B"
/clone lib="MOI GGAP Mam4"
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Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG975353 796 bp mRNA linear EST 12-JUN-2001
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 796)
NIH-MGC http://mgc.nci.nih.gov/.
620 TATGCTGAGCTGCTGGAAGAGCATCGGAACTCGCAGAAGCAGATGAAGCTCCTGCAGAAG
                                                                                                                                                                                   200 LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: Grapbs-r@mil.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рe
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10975 rown column: 24
High quality sequence stop: 780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                      220 LeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArg 234
                                                                                                                                                                                                                                                                                                                                                    CTGGCCCGAAGCAAGCTTGAGAGTCTGTGCCCCGGAGCTGCAACGG 783
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: June 8, 2004, 12:35:08 Job time: 3911.61 secs

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Perfect score: Scoring table:

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Bovine em Human bon

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Human ova Bovine em Gene MYH1

Ade45661 F Abq55358 F Abn74510 E Abk35570 C

Human car

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Human cer Human cDN

Farnesyl

Ade85060

Human smc

Drosophil DNA encod

Human DNA

Aav88391 Acd13448 B

Human

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Low density lipoprotein binding protein; LDL binding protein 3; LBP-3; receptor; human; atherosclerosis; diagnosis; therapy, vaccine; ss.
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/*tag= b
/note= "Claim 2
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22.3.8 11575
23.8 1233
23.8 1734
20.4 2526
19.5 4307
17.7 334
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  Command line parameters:
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-MODEL=france+ p2n.model -DEV=xlh
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-LOOPEXT=0 -UNITS=bits -STAFT=1 -TRNS=-1 -MATRIX=biosum62 -TRANS=human40 -Cdi
-LIST=50 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50
-MODEL=LOCAL -OUTFMT=pto -NORM=ext -HEAPIXE=500 -MINLENE=0 -AALIGN=50
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-NO_MMAP -LANGEQUERY -NGG SCORE=0 - WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=0 -YARADP=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=6
-FGAREXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDF=6 -DELEXT=7
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Aah26496 Human low
Aah26501 Human low
Aba09908 Human LDL
Aak52874 Human pol
Acc46153 Human dit
Acc46139 Human dit
Aav32836 Rabbit lo
                                                                                8, 2004, 06:37:54 ; Search time 598.959 Seconds (without alignments) 3759.096 Million cell updates/sec
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1 KSSPGQPBAGPBGAQBRPSQ.....APSTBASGQTGPQBPTSARA 530
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                            OM protein - nucleic search, using frame plus p2n model
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Delop 6.0, Delext
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(BOST-) BOSTON HEART FOUND INC
   96US-0031930P.
97US-0048547P.
                           WPI; 1998-322455/28
P-PSDB; AAW49042.
                     RS,
                                                 subjects at risk
                    Lees
   27-NOV-1996;
03-JUN-1997;
                     Lees AM,
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Arjona AA;

This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-3 (see AAW49042). It was isolated by screening human liver, ancrta and foetal brain cDNA libraries with rabbit LBP-3 cDNA. CDNA clones (see AAV32834-39) and encoded trabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene formation of atherosclerotic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying Claim 10; Fig 17; 47pp; English

Sequence 4697 BP; 1097 A; 1198 C; 1289 G; 1113 T; 0 U; 0 Other;

242 GCCGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCAGCAGGCTCCTCGGAAGCCGGAG 122 182 81 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100 GAGGATGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTAT 302 120 362 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 141 ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMet 160 363 AAGGGGGATCCAAACACAGAAGAGATCCGGCAGAGGGGGCGAGGTCGGAGACCGAGACCAT 422 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 20 9 80 AAAAGCAGCCCAGGACAACCGGAAGCAGGACCCGAGGAGCCCAGGAGCGGCCCAGCCAG 21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 40 41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 303 GTGGCAAGGAATGGGGAGCCTGAACTCCAGTAGTCTATGGAGAGAAGGAACCCTCC 101 ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-023-523-8 (1-530) x AAV32839 (1-4697) 1.4e-157 2702.00 100.00% 100.00% Percent Similarity: Best Local Similarity: 63 61 121 Query Match δ a d ò dd ò g ò 음 셤 ò ð g δ d

qq	423 C	GAAGGCCACAGGAGAAAAAAAGGCCAAGGGTTTGGGGAAGGAGATCACGTTGCTGATG 482
٥٨	161 G	GlnThrieuAsnThrleuSerThrProGluGluLysbeuAlaAlaLeuCysLysTyr 180
Ор	483 C	TGAGTACCCCAGAGGGGAGCTGGCTGCTCTGTGCAAGTA
ò		AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLySLeuLeuGlnLysLys 200
Dp	543 G	AGCACCGGAATTCACAGAAGCAGATGAAGCTGCTACAGAA
λō i	01	CA
අූ .	03	AGCCAGCTGGTGCAAGAAAGGACCACCTGCGGTGAGCAAAGGCCGTCCTG 66
Š 7	21 A	LaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 24
a D	m	GGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGCTCCCTCAAG 72:
8 8	٦ ,	9
<u>a</u> (57	GACCICGCAC 78
දු දු	261 PF 783 TT	PheGinValThrLeuAsnAsplieGinLeuGinMetGluGinHisAsnGluArgAsnSer 280 TTCCAGGGGACACATGAETGAETGAETTGAETTGAETGAETGAETGAETGAET
ò	81	leGluGlnTvr 3
QC	843 AA	
δλ	301 G1	InglnGlnLeu 32
QQ	903 GA	AAACACAAGGACCTACAACAGCAGCTG 96
à	321 Va	JeulysGluAlaGluGluArgHisGln 34
qq		GGATGCCAAGCTCCAGCAGCCCAGGAGGTGCTAAAGGAGGCAGAAGAAGAGCGCCCCC
ð 4	341 Arg	3luLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 36
3	9	SAGAAGGAIIIICICCIGAAAGAGGCAGIAGAGICCCAGAGGAIGIGIGAGGTIGAIG 10
දු දු	361 Lys(SedinGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380
δ	81	3lnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 40
QC .	1143 TT	
λ	01	hrMetTyrArgSerArgTrp 42
ΩP	03	
ζ	21 9	luSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 440
q	თ	scadcaacaacccingciidagaidgcigagagaaaaacagiccdggaiaaagaa 13
à	-Fe	uGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr 46
qq	1323 CT	CGAGGGCCTGCAGGTAAAAATCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGAC
ģ	61 G1	uArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeu 48
ПЪ	1383 GAC	GCGCAATGACCTGAACAAGGGGTACAGGACCTGAGTGGCTGGC
λ̈́O	81 Th	RASPSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerPro 50
qq	1443 ÁC	igacagiggeectgagaggaggeeagaggeectgageeteaageacteece
ò	501 Ard	9ValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520

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US-10-023-523-8 (1-530) x AAH26496 (1-4697)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 3 (LBP-3, see AAB82804). Clones were isolated from human foetal brain, liver and aorta cDNA libraries using rabbit LBP-3 cDNA as probe. A full-length cDNA clone is given in AAH26501, and a genomic DNA sequence is given in AAH26497. LBP-3 nucleic acids are among claimed polypucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
1503 AGGGTCACAGAAGCGCCTTGCTACCCAGGAGCACCGAGCACCACAAGCATCAGGCCAGACT 1562
                                                                                                                                                                                           Low density lipoprotein binding protein 3; LBP-3; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; 1290 G; 1113 T; 0 U; 0 Other;
                                                                                                                                                                     Human low density lipoprotein binding protein 3 (LBP-3) cDNA.
                                    521 GlyProGlnGluProThrSerAlaArgAla 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arjona AA;
                                                                                                                                                                                                                                                                Location/Qualifiers
3. 1596
/*tag= a
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                                                                                             AAH26496 standard; cDNA; 4697 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOST-) BOSTON HEART FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
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                                                                                                                                                                                                                                              Homo sapiens.
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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.4e-157 2702.00 100.00% 100.00% 100.00%

Percent Similarity: Best Local Similarity: Query Match: DB:

Gaps:

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GTGGATGCCAAGCTCCAGCAGGCCCAGGAGTGCTAAAGGAGGCAGAAAAAGGCGCACCAG 1022
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The present sequence is that of the coding region of the human gene (see also AAH26496) encoding novel human low density lipoprotein binding protein 2 (IBP-3, see AAB82808). The gene was isolated from a genomic DNA library using 1BP-3 conh as probe. The IBP-3 protein predicted from the present sequence differs from that predicted from a cDNA clone (see AAB82804) in that it contains an additional 16 amino acids at its N-cermins (the cDNA is a 5' truncation) and has Asn at amino acid position 130 rather than Tyr: LBP-3 nucleic acids are among claimed cof binding to native and methylated LDL. Also claimed are isolated LBP colymucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP colympeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for treating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or cemptained or nucleic acid, and vaccine compositions, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAG 648
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Claim 8; Fig 8A; 143pp; English.
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                                                    .083 AAGCAGCAAGAACCCACCTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAG
                                                                                                                      New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                         .203 AAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACCATGTACCGGTCCCGGTGG
                                                                                                                                                                                                                                GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu
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                                 LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu
                                                                                               PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu
                                                                                                                                                               LysMetThrLysLysleLysLysLeuGluLysGluThrMetTyrArgSerArgTrp
                                                                                                                                                                                                                                                             263 GAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGAAAACAGTCCGGGATAAAGAA
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                                    AlaargSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 240
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11-JAN-2002 (first entry)

Human LDL binding protein homologue-encoding cDNA, SEQ ID NO:784.

cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation, tissue growth, immunomodulator; activin, inhibin; chemotaxis, chemokinesis; thrombolysis; oncogenesis; proliferation; metastessis, cancer; tumour; heamatopoietic disorder; proliferation; metastessis, cancer; tumour; heamatopoietic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis, coronary heart disease; arcerial ischaemia; bone disorder; osteoporosis; vascular growth disorder; call culture; drug screening; qene therapy; antinflammatory; cell culture; drug screening; gene therapy; antinflammatory; antiarthritic; haemostatic; antiarthritic; demostatic; antiarthritic; astochoic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US003800

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. P-PSDB; ABB11764. Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis

Claim 1; Page 693-694; 1963pp; English.

concentration bolypepides, and recombinant polypepides, and sequences Abblob25-AbbA0574 represent laby mover number of sequences Abblob25-AbbA0574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of detecting the nucleotides of nucleotides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the competition are not properties of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptides of the invention activities activities, including cytokine, cell proliferation or cell differentiation activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; chemocopies required activities; homogonic or chemochatory activity; activin. or inhibin-related activities; chemocopies required activities; becaptor or liagand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Compending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemacopolesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemacopolesis, or representing or ameliorating medical activities polypeptides and nucleotides of proliferative retinopathy, atherocaclerosis, occonary heart disease.

Conditions, e.g., by protein or gene therapy. Such conditions include activities and include activities involved with tissue regeneration and repair (or nucleic acide encoding them) may be used to promote wound repair (or nucleic acide encoding them) may be used to promote wound immunomodulatory activities un activity may be used in cell cu Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

ABA09008 standard; cDNA; 2523 BP.

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cell growth. For example, such polypeptides may be used to
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\$88 888 888	promote cell g manipulate ste that can be us autoimmune dis may also be us screening tech novel human po	promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by lilness, autoimmune disease or accidental damage. The polypeptides and nuclectides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention	
ŏs	Sequence 2523	BP; 666 A; 626 C; 794 G; 437 T; 0 U; 0 Other;	
Alignm Pred, J Score: Percent Best Lo	ent Scores No.: t Similari ccal Simil Match:	2.55e-157 Length: 2523 2633.00 Matches: 529 99.81% Conservative: 0 ty: 99.81% Mismatches: 1 99.67% Gaps: 0	
US-1	0-023-523-8 (1-	530) x ABA09008 (1-2523)	
ζο, i	н ;	rProglyginProgluAlaglyProgludlyAlaglnGluArgProserGln 20	
a .		SAGUGGUUCAGUUAG Z	
· 중 원	21 AIAAI 227 GCGGC	AlaAtakroniaaatoludiaagiudiyykrodiyserselialarromigiyskrodiu 40 	
δ	41 GlyAL	adlnAlahrgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60	
QQ	287 GGGGC	GGGGCTCAAGCCAGAAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGG 346	
ò	61 ArgGl	ArgGinLeuGluAspileLeuSerThrTyrCysValAspAsnGanGlyGlyBroGly 80	
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දු දු	81 Gluas 407 GAGGA	GluaspGlyalaGlnGlyGluProAlaGluProGluaspAlaGluLysSerArgThrTyr 100 	
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qq	707 GCTGA	CAGATGAAGCTCCTACAGAAAA	
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b c	221 AlaArc 827 GCCGC	gSerlysleuglugerleugysarggluleuginarghisasnargserleulys 240 	
δ	241 GluGl	GluGluGlyValGlnArgAlaArgGluGluGluGluUGluLysArgLysGluValThrSerHis 260	
QQ	887 GAAGAA	AGCGGGCCCGGGAGGAGGAGAAGCGCAAGGAGGTGACTCGCA	
à	261 PheGlr	PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280	

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                      947 TTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACAGCACAATGAGCGCAACTCC 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 GluArgAsnAspleuAsnLysArgValGlnAspleuSerAlaGlyGlyGlnGlySerLeu 480
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                                                          281 LysleuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr
                                                                                                                                                                                                                                 321 ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln
                                                                                                       1007 AAGCTGCGCCAAGAACATGGAGCTGGCTGAGAGGCTCAAGAAGCTGATTGAGCAGTAT
                                                                                                                                                  301 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu
                                                                                                                                                                        1067 GAGCIGCGCAGAGAGCAIAICGACAAAGTCTICAAACACAAAGACCTACAACAACAGCAGCIG
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1727 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 GlyProGlnGluProThrSerAlaArgAla 530
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WO200157190-A2

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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                Xu C, Cao Y;
, Chen R, Wang ZW;
                                                                                                                                                Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, X
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                               Claim 1; Page 4687-4688; 6221pp; English
                                          03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00598075.
19-UUL-2000; 2000US-0063035.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0063325.
30-NOV-2000; 2000US-00633325.
                          05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                     WPI; 2001-476283/51.
P-PSDB; AAM79741.
                                                                                                                               (HYSE-) HYSEQ INC.
         09-AUG-2001
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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetric activity in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 2523 BP; 666 A; 626 C; 794 G; 437 T; 0 U; .0 Other;

es: 2.55e-157 Length: 2523 2693.00 Matches: 529 1rity: 99.81% Conservative: 0 Mismatches: 1 99.67% Indels: 0 4 Gaps: 0	-8 (1-530) x AAK52874 (1-2523)	LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 20	AAAAGCAGCCCAGGAACCAGGAAGCAGGACCCGAGGAAGCCCAGGAGCGCCCAGGCAG	AlaAlaProAlaValGluAlaGluGlyProGlySerGlnAlaProArgLySFroGlu 40	GCGGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAG 286	GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60	GGGGCTCAGCAGCGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGGTGAGG 346	ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80	CGCCAACTGGAAGACATACTGTGTTGGGACATAACCGGGGGGCCCCGGGC 406	GluaspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100	GAGGATGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTAT 466
Alignment Scores: Pred. No.: Score: Similarity: Best Local Similarity Query Match:	US-10-023-523-8	у 1	167	у 21	Db 227	Oy 41	Db 287	Qy 61	Db 347	Qy 81	Db 407
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	121	sGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 14	
	141	uLeuMet 16 GCTGATG 64	
	161	ITHELEUASHTHELEUSBETHEPFOGIUGIULYSLEUAJAAIALEUCYSLYSLYSTYE 18 	
	181	AlagluleuleuglugluhisargasnSerglnlysglnMetlysLeuleuglnlysLys 200 	
	201	nserGlnLeuvalGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 22 	
	221	rLėuLys 24 CCTCAAG 88	
	241	JGIUGIYVAIGIDARGAlaArgGluGluGlUGIULIYSARGIYSGIUVAIThrSerHis 26 	
	261	sGinLeuginMetGludinHisAsnGluArgAsnSer 28 	
	281	IysieuargGlnGluaanMetGluLeualaGluargLeuLysLysLeuIleGluGlnTyr 300 	
	301	GluLeuArgGluGluHis1leAspLysValPheLysHisLysAspLeU 	
	321	ValAspalalysteuginginalagingiuMetteulysgiuAlagiugluargHisgin 34	
	341	ArgGlulysAspPheLeuLeulysGluAlaValGluSerGlnArgMetCysGluLeuMet 36	
	361	LysglnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 3	
	381 1307	PheginasnThrieuSerLysSerSerGluValPheThrThrPheLysGlnGluWetGlu 40 	
	401	LysMetThrLysLysLleLysLysLeuGluLysGluThrT 	
	421	alargaspLysGlu 44 	
	1487	LeuGludlyLeuglnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr 46	

polynucleotide sequences at least 90% identical to the dithp cDNA

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1606
                                                               1666
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                                           500
                                                                                      520
                                                                                                                                                                                                                                                                             Human; dithp; diagnostic and therapeutic polymucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genocyping; transgenic animal; knock in; extracellular signalling; gene; ss.
             GluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlyGlnGlySerLeu
                                         ThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro
                                                               1607 Actigacadececercadadadadadadadadadacececece
                                                                                                 1667 AGGICACAGAAGCGCCTTGCTACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACT
                                                                                    ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr
                                                                                                                                                                                                                                                            Human dithp extracellular signalling protein-encoding cDNA
                                                                                                                                         1727 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1756
                                                                                                                              521 GlyProGlnGluProThrSerAlaArgAla 530
                                                                                                                                                                                              ACC46153 standard; cDNA; 5085 BP
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2001US-0280067P.
2001US-0280068P.
2001US-0291280P.
2001US-0291829P.
2001US-0291849P.
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                                                                                                                                                                                                                                          (first entry)
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29-MAR-2001;
16-MAY-2001;
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CC recombinant production adjusted and theas was least by a factorial to the altupy curva compounds sequences of the invention; recombinant vectors, host calls and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of screening for compounds which specifically bind a DITHP protein; and methods of disposes in the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP protein; and methods of disposes of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic proliferative disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dith nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human isease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a ditho DNA encoding a DITHP procein which has extracellular signalling activity. Note: The sequence data for the primer intering from protein animal of the primers of the primers of the primers of the primers of the primers of the present sequence represents a ditho DNA encoding a DITHP procein which has extracellular signalling activity. Note: The sequence data for the primer intering the discorder of the primers of th

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Sequence 5085 BP; 1178 A; 1310 C; 1407 G; 1190 T; 0 U; 0 Other;

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Matches: Conservative: Mismatches: Indels:

5.5e-157 2693.00 99.81% 99.81%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Gaps: (1-5085)

US-10-023-523-8 (1-530) x ACC46153

160 387 447 507 567 100 627 120 687 747 807 161 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr 180 40 9 80 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGluGluArgProSerGln 21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 388 GCGGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCAGCCCAGGCTCCTCGGAAGCCGGAG GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 448 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGC 508 CGCCAACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCCGGC GAGGATGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAAGATCCCGGAAGTCCCGGACCTAT ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer AAGGGGGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCAT CGAAGGCCACAGGAGAAGAAAAAGCCAAGGGTTTGGGGGAAGGAGTCACGTTGCTGATG ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr GTGGCAAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGAAGGAACCCTCC ArgArgProGlnGluLysLysLysBlyLysGlyLeuGlyLysGluIleThrLeuLeuMet rH 41 101 61 81 688 268 121 ò a ઠે ઠે g ₽ g g d à g В ò à ò

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Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin I,
David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;

Daughtery SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R,

Daffo A, Jones Dufour GE, Hil Daughtery SC,

WPI; 2003-129518/12. P-PSDB; ABR41210.

2001US-0299776P 2001US-0300001P

19-JUN-2001; 20-JUN-2001; 20-JUN-2001;

(INCY-) INCYTE GENOMICS INC.

Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Claim 2; SEQ ID NO 74; 591pp; English.

The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to

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1888 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1917
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29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-0280068P.
16-MAY-2001; 2001US-029180P.
17-MAY-2001; 2001US-0291849P.
17-MAY-2001; 2001US-0291849P.
20-UJN-2001; 2001US-0299428P.
20-UJN-2001; 2001US-0299476P.
                                       ACC46130 standard; cDNA; 6577
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                                                          ACC46130;
                   RESULT 7
ACC46130
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Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J; Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR; Daughtery SC, Dam TC, Liu TF, Ngryen DA, Kleefeld Y, Gerstin Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

(INCY-) INCYTE GENOMICS INC.

2003-129518/12. P-PSDB; ABR41186 Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Claim 2; SEQ ID NO 51; 591pp; English.

The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP, ABR4136-ABR4812). The invention also relates to proteins (DITHP, ABR4136-ABR4812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transpenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins, antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleic and protein sequences; methods of sessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other call confiferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; and connective tissue disorders. They may also be used to

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GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1048 GAAGAAGGTGTGCGGGGCCCGGGAAGAGGAGGAGGAAGCGCAAGGAGGTGACCTCGCAC
                                                             PheglnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Low density lipoprotein binding protein, LDL binding protein 2, receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine;
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Location/Qualifiers 61. .1734

/*tag= a 348. .390 /*tag= b /note= "Claim 22"

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(BOST-) BOSTON HEART FOUND INC.
  Oryctolagus cuniculus.
                                                                WPI; 1998-322455/28.
P-PSDB; AAW49039.
                                             27-NOV-1996;
03-JUN-1997;
                                       26-NOV-1997;
                            WO9823282-A1
                misc_feature
                                 04-JUN-1998,
                                                           Lees AM,
        Key
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Lees RS, Law SW, Arjona AA;

96US-0031930P. 97WO-US021857.

This cDNA clone codes for novel rabbit low density lipoprotein (LDL) binding protein LBP-3 (see AAM49039). It was isolated by functional screening of a cDNA library, produced from balloon-dendchehialised healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to bind both native and methyl LDL. cDNA clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An chorded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in an aspect of LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for cheranting if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerotic plaque; and methods for treating a cell compation of atherosclerotic plaque; and methods for treating a cell vaccine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying Sequence 4722 BP; 997 A; 1332 C; 1430 G; 963 T; 0 U; 0 Other; Claim 7; Fig 14; 47pp; English. subjects at risk

Length: 4722 Marches: 492 Conservative: 12 Mismatches: 25 Indels: 13 Gaps: 3	6 (1-4722)	LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 20	AAAAGCAGCCCGGGACCGGAAGCAGGAGCGGAGGAGCCCAGGGGCCGGCCCGG 168	21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 40	169 CCGGCCCCGCCCGAGAGCCGAAGGTGCCAGCAGCCAGGCCCGGGAGGCCGGAG 225	41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60	226 GGGGCTCAAGCCAAAACTGCTCAGCCCTGGGGCTCTGTGATGTCTTCTGAGGAGCTGAGC 285
5.75e-143 2465.50 92.99% 90.77% 91.25%	x AAV3283	rProGlyGlnF	CCGGGACAGC	AlavalgluA	CGCCGAGAAG	AlaArgThr	AGCCAAAACTO
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-10-023-523-8 (1-530) x AAV32836 (1-4722)	1 LysSerSer	109 AAAAGCAGC	21 AlaAlaPro	169.00660000	41 GlyAlaGlr	226 GGGGCTCAA
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Tredgl	pglyal rggggr	aArgas AAGGAA	sGlyAs 	gArgPr GAGGCC	nThrle GACACT	aGluLe GGAACT	nSerG1 GAGCCA	aArgSe ccccAG	uglugl AGAAGG	eGlnVa :: CCAGAT	sLeuAr GCTGCG	uLeuAr GCTGCG	1AspA1 GGACGC	ggluby ggagaa	rsGlnG] GCAACP	eGlnAs ccAGA	sMetTP GATGAC	userse.
Arggl:	GAGGA	ValAl GTGGC	SerLy 	HisAr CACCG	MetG1 ATGCA	Tyral TATGO	Lysg1 AAGCA	Leual 	Lysgl AAGGA	HisPh CACTT	SerLy TCCAA	TyrG1 TACGA	LeuVa	GlnAr CAGCG	MetLy ATGAA	GluPr	GluLy	TrpG]
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                                             1426 GAGCTGGAAGGCCTGCAGGTGAAAATCCAGCGGCTGGAGAAGCTGTGCCGGGCACTGCAG
                                                                 ThrGluArgAsnAspleuAsnLysArgValGlnAspleuSerAlaGlyGlyGlnGlySer
                                                                                                                  ---GluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr
                                                                                                                                                                               509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla
                                                                                                                                                                                                                                                                                                                                                      Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                    Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA
                                                                                                      LeuThrAspSerGlyProGluArgArgPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOST-) BOSTON HEART FOUND INC
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2000US-00616289.
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The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 3 (LBP-3, see AAB22801). The cDNA was solated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel

treating,

New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.

Claim 5; Fig 14; 143pp; English

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polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
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                                                                                                                                                          Sequence 4722 BP; 997 A; 1332 C; 1430 G; 963 T; 0 U; 0 Other;
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                                                                                                                                               300 TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 319
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HisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsn
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

WPI; 2001-639362/73. P-PSDB; ABG00839. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631.

WO200175067-A2

11-OCT-2001.

Homo sapiens.

Claim 1; SEQ ID NO 830; 103pp; English.

biodiversity.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic conding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in procession of commentations. Note: The sequence date for this patent directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGGAGGAGCTGAGG 681
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61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80

1762 GTATTCACCACATTCAAGGAGATGGAAAAGATGAAAAGATCAAGAAGCTGGAG 1821	Qy 498 SerSerProArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSer 517 Db 2112 ATGGCTCCCACATCAGCCAA	Human polynuc Human; cytoki vaccine; pept tissue growth nervous syste Homo sapiens. WOZO0157190-P	PR 03-FEB-2000; 20000US-00560875. PR 27-APR-2000; 2000US-00560875. PR 27-APR-2000; 2000US-00560875. PR 19-7UL-2000; 2000US-00563935. PR 19-FEB-2000; 2000US-00563561. PR 19-CCT-2000; 2000US-006633561. PR 20-CCT-2000; 2000US-00663325. PR 30-NOV-2000; 2000US-00693325. PR 4VSE-) HYSEQ INC. XX PA (HYSE-) HYSEQ INC. XX PI ma Yr, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; PI Wa Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; XX VX XX VX VX VX VX VX VX VX VX VX VX
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                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or egeptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK22581), 2111
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Conservative:
Mismatches:
Indels:
              Page 1605-1607; 6221pp; English.
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                                                                                                                                               TyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThr
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets on unclaic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airway, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating conditions, pulmonary vasoconstriction, allergies, asthma, impaced respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD) and cancers such as leukaemias, lymphomas, containings, and cancers which may metastasise to the lungs, including carcinomas, and cancers which may metastasise to the lungs, including carcinomas, and cancers which any metastasis to the lungs, including carcinomas, and cancers which activates adenosine content of the content of the adenosine which activates adenosine receptors causing chroniconstriction and inflammation. AAA32131 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present contention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1860 (AAA33233 to AAA3392) are specifically claimed ONS from the present invention. N.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1259-1260; 1343pp; English
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                                                                                                                                                                              1791 AATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCCAGCTGGTGCAAGAAAG
                                                                                                                                                                                                          AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu
            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                    US-10-023-523-8 (1-530) x ABZ34807 (1-1793)
              8.376-98
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                                       Percent Similarity:
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                                         ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenosine receptor related polynucleotide 2nd SEQ ID NO:92
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Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeu
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                                                                                                                                                                                                                                                                 AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys
                                                                Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;
                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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952 GTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGGCCCTGAGAGGGGG
                                                                            ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla
                                                                                                                                                                                                                                                                                                            antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischemenic condition; pulmonary vasoconstriction; asthma, respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                 489 ProGluGlyProGlyAlaGlnAlaProSerSerProArqValThrGluAlaProCysTyr
                                              Human, adenosine receptor, low adenosine antisense oligonucleotide,
phosphorothioate, impaired respiration; inflammation; allergy,
allergic disease, bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                       Human adenosine receptor related polynucleotide 2nd SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                      cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                       AAA35217 standard; DNA; 1793 BP.
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New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

99WO-US017712, 98US-0095212P,

3-AUG-1999; 03-AUG-1998;

24-FEB-2000.

WO200009525-A2.

(UYEC-) UNIV EAST CAROLINA.

WPI; 2000-205971/18.

Disclosure; Page 1259; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, altialergic, and/or inflammation. The ON can have antihiflammatory, antialergic, antiasthmatic: cytostatic and analgesic activities. The compositions are useful for the treatment of disease associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs pulmonary vascocnstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (OCDPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers such as leukaemias, lymphomas, obreast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing

The state of the s

Manager of American States

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nucleotide sequences given in the sequence listing from the present invention, which correspond to SEO ID NO:1 to 2815, and then the last 185 sequences are also called SEO ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA33323 to AAA33929) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
  bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
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listing
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Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;

			* (5 5 1	0 0 0 0 17 505 10 11	, , , ,	
Alignmen Pred. No Score: Percent Best Loc Query Ma DB:	nt Sco D.: Simil Simil tal Si	res: arity: milarity:	2.15e-95 1688.00 99.12% 99.47% 62.47%	Length: 1793 Matches: 339 Conservative: 0 Mismatches: 1 Indels: 0		
:0-01-SD	23-523	-8 (1-530)	× AAA35217 (1-	1793)		
δλ	189	AsnSerGl	nLysGlnMetLysLeu	ureugjutystysgjusergju	LeuValGinGluLys 208	
Db	1791	AATTCACAG	_E	CTACAGAAAAAGCAGA	GCCAGCTGGTGCAAGAGAAG 1732	~
ζŏ	209	AsphisLeuA	rgGlyGluHisSe	rLysAlavalLeuAlaArgSeri	Lysheugluserhen 228	
Db	1731	GACCACCTG		 	_8 _8	m
δ	229	CysArgGluL	LeuGlnArgHisAsnA	ArgSerLeuLysGluGluGlyVa	alGlnArgAl	
qq	1672	TGCCGTGAG	CGTGAGCTGCACGGCACAACCGCT		GTGTGCAGCGGGCCCGG 1613	м
ò	249	GluGluGluC	uGluLysArgLysGluV	alThrSerHisPheGlnVal	ThrieuAspAspile 268	
DP QC	1612	GAGGAGGAGGAGAAG	_ც		ACACTGAATGACATT 1553	
ò	269	GlnLeuGlnMe	MetGluGlnHisAsnC	sasnGluargasnSerLysLeuargGl	SingluAsnMetGlu 288	
원	1552	CAGCTGCAG	ATGGAACAGCACAATC	GCTGCAGATGGAACAGCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATG	CAAGAGAACATGGAG 1493	м
λŏ	289	LeuAlaGluA	trgLeuLysLysLeuI	lleGluGlnTyrGluLeuArgGl	SlugluHisileAsp 308	
ΩÞ	1492	CTGGCTGAGA	GAGGCTCAAGAAGCTGAT	TGAGCAGTATGAG	CTGCGCGAGGAGCATATCGAC 1433	m
\$	309	LysValPheLy	ysHisLysAspLeuGl	1GlnGlnLeuValAspAl	alysteuglnglnala 328	
ДD	1432	AAAGTCTTCA	AAAGTCTTCAAACACAAGGACCTACA	JAACAGCAGCTGGTGGATGCCAA	AAGCTCCAGCAGGCC 1373	m
δ	329	GlnGluMetL	euLysGluAlaGluGl	uArgHisGlnArgGluLy	sAspPheleuleulys 348	
Db	1372	CAGGAGATGC	TAAAGGAGGCAGAAG	CTAAAGGAGGAGAAGAGCGGCACCAGCGGGAGAAGGATTTTCTCCTGAA		
λŏ	349	GluAlaValG	GluSerGlnArgMetC	CysGluLeuMetLysGlnGlnG	GluThrHisLeuLys 368	
Dp	1312	GAGGCAGTAGAGT	CCCAGAGGAT			_
δ	369	GlnGlnLeuA	labeuTyrThrGluLy	age -	nAsnThrLeuSerLysSer 388	
ΩP	1252	CAACAGCTTG	CCCTATACACAGA			
δ	389	SerGluValP	PheThrThrPheLysG	GlnGluMetGluLysMetThri	LysLyslleLysLys 408	
Db	1192	AGCGAGGTATTCA	TCACCACATTCAAGCA	GGAGATGGAAAAGATGACT	SATCAA	
λõ	409	LeuGluLysGl	uThrThrMetT	yrArgSerArgTrpGluSerSerA	erAsnLysAlaLeuLeu 428	
Db	1132	CTGGAGAAAG	GAAACCACCATGTACO	CCACCATGTACCGGTCCCGGTGGGAGCAGCAACAAGG	CCCTGC	
<i>≿</i>	429	GluMetAlaGl	uGluLysThrValA	rgAspLysGlu	euGlnVallysile 448	
op.	1072	GAGATGGCTG		GGGATAAAGAACTGGAGGGCC	CTGGAGGCCTGCAGGTAAAATC 1013	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammation; immunosuppressive; antisathmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypotrension; emplyemen; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antisthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and
GinArgieuGiuLysieuCysArgAlaieuGinThrGluArgAsnAspLeuAsnLysArg
                                                                 ValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArg
                                                                                                   489 ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr
                                                                                                                                                        ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla
                                1012 CAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACAGAGCGCAATGACCTGAACAAGAGG
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          immunoglobulins and antibodies, receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adensein melecules and their receptors, cytokine and chemokine receptors, adensein melecules and their receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peripheral nervous and non-nervous system peripheral nervous and non-nervous system ceceptors, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonuclectides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstruction) and/or lung inflammation, allergyies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstruction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of fragments and antisense oligonucleotides used in the exemplification of
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peptide factors and transmitters, transcription factors,
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(EPIG-) EPIGENESIS PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGlu
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                                                                                                                                                                                                                                                                                                                                                                                                               condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nypertension, emphysema, chronic obstructive pulmonary disease (COPD)
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                          GAGGCAGTAGAGTCCCAGAGGATGTGTGTGAGCTGATGAAGCAGCAAGAGAGCCCACCTGAAG
                                               CAGGAGATGCTAAAGGAGGCAGCAGCGGCACCAGCGGAGAAGGATTTTCTCCTGAAA
                                                                                                                                                                                                                                                                                              1252 CAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLys
                                                                                                                          GlualaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLys
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Pabalan J, Aguilar

Sandrasagra A, Katz E,

Li Y, Sa Tang L,

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WPI; 2003-229219/22.
Nyce JW,
Miller S,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or regions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antihiflammatory steroid and ubiquinone. A composition of the invention has antihiflammatory, antiallargic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antihilammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung all mamation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at first property disease or condition. Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Disclosure; SEQ ID NO 12276; 872pp; English ubiquinone

Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;

Alignment Pred. No. Score: Secret: Sec	112 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10 10 10 10 10 10 10 10	2.15e-95 11arity: 11arity: 99.12* 11arity: 99.12* 62.47* 4snSerGlnLysGlnMetLysLev AATTCACAGAGCAGATGAAGGT 11	Length: Matcheres Conserve Mismatcl Indels: Gaps: -1793) ILEUGINLY ICTACAGAA CAACC-GT CAACGCC-GT CA	1793 11793 11793 1189 1189 1189 1298 1399
qq	1552	CAGCTGCAG	CTGCAGATGGAACAGCACA	CAATGAGCGCAACTCCAAGCTGCGCCAAGAGAA	SCTGCGCCAAGAGAACAT
δ	289	Levalagiv	uArgleulyslysleuil	eGluGlnTyrGl	uLeuArgGluGluHis
QQ	1492	CIGGCIGAGA	GCT		SCTGCGCGAGGAGCATAT
ò	309	Lysvalph	eLysHisLysAspL	euGlnGlnGlnLeuVa]	AspalaLysLeuGlnGl
QQ	1432		AAAGTCTTCAAACACAAAGGACC	CTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCA	GATGCCAAGCTCCAG

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GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLys
               1252 CAACAGCTTGCCCTATACACAGAGAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGC
                                                                                                                                                                       SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLys
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                                                       349 GluhlaValGluSerGluhrgMetCysGluLeuMetLysGluGluThrHisLeuLys
                                                                                                             369 GlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSer
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Human, antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory; antiallergic; antianflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

lung inflammation; respiratory disease; ds ABE297033/C
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Human; antisense; lung dysfunction antianflammatory steroid; ubiquino with antianflammatic; hypotensive; immuno antiantense gene therapy; respiratory with antianflammatic, hypotensive; immuno antiantense gene therapy; respiratory with lung inflammation; respiratory dis XX
Homo sapiens.
XX
WO200285308-A2.
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PP 23-APR-2002; 2002WO-US013135.
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Z4-APR-2001; 2001US-0286137P.
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GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLys 1372 CAGGAGATGCTAAAGGAGGCAGAAGAGCGCCACCAGCGGAGAAGGATTTTCTCCTGAAA GlualaValGluSerGlnArgMetCysGluLeuMetLysGlnGluThrHisLeuLys LeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeu

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SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLys

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antiense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entinflammatory steroid and ubjuding the composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of, or reducing sensitivity to adenosine reducing levels of corrector, producing bronchodilation, increasing levels of ubjuingne or Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Aguilar D; Pabalan J, Disclosure; SEQ ID NO 12275; 872pp; English Katz E, Sandrasagra A, K ,, Shahabuddin S; Li Y, Sar Tang L, WPI; 2003-229219/22 ubiquinone Nyce JW, Miller S,

Sequence 1793 BP; 339 A; 546 C; 444 G; 464 T; 0 U; 0 Other;

AATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCAGCTGGTGCAAGAAGAAG 1732 TGCCGTGAGCTGCACGGGCACAACCGCTCCATCAAGAAGAAGGTGTGCAGCGGGCCCGG 1613 LeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAsp 308 189 AsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLys GluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAsplle 1612 GAGGAGGAGGAGAAGGCGAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATT 1552 CAGCTGCAGATGGAACAGCACAATGAGCGCAACTCCAAGGCGCCAAGAGAACATGGAG CysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArg GlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGlu Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-023-523-8 (1-530) x ABZ97033 (1-1793) 2.15e-95 1688.00 99.12% 99.12% Best Local Similarity: Percent Similarity: Alignment Scores: 1791 1731 1672 249 209 229 269 289 Query Match: g qq à. g à $\dot{\delta}$ g ò

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1073 1013 448 468 488 893 508 833 IL-14; B-cell growth factor; proliferation; differentiation; replication; non-Hodgkin's lymphoma; systemic lupus erythematosus; systemic necrotising vasculitis; transplant; ss. GluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIle CAACGGCTGGAGAAGCTGTGGGCACTGCAACAGAGGCGCAATGACCTGAACAAGAGG CTGGAGAAAGAAACCACCATGTACCGGTCCCGGTGGGAGAGCAGCAACAAGGCCCTGCTT 1072 GAGATGGCTGAGGAGAAAAGAGTCCGGGATAAAGAACTGGAGGCCTGCAGGTAAAAATC ValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGluArgArg CCAGGAGCACCGAGCACAGAGCATCAGGCCAGACTGGGCCTCAAGAGCCCACCTCCGCC 449 GinArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArg 952 Gracaddaccreadrecredrecededecreercecreacadacaecereadadae ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla AAQ66987 standard; cDNA to mRNA; 1854 BP. Location/Qualifiers 73. .1770 /*tag= a 93US-00005156 94WO-US001101 (revised)
(first entry) Interleukin 14 gene. 767 Argala 530 WO9416074-A2 sapiens 18-JAN-1994; 15-JAN-1993; 25-MAR-2003 19-MAR-1995 1132 832 529 429 469 489 892 509 RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                             GluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAla
                                                                                                          GAAACCACCATGTACCGGTCCCGGTGGGAGAGAGCAGCAACAAGGCCCTGCTTGAGATGGCT
                                                                                                                                                                       1079 GAGGAGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAATCCAACGGCTG
                                                                                                                                                                                                      GluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGlnAsp
                                                                                                                                                                                                                                                                LeuseralaglyglyglnglyserLeuThraspserGlyProGluArgArgProGlu-Gl
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GCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAGCGAGGTA
                            PheThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLeuGluLys
                                                                                                                                                GluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGlnArgLeu
                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 13025; 2537pp + Sequence Listing; English
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Otsuki
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A, Nagai I
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Sugiyama T, Wakamatsu
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00241899.
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                                                                                                                                                                                                                                    The sequence is that of a gene encoding a high molecular weight B cell growth factor which stimulates B cell proliferation and inhibits B cell differentiation, termed interleukin 14. IL-14 can be used to interfere with the replication of B cells and to treat B cell non-Hodgkin's lymboma, systemic lupus errythematosus and systemic necrotising vaculitis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                High molecular weight B cell growth factor - able to stimulate B cell proliferation and inhibit B cell differentiation, useful to treat e.g. systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGlu
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                                                                                                                                                                                                                                                                                                                                          Sequence 1854 BP; 350 A; 559 C; 456 G; 489 T; 0 U; 0 Other;
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Matches:
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* HUMAN SERVICES.
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P-PSDB; AAR55800.
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complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. The polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence 3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the partection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs rapesent human cond methods. AAH13622 represent human amino acid sequences; and AAH13622 to AAH13622 represent consideration of the consideration of the expression of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration consideration of the consideration of the consideration of the consideration consideration of the consideration consideration of the consideration consideration consideration of the consideration consideration consideration of the consideration consideration consideration consideration consideration consideration consideration consideration consideration consideration consideration considerat
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Sequence 2045 BP; 672 A; 421 C; 506 G; 446 T; 0 U; 0 Other;

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	AlagluGlyProgly sccccaccccca	-ProgluglyalaglnalaargThralaglnSer rgaaattGGCaCaatGGAAGAAGCTGGAATTTGT	AspileLeuSerThr SATATTCTTCAACAT	slnGlyGluProAla rrgcaaGaGGarGaA	slyGluProGluPro	AsnThrGluGluIle GAAGCT	iluLysLysLysAla ::: ACAAAGAAAAACT	snThrLeuSerThrPro 	iluGluHisArgAsn AGGAGCAGGAGT	alginglulysasp ::: TGAAAGAGAAGTT	enGluSerLeuCys
2045 284 71 132 39 8	Valglu ACTGAGG	GlnAla ATGGAA(LeuGlu	GlyAlaC ::: CATTCAI	ArgAsn(AspPro/ 3GA	ProGlnC ::: AACAGG	Leuasn1 CTAAAC	LeuLeuC CTTCTGC	SlnLeu\ ::: CAGATTC	SerLysi
Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-2045)	GluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly 	AAGTT	GlyalabeuargaspvalserGluGlubeuserargGlnbeuGluaspilebeuserthr 	TyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAla 	GluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro 	ThrProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluG : :	ArgGlnSerAspGluvalGlyAspArgAspHisArgArgProGlnGluLysLysLysAla 	LeuglyLysglulleThrLeuLeuWetglnThrLeuAsnThrLeuSerThrPro 	LeuCyslyslysTyzAlaGluLeuLeuGluGluHisArgAsn 	SerginiysginMetlysLeuleuginiyslysginSerginleuValgingiulysAsp gitcagaagcaaatgaagatcctgcagaagaagcaagcccagattgtgaaagagaaagt	HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys
1.96e-70 1285.00 67.49% 53.99% 47.56% A AAH15042	aGlnGluArgPr ::: scgggaagag	SerSerGlnAlaProArgLys :::: ::: CGGCGACCCGCGGGAG	JArgAspValSe 3GTGAAAGCAGA	laspasnasngl: 	ASPAlaGluLy. :: CTTTATAACAGA	lvalTyrGlyGl CACGCAAGAATC	rAspGluValGl - rccccTGATGG	JGlyLysgluIl AGGAAAGAAGT	GluGluLysLeuAlaAlaLeuCy 	SGlnMetLysLeu SCAAATGAAGATC	glyGluHisSe.
res: arity: milarity: -8 (1-530)				TyrCysVa CAA			ArgGlnSer CGAACAGA1	LysGlyLeuGlyLy TTAGGAAA			
sco: imili l sil ch:	12	32	190	70	304	110	130	150	170	190	210
Alignment S Pred. No.: Score: Percent Sir Best Local Query Match DB:	QY Bb	oy Ob	- & - q	QY	oy da	č qa	oy QD	20 20	- & - da	දුරු දුරු	, VQ

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628 230 688 250	CACTTGCAGAACGTAGCTATCTTGGCAAGAAGCTAGAATCTCTTTGC 687 ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu 249 ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu 249 AdaGaACTTCAGCTCACATAAGACGTTAAAGAAGAAAATATGCAGCAGGAAG 747 GluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAsnBelleGln 269
748 270 808	SANGARGANCEACGIANAGANGCAACIGCAACAIIICCAGAIIACCIIAGAIGAGAIIICCAGAIIACCIIAGAIGAGAIIICCAGAIIACCIIAGAIGAGAIIICCAGAIIACCIIAGAIGAGAIIICCAGAIIAGAIGAGAIIICCAGAIIAGAIGAGAIICCAGAGAAGAIICCAGAGAACAIICGAGAACAIICGAGAACAIICGAGAAACTCCGACAGGAAACAIICGAGAAACTCCAGACAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAACAIICGAGAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAAAACAIICGAGAAAAACAIICGAGAAAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAGAAAAACAIICGAAAAAACAAAAAAAA
290 868	∢ v
310 928	ValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGln 329
330 988	GlumetLeulysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeulysGlu 349 :::::::
350	4=8
370	
390 1168	ნ <u>—</u> წ
410 1228	GlulysgluthrthrmetTyrargSerargTrpGluserSerashjysalaleuleuGlu 429 GaaaagaaacaataatttrggcGtaccaaatgggaaaacaataataaagaacttctGcaa 1287
430	MetalagluglulysThrValargasplysGluleugluglyLei
450 1348	
47	Gln
1408	GAAGTCCTGAAAGAGCAGGTATCCATCAAGCGGCCATCAAAGCGGGCGAAAGAGGGTTTA 1
473	rleninraspoerciyriosidargargriosid 49
491	GlyPro
50	sTyrProGlyAlaPro 512
1588	 CAAAAGCCCCCGTCCA
0301	standard; cDNA; 2045 BP.

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WPI; 2002-372001/40.
          Benson DR,
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cancer; cytostatic; tumour; vaccine.
                                      Human lung cancer associated full length cDNA DMSM-181
                                                                                                                                                                                                                                                                                                                  22-SEP-2000; 2000US-0234837P.
10-OCT-2000; 2000US-0239440P.
29-JUN-2001; 2001US-0301928P.
                                                                                                                                                                                                                                                                       20-SEP-2001; 2001WO-US042232
15-JUL-2002 (first entry)
                                                                                         ss; gene; lung
                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                  WO200224057-A2.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                28-MAR-2002
                                                                                              Human;
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encoding the proteins, useful diagnosing or monitoring lung New tumor lung proteins and nucleic acids as vaccines and for treating, preventing, cancer.

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Mohamath R,

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Page 175-176; 189pp; English. Claim 1;

The invention relates to an isolated polynuclectide comprising a sequence selected from 183 human DNA sequences (appearing as ABX70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the polynucleotide operably linked to an expression vector of; an isolated cell transformed or transfected with an expression control sequence; a host cell transformed or transfected with an expression vector of; an isolated cell transformed or transfected with an expression vector of; an isolated cell transformed or transfected with an expression vector of; an isolated cell transformed or transfected with an expression vector of; an isolated cell polypeptide; an enthod for detecting the presence of a cancer in a patient of a fusion protein comprising at least the polypeptide and incleased to expending T cells specific for a tumour protein; an isolated T cell population comprising T cells specific for a tumour protein; an isolated T cell population comprising T cells specific for a tumour protein; an isolated T cell population a first component selected from the polynucleotides, proteins, antibodies, fusion of component selected from the polynucleotides, proteins, and a second component selected from the polynucleotides, proteins, and an expension of selection reagent consisting of a reporter group. The polypeptides are useful as vaccines for the treatment or prevention of tung cancer, and for diagnosis and monitoring of such cancer. The compusion of an expense of polynucleotides may be used as probes or primers for inclease for inhibiting expression of tumour polypeptides and proteins in tumour cells specific for a tumorous protein. The collynucleotides may be used as probes or primers for inclease for inhibiting expression of tumour polypeptides and proteins in tumour cells in tumour cells. The present sequence is one of the 183 lung cancer associated polynucleotides

G; 446 T; 0 U; 0 Other; Sequence 2045 BP; 672 A; 421 C; 506

	2045	284	71	132	39	8	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	
	1.96e-70	1285.00	67.49%	53.99%	47.56%	9	
Alignment Scores:			t Similarity:	Ltv	Ouerv Match:	DB:	

12 GluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly 31 US-10-023-523-8 (1-530) x ABK70301 (1-2045)

1107 GlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSer 389 AlaGluargLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLys 309 AlavalGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGln 369 ValPhelysHisLysAspleuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGln 329 229 687 249 747 269 289 808 GCCCAGCTGGAGCAGCATGACATCCACAACGCCAAACTCCGACAAGGAAACATTGAGCTG 867 ArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAla 149 507 345 110 ThrProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIle 129 346 GCATACTGCACGCAAGAATCAAGAAGAAATCCCTGGGGGA------GAAGCT 393 90 GluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro 109 CAA-----GGCTCAAATTGTGGTGGCACAAGTAACAAGCATTCATTGGAAGAGGATGAA 303 868 GGGGAGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAAGAACACTTGATAAG |||| |||||||:: GCGACAGBATCGAGGCACAAATACGAAATGAAACAGCAGGAAGTACAACTAAAACAG GluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsn SerginiyaginmetiysLeuleuGiniyaiyaginSerginLeuValGinGluiyaAsp ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu GluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGln LeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeu 330 GluMetLeulysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeulysGlu LysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrPro HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys 32 SerSerGlnAlaProArgLys-----ProGluGlyAlaGlnAlaArgThrAlaGlnSer 70 TyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAla 30 cggcgacgcacccccccccacaaagtttgaaattcgcacaatggaagaagctggaatttgt 50 GlyAlaLeuArgAspValSerGluGluLeuSerArgGinLeuGluAsplieLeuSerThr 104 GGCAGTGACTTTATAACAGAACAGGAATTTGGTGAGC-----1048 270 290 310 928 394 150 208 999 250 170 190 210 628 230 688 748 50 154 \$ g \$ g 8 8 8 8 ò g ò g g 8 8 8 Д ò q à 8

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Example 2; Page 319-320; 678pp; English.

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CAGCTITICICITITATATGGATAAGTTTGAAGAATTCCAGACTACCATGGCAAAAAGCAAT 1167
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                                                                                                       MetalaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIleGln 449
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                                                               GluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGlu 429
                                                                                                                                                                                            ----Aspleu 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; gene; p53 modifier; cytostatic; cancer; cytostatic; antiangidgenic; antiangoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                 GluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLeu
                                                                                                                                                                                                                                                                                           SerAlaGlyGlnGlySerLeuThr----AspSerGlyProGluArgArgProGlu
                                                                                                                                                                                                                                                        .468 GCAACACCTGTGATGCAGCCCTGTACTGCCCTGGATTCTCACAAGGAGCTGAACACTTCC
                                                                                                                                                 450 ArgieuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgVal
                                                                                                                                                                                                                                                                           491 GlyPro-----GlyAlaGlnAlaProSer-SerProArgValThrGluAlaProCy
                                                                                                                                                                                          Human DNA encoding a p53 modifier, SEQ ID 67.
                                                                                                                                                                                                                                                                                                                                          1588 CAAAAGCCCCCGTCCA 1603
                                                                                                                                                                                                                                                                                                                                                                                     ACD13396 standard; cDNA; 1618
                                                                                                                                                                                                                                                                                                                       sTyrProGlyAlaPro 512
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Sequence 1618 BP; 558 A; 330 C; 363 G; 367 T; 0 U; 0 Other; nucleic acid encoding a p53 pathway modifying protein

Length:
Matches:
Conservative:
Mismatches:
Indels:

3.08e-70 1280.00 80.26% 65.90%

Best Local Similarity: Percent Similarity:

Query Match: DB:

Gaps: (1-1618)

US-10-023-523-8 (1-530) x ACD13396

The invention relates to identifying (M1) a candidate p53 pathway condusting agent, by contacting an assay system comprising a purified HM condusting agent, by contacting an assay system comprising a purified HM brosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference of activity, and detecting a test agent-biased activity of the assay system. Contacting a cell affective in p53 pathway of a cell (comprising contacting a cell affective in p53 tunction with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid cequence, where p53 function is restored, modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising) (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likellhood disease) (M1) is useful. Contacting breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Condulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defect in the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway such as, angiogenesic, appointed or proliferation of the cell, so that the cell cycles normal colliferation of progression through the cell cycle (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, also and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and an analysism and analysism and analysism and ana

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166 LeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGlu
                                                                                                                                                                                              226 GluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 CAGGCACGAGAGAAGAAGAAGAACGACGTAAAAGAAGCAACTGCACATTTCCAGATTACCTTA
146 LysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThr
                      69 CTTTCAACCCCAGAGGAGAAGCTGGCAGCTCTCTGTAAGAATATGCTGATCTTCTGGAG
                                                                                                                                                                   186 GluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuVal
                                                                                                                                                                                                                                                                                                                                                                           249 GAATCTCTTTGCAGAGAACTTCAGCGTCACAATAAGACGTTAAAGGAGGAAAATATGCAG
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                                                                                                                                                                                                                                                        206 GlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.
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Funke RP;

Ď, H

Belvin M, Francis-Lang H,

Plowman GD,

Friedman L,

WPI; 2003-156859/15. P-PSDB; ABO07222.

(EXEL-) EXELIXIS INC.

05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P.

03-JUN-2002; 2002WO-US017382

205 188

68

248 245 308 368

286 AshMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArgGluGlu 305

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US-10-023-523-8 (1-530) x ACC68992 (1-4174)
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 230-231; 240pp; English.
                                                                                                                                    2001US-0327446P.
2001US-0345837P.
2001US-0343903P.
2001US-0334020P.
                                                                                                                                                                                  2001US-0340226P.
2002US-0345008P.
                                                                                                                                                                                                        2002US-0365645P
                                                                                                                                                                                                                   2002US-0379887P
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1265.50
61.51%
46.39%
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                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                               WPI; 2003-363137/
P-PSDB; ABR43284.
                                               WO2003025129-A2
                                                                                                                                                26-OCT-2001;
02-NOV-2001;
27-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                   or infections
                                                                                                               14-SEP-2001;
28-SEP-2001;
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                                                                  27-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                     969 AATGAGAAGGTGGAAGTCCTGAAAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCG 1028
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325
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                                                                              GinGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPhe 345
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                                                                                                                                               TTATTAAAAGGAGGAGAAATGAAGGCACAAAATACGAACAAATGAAACAGCAAGAAGTA 668
                                                                                                                                                                      366 HisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu 385
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                                  HislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeu
                                                CACATTGATAAGGTGTTCAAACATAAGGAACTGCAACAGCAGCTCGTGGATGCCAAACTG
                                                                                                   Human neurotransmission-associated protein NTRAN-14 cDNA SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                        AlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGln
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proteins given in ABR43271 to ABR43295, designated NTRAN-1 to NTRAN-25

(1). (1) have eveckatatic, antiatreriosciercic, anticonvulsant,

notropic, neuroprotective, cerebroprotective, anti-HTV, antiallergic,
antiinflammatory, thyromimetic and antidiabetic activities, and can be
useful in diagnosing, treating and preventing diseases or conditions
associated with the decreased expression or overexpression of NTRAN, such
as call proliferative (e.g. cancer, attroke), immune/inflammatory (e.g. applepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AlDS,
allergies), developmental (e.g. hypothyroidism, Cushing's syndrome) or
endocrine (e.g. diabetes) disorders, or infections. They are also useful
in assessing the effects of exogenous compounds on the expression of
nucleic acid and amino acid sequences of NTRAN. The NTRANs or their
fragments are useful in screening compounds for effectiveness as agonist
or antagonist of the polypeptides, or in altering the expression of the
target polymuclectide and compounds that specifically bind to or modulate
the activity of the polypeptide
Honchell CD, Warren BA, Borowsky ML, Griffin JA, Li JX, Lee SY;
Yue H, Forsythe IJ, Marquis JP, Gietzen KJ, Baughn MR, Tran UK;
Lehr-Mason PM, Tang YT, Ramkumar J, Emerling BM, Lee EA, Elliott VS;
Hafalia AJA, Duggan BM, Chawla NK, Kable AE, Chang H, Khare R;
Becha SD, Jin P, Lee S;
                                                                                                                                                                                                                                                                                                                                                                                                    New human neurotransmission associated proteins (NTRAN), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NTRAN expression e.g. cancer, AIDS, diabetes, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||||
cCTICTGATACTACTCCCAAGATGGAGGCTAATCACTCTGAACAGCTCTCAGGGGAACGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4174 BP; 1331 A; 924 C; 962 G; 957 T; 0 U; 0 Other;
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Location/Qualifiers

Key

Oy 374 TyrThrGluLysPheGluGluPheC	Oy 394 ThrPheLysGlnGluMetGluLysh	414	Db 1515 GCCACATGGAAAGCCCGATTTGAG	1	Oy 454 LeuCysArgAlaLeuGlnThrGlu	474	Db 1695 ATATCTGAAAAGGATGACCAAAGT	1755	Oy 491	Db 1815 CTGGCCACAGCCTTCATGATATTY OV 492	1	Oy 499 SerProArg	Db 1935 CAACCCCTTGATCCCTTCACGG	1995	24 56	ID AAX80156 standard; cDNA; 4723 BP. XX AAX80156; AC AAX80156;	XX DT 16-AUG-1999 (first entry)	XX DE Neurite extending activity protei	XX XX Neurite extending activity; anti- XX dementia; ds. XX	18 Sp.	FH Key Location/Qualifie FT CDS 196. 2226 FT CDS /*tag= a	911147897-A.	2-JUN-1999.	EF 13-NOV-1997; 9/0F-00531242. XX 13-NOV-1997; 97JP-00331242.	XX PA (AGEN) AGENCY OF IND SCI & TECHN XX
29GlyproGlySerSerGlnAlaProArgLysPro 39			54 AspvalSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAsp 73	74 AsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAsp 93 .:: ::: ::: :::	AlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValVal		114 TyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluLleArgGLnSerAsp 133	134 GluvalGlyAspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLeuGly 153		135 AAAGAAGCCAACCTGCTAATGCAAATCTGAAGTTGCAAACACGGGAAGAAGTTT 794	174 AlaAlaLeuCysLysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln 193	795 GATTITITATITOAAGAAGTAIGCTGAATTGCTGGATGAACATCGTACTGAGCAAAAAAGAAG 854	194 Met.byslettedtalphysbysgdinderginergationtunysasphishergaty 215 855 TIABAAGCTCCTCCAAAAGAAACGAACGACTACAAATCAAAAAGAAAAGGACCAGTIACAAGG 914	214 GlubisSerLyshlavalLeuAlaArgSerLysleuGluSerLeuCysArgGluLeuGln 233	sacrialCcicocicoamoczaniiosasacicioioccosozociocza raSerLeuLvsGluGlüGlvValGlnArqAlaArqGluGluGluGluLvs	CARCAGACTCTGAAGGAAGAGGGGCTTCAGCGGGCACGTGAGAAAAAAAA	alThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGlu	TCACAAGCCATTTCCAGAGTACCCTCACGGACATCCAGGCCAGATCGAG	274 GlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeu 293 :::	294 LysLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHis 313	TCGATCACATATGACTCAGAGAGGAGCATCTGGACAAATATTTAAACA	314 Lysabbedginginginguvalaspalalysegdingingingingingeleguis 1215 Agagaactgcagcagaagctggtggatgcaaggcttgagcaggcccaagaatgatgaag 1274	GlualaglugluargHisGlnArgGlubysAspPheLeuLeuLysGlualaValGluSer	1275 GAAGGGAGGAGGACACAAAACGAAAAGGAATATTGGTGAACCAGGCAGCAGAGTGG 1334 se claaramar cyschiteiwattyschichidhidhidhidhidhidhidhidhidhidhidhidhidh	1335 AAACTTCAGGCGAAAGTGCTGAAGGAGCAAGACAGTCCTGCAGGCTCAGGTCACTCTC 1394
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AGAGGAGGTTAATAGTGTCCAAACCGCCGTGAAAAAT 1814
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|Gagaaacgaactccacaaaaaarcagagacgcagaa 1694
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                                                                                              TCAGCACAACTCCGATGAAGAGCCAGAGTCAAACGTC 1754
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                                                                                                                                                                                                                                                                                                                                                                                                               :::
TCAGGAGAGTGCTGACGCCGCTCTCAAGGAGCCAGAG 1934
                                                                                                                                                                                                                                               rAspSerGlyProGluArgArgProGluGly----- 491
                                                                                                                                                                                                                                                                                                                                                                                              491
eGlnAsnThrLeuSerLysSerSerGluValPheThr 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -dementia; memory; brain function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yProGlnGluProThrSerAla 528
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238 SerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluLysArgLysGluVal 257
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1747 AGCGACGGCAGCA 1759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 GluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 ArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThr 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCys 177
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                                                                                                                                                                                                                                                                                                                                                                                                                        526 AAACCAGCTCCTGGAGATGCTTCA-----AGAGCAAAGGAGCCCAGTGCCAGC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  748 CAGAAGAGCCAGGCCCAGATCACCAAGAGAAGGACCAGTTGCAGAGTGAGCACAGCCGA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GinLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AspGlyAla------GlnGlyGluProAlaGluProGluAspAlaGluLysSer 97
                                                                                                                                                                                                                                                                                                                                                                                              22 AlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGly 41
                                                                                                                                                                                                                                                                                                                                           2 SerSerProGlyGlnProGluAlaGlyProGluGlyAlaGluGluArgProSerGlnAla 21
                                                                                                       The present sequence encodes a protein (I) which has neurite extending activity. (I) may be administered to patients to prevent dementia or to improve memory and brain function. (I) is also used as a neurite-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 AlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AlavalLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg
                                        New protein with neurite extending activity - useful for treating
                                                                                                                                                                            Sequence 4723 BP; 1510 A; 1038 C; 1025 G; 1150 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                                 Claim 3; Page 5-8; 9pp; Japanese.
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1240.00
65.87%
49.72%
45.89%
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                P-PSDB; AAY17863
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1288 TTTGAAGAATTTCAGAAACATTGACCAAAAGCAATGAAGTGTTTGCTACCTTCAAACAG 1347
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                                                                                                                  298 GluGlnTyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGln 317
                                                                                                                                                                                                                                                                                                                                                                                                                                           318 GlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGlu 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 ArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCys 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 PheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGln 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 GluMetGluLysMetThrLysLysLysLysLeuGluLysGluThrThrMetTyrArg 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 SerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArg 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AspiysGluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAla 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 AlaGlyGlyGlyGlnGlySerLeu---ThrAspSerGlyProGluArgArgProGluGly-Pr 492
                                                                                                                                                                                                       278 ArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIle 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 GluLeuMetLysGlnGlnGluThrRisLeuLysGlnGlnLeuAlaLeuTyrThrGluLys 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 LeuGinThrGluArgAsnAspLeuAsnLysArgValGlnAspLeu-----Ser 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 -----TyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGl 524
258 ThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGlu 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 oGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCys-------
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This cDNA clone, designated 091-132020 (ATCC 98143), which is not full-length, codes for a 46 kDa BRCA1 modulator protein (see AAW37883) that binds to the tumour suppressor gene product BRCA1, and which is characterised by a single leucine zipper domain. 3 cDNA clones (see also AAV29062-63) coding for BRCA1 modulator proteins (see AAW37881-83) were isolated from a HeLa cDNA library using a yeast two-hybrid assay with a GAL4-BRCA1(8-1293) fusion as bait. Vectors and host cells comprising the isolated nucleic acid sequences are claimed, as well as a process for producing BRCA1 modulator protein by culturing these host cells. BRCA1 modulator proteins and nucleic acids can be used to diagnose diseases involving unwanted cell growth, e.g. breast cancer, and to identify compounds that alter BRCA1 interaction with BRCA1 modulators for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GCGACTGAGGCCGGACGGGGCGGACGCCGCGCGCGCGCAGAAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 TGGCACAATGGAAGAAGCTGGAATTTGTGGGCTAGGGGTGAAAGCAGATATGTTGTGTAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTCAATCAAATGATATTCTTCAACATCAA-----GGCTCAAATTGTGGTGGCACAAG 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer antigen 1 modulator protein - useful for diagnosing diseases involving unwanted cell growth, e.g. breast cancer, and 1 producing therapeutics for treatment of such diseases.
BRCA1 modulator protein; 091-132020; breast cancer antigen 1; tumour suppressor protein; diagnosis; therapy; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1191 BP; 449 A; 228 C; 302 G; 212 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                        Location/Qualifiers
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69.01%
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38.77%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ONYX-) ONYX PHARM INC
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P-PSDB; AAW37883.
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                                                                                              Homo sapiens
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                                     TAACAAGCATTCATTGGAAGAGGATGAAGGCAGTGACTTTATAACAGAGAACAGGAATTT
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Modulator proteins that bind to and modulate the activity o
tumor suppressor gene product, useful for the treatment of
                                   Modulator protein; BRCA1; tumour suppressor protein; ovarian cancer; cell growth; cell proliferation; ds.
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/*tag= a
/note= "no termination codon given"
                    cDNA 091-132Q20 encoding a BRCA1 modulator protein.
                                                                     Location/Qualifiers
                                                                                                                                                                                 Lingenfelter C,
                                                                                                                                       97US-00968751
                                                                                                                                                     97US-00968751
      (first entry)
                                                                                                                                                                   PHARM INC
                                                                                                                                                                                               WPI; 1999-517952/43.
P-PSDB; AAY30151.
                                                                                                                                                                                                                                    breast cancer
      27-OCT-1999
                                                                                                                                                                   XXNO (-XXNO)
                                                                                                                                      13-AUG-1997;
                                                                                                                                                     13-AUG-1997;
                                                                                                                                                                                 Rubinfeld B,
                                                         Homo sapiens
                                                                                                          US5948643-A.
                                  Modulator
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The present sequence encodes a modulator protein, that binds to and modulate the activity of the BRCA1 gene product (BRCA1). The BRCA1 protein has been characterized as a tumour suppressor protein.

Alterations in the amino acid sequence of BRCA1 causes breast and ovarian cancers by removing the controls on cell growth and proliferation.

Research has shown that different regions on the BRCA1 molecule have different effects on cell growth and tumour suppression (e.g. full length truncated BRCA1 has no effect on breast cancer cell growth but will inhibit ovarian cancer cell growth. It has been suggested that different host cell factors (e.g. proteins) interact with different regions of the BRCA1 to control its function. The identification of these proteins (e.g. BRCA1 to control its function and treatment of novel diagnostic methods and new therapeutics for identifying and treating cancers caused by changes in the expression or activity of BRCA1 of the BRCAl Claim 1; Fig 3; 35pp; English

BP; 449 A; 228 C; 302 G; 212 T; 0 U; 0 Other; Sequence 1191

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 1191
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                           Percent Similarity:
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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorders, arthritis, inflammation, ss.
242 AATATGCAGCAGGCACGAGAAGAAGAAGAACGACGTAAAAGAAGCAACTGCACATTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 LysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 ACTACCATGGGAAAAAGGAATGAATGTTTCA-ACCTTCAGACAGGAAATGGGAAAAGAT
                                                                             243 GlyValGlnArgAlaArgGluGluGluGluGluLysArgLysGluValThrSerHisPheGln
                                                                                                                                                           263 ValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeu
                                                                                                                                                                                                                                     283 ArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeu
                                                                                                                                                                                                                                                            362 CGACAGGAAAACATTGAGCTGGGGGAAGCTAAAGAAGCTCATCGAACAGTACGCACTG
                                                                                                                                                                                                                                                                                                             303 ArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAsp
                                                                                                                                                                                                                                                                                                                                        323 AlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                             542 AGAGAGTITITATTAAAAGAAGCGACAGAATCGAGGCACAAATACGAACAATGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 GlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGln
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                                                                                                                                                                                  302 ATTACCTTAAATGAAATTCAAGCCCAGCTGGAGCAGCAGCATGACATCCACAACGCCAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 AsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 8292.
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGlu 182
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                                                                                                                                                                              Human breast cancer associated antigen nucleotide sequence SEQ ID NO:48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric and prostate cancer associated diagnosing and treating a condition an abnormal amount of a protein, e.g.
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                                                                                                                                                                                                                 breast cancer; gastric cancer; prostate cancer; diagnosis; associated antigen; cytostatic; cancer vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 G; 149 T; 0 U; 3 Other;
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                                                               BP
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antigen precursors, useful for
characterized by expression of
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                                                               AAF22469 standard; cDNA; 823
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925.50
86.55$
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Query Match:
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10-SEP-1999;
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                                                                                                                                                                                                                                         cancer
                        RESULT 27
AAF22469
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019340) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed apecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                 lated nucleic acids and polypeptides, useful for preventing diagnosing treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln 340
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                                                                                                                       Claim 1; SEQ ID NO 8292; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1501 BP; 473 A; 375 C; 393 G; 259 T; 0 U; 1 Other;
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810.00
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P-PSDB; AAO08301.
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987 TCTCAGGAGAGTGCTGACGCCGCTCTCAAGGAGCCAGAGCAACCCCCTCTGATCCCTTCA 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 ArgvalThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520
527 GAGAACTGTAACAAAGCTCTGTTGGACATGATTGAAGAGAAAGCACTGAGAGCTAAAGAA 686
                                  141 LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr 460
                                                                                                          461 GludrgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeu 480
                                                                                                                                           747 GAGAGAAACGAACTCCACAAAAAATCAGAGAGGCAGAAATATCTGAAAAGGATGACCAA 806
                                                                                                                                                                                                                                                                                                                                    491
                                                                                                                                                                                                                                                                                                                                                                        927 ATTCATCATCCAGAGTCAACCCCGCACCAGTCCAAAGAAACCCAACCCGAAATAGGCAGT 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing, preventing or
                                                                                                                                                                                                                                                                                                  867 GCAGAGGAGGTTAATAGTGTCCAAACCGCCGTGAAAAATCTGGCCACAGGCCTTCATGATA
                                                          Human, diagnostic, drug screening, forensics, gene mapping,
biodiversity assessment, Parkinson's disease, Alzheimer's disease,
neurodegenerative diseases, anaemia, platelet disorder, wound, burns,
                                                                                                                                                                                                                                                                                                                                                                                                             --------ProGlyAlaGlnAlaProSerSerPro------
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Wang Z, Weng G;
                                                                                                                                                                                   481 ThrAspSerGlyProGluArgArgProGluGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human novel cDNA contig sequence, SEQ ID NO:2531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ren F, Xue AJ, Zhao QA,
Wang D, Ma Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 GAIGCIGAACCICCCICCAAGGCC 1130
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Zhou P, Ghosh M, Wang D, Ma
Haley-Vicente D, Drmanac RT;
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treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                            Example 2; SEQ ID NO 2531; 1185pp; English.
                                                                                     cancer.
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The invention relates to 971 novel human cDNA sequences (ADC29919-CC The invention are lates to 971 novel human cDNA sequences (ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of invention further discloses methods of the invention of applying the of the invention. The invention further discloses methods of polymucleotide probes ampliant and antibodies for arriving out the methods of the invention methods for the identification of compounds that modulate the applying and polymetrion and/or monoclonal antibodies for carrying out the methods of the invention and/or monoclonal antibodies for carrying out the methods of the conting sequences corresponding to the compounds that modulate the appropriate sequences corresponding to the compounds that modulate the conting sequences corresponding to the compounds that modulate the conting sequences corresponding to the conting for polypeptides of the invention are useful in diagnostics, drug screening, forensics, game mapping, in the definition of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of disease and other neurodegenerative diseases, anaemia, platelet also used for treating diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating be used be been as photocial and as food supplements. The present sequences are propered and as food supplements. The present sequences and not an expending the present sequences and method and sequences and method and products expending the present sequences and method as polype and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1501 BP; 473 A; 375 C; 393 G; 259 T; 0 U; 1 Other;

241 GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis 260 147 TTCCAGAGTACCCTCACGACATCCAGGCCAGATCGAGCAGCAGCAGGAGGAAATATG 206 LysleuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 300 ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluArgHisGln 340 341 ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 360 PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-023-523-8 (1-530) x ADC32449 (1-1501) 3.09e-41 810.00 63.22\$ 47.70\$ Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: 281 207 261 301 321 No. ò ò 셤 à g, ò 엄 à g

266

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10-APR-2003.
     Tang TY,
Zhou P,
           cancer.
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    Ren F, Xue AJ,
Wang D, Ma Y, P
Drmanac RT;

24-SEP-2002; 2002WO-US030474.
                              24-SEP-2001; 2001US-0324631P.
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P-PSDB; ADC31613.
                                                                                                    Zhang J,
Ghosh M,
                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                    Haley-Vicente D,
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Wang J, Wang Z,

Zhao QA, Asundi V,

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 724; 1185pp; English.

The invention traders to you much that the invention also relates to you much that the properties they encode (AbC30890-AbC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or invention declared condition; kits comprising polymuclectide probes and/or monoclonal antibodies for carrying out the methods of the invention capturession or activity of the polymuclectide and/or polypeptide, and 767 expression or activity of the polymuclectide and/or polypeptide, and 767 expression or activity of the polymuclectide of the invention (AbC31861-AbC32627) and the polymuclectide and/or polypeptide, and 767 expression or activity of the polymuclectide of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of that and products dependent on DNA and amino acid sequences. They are cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at also used for treating diseases such as Parkinson's disease, Alzhelmer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or invention relates to 971 novel human cDNA sequences (ADC29919ftp.wipo.int/pub/published_pct_sequences.

Sequence 1782 BP; 564 A; 425 C; 445 G; 348 T; 0 U; 0 Other;

Length:		Mismatches:	Indels:	Gaps: 2
Alignment Scores:	Score: 810.00	Best Local Similarity: 47.7		DB:

US-10-023-523-8 (1-530) x ADC30642 (1-1782)

260		146
alginarglaargjugjugjugjulysarglysgjuvalThrSerHis 260		87 GAAGAGCGCTTCAGCGGGCACGTGAGGAAGAAGAAAAAAGGAAAGAAA
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261 PheGinValThrLeuAsnAspileGinLeuGinMetGluGinHisAsnGluArgAsnSer 280

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Db 1	47 TICCAGAGTACCCTCACGGACATCCAGGGCCAGATCGAGCAGCAGCAGAGTGAGCGAATATG 206
2	81 LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr
Db 2	
3	01 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu 320
Db 2	67 GAGCTCAGAGAGCATCTGGACAAATATTTAAACACAGAGAACTGCAGCAGAAGCTG 3
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3	27 GTGGATGCAAAGCTTGAGCAGGCCCCAAGAAATGATGAAGGAAG
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Db 7	47 GAGAGAAACGAACTCCACAAAAAATCAGAGACGCAGAAATATCTGAAAAGGATGACC
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Db 10	047 cedearricadadaercecerecereceraacrecteagereaagedegaageagr 1106
8	521 GlyProGlnGluBroThrSerAla 528
Db 1:	gcrgaaccrcccrccaagg
AAH26	497 standard; DNA; 22255 BP.
AC AAH26	.~
DT 12-NOV	7-2001 (first entry)

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Low density lipoprotein binding protein 3; LBP-3; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
         Human low density lipoprotein binding protein 3 (LBP-3) gene.
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14-JUL-2000; 2000US-00616289.
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P-PSDB; AAB82809.
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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 3 (LBP-3, see AABB2809). The DNA was isolated from a human genomic library by screening with LBP-3 cDNA (see AAB2501). The open reading frame spans 10 exons. Human LBP-2 nucleic caids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for treating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
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                                                                                                                                                                                                                                                                                             BP; 5195 A; 5302 C; 5924 G; 5834 T; 0 U; 0 Other;
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Matches:
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The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, nearestatic and thrombolytic activity, receptor/ligand activity, auti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Racie LA, Merberg D, Treacy M;
                                                                                                                                                                                         Expressed sequence tag; secreted protein; haematopoiesis regulator; itsuse growth; activin; inhibin; tumour invasion suppressor; EST; in chemotaxis; chemotaxis; dhemotaxis; dene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 529 BP; 151 A; 146 C; 168 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 381; 641pp; English.
                                    AAV88391 standard; cDNA; 529 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lavallie
                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US006956
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mccoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070078/06.
                                                                                                                                                   EST clone GP232
                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1998;
                                                                                                               12-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1998
RESULT
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Conservative:
Mismatches:
Indels:
         Length:
Matches:
          68e-36
                713.00
99.28%
98.56%
26.39%
2
Alignment Scores:
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GCGGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAG 223 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArglysProGlu 40 41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60 1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln US-10-023-523-8 (1-530) x AAV88391 (1-529) Percent Similarity: Best Local Similarity: 21 Query Match: DB:

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343
                 224 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGC 283
                                                                                                                                        GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100
                                                                                                                                                                                   403
                                                                                                                                                                                                                        ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modularing agent, by contacting an assay system comprising puritied HM polypeptide (human orthologue of genes that modify the p53 pathway in brosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent. Les system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; gene; p53 modifier; cytostatic; cancer; cytostatic;
antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer;
kidney cancer; lung cancer; ovarian cancer; anglogenesis; cell cycle;
apoptotic disorder; cell proliferation disorder.
                                                                                                                                                                                                                                                                                                     LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp 139
                                                                                                                                                                                                                                                                                                                                           464 hagggggarccaaacacagaagarccggcagagrgacgagaggaggagaa 520
                                                                                                ceccaacresaadacaracreacacaracrerereresacaaraaccadededececeeec
                                                                                                                                                                  944 GAGGATGGGCACACAGGGTGAGCCGGCTGAACCCCGAAGATGCAGAAAGTCCCGGACCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Funke RP;
                                                                                                                                                                                                                                                              404 GIGGCAAGGAAIGGGGAGCCIGAACCAACICCAGIAGICAAIGGAGAGAAAGGAACCTCC
                                                         61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
Identifying modulators of the p53 pathway for use in treating apopt or cell proliferation disorders, comprises screening for agents the modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying (M1) a candidate p53 pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Belvin M, Francis-Lang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA encoding a p53 modifier, SEQ ID 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 320-351; 678pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                          ACD13448 standard; DNA; 115756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-2002; 2002WO-US017382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Friedman L, Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathway in Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-156859/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABO07223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACD13448;
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                                                                                                                                                                                                                     101
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whether the comparing the results with a control; and (u) is useful for identifying modulators of the p53 pathway. A probe for HM expression in susful for identifying modulators of the p53 pathway. A probe for HM expression in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and the reapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptoric or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and the p53 function of the cell, so that the cell undergoes normal proliferation of the cell, so that the cell undergoes normal also useful for treating defects in the p53 pathway of a cell, thus restoring proliferation or progression through the cell undergoes normal also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell prolliferation disorders. The present sequence is an HM	useful useful useful useful pression cancer, level. level it cand or cell max and max and storing is an HM
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	82555 GCI 390 uVa 82595 GGI 401 82654 GCI 401	82714 TCT 401 82774 AGT 401	82894 GAG 401 82954 TGC 401 83014 GCG 401 83074 GGG	83134 CTT 401 83194 TCC 401 83254 TGA 401 83314 GGT
6 8 6 8 6 8 6 8 6		6 6 6 6 6	8 8 8 8 8 8 8 8	
expression; (c) comparing the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 pathway of a cell, undergoes normal the p53 innexion or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence is an HM nucleic acid encoding a p53 pathway modifying protein	Scores: milarity: Similarity: Similarity: S23-8 (1-	305 GluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys 324 :::	CTCAGCTCATAGCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTTGA GTACCAGTCTGAGAGCGTCAGTGGGTCTGGTGCTTGTGGCTAAAAACCAAACA TAGCCCCTGGGGGGTTTGTGGTGTTTGTGGTTGTTGGGTAAAACCAAACA TAGCCCCTGGGGGGCTTCTGACAGGATCTGGGTTCTTGTCTTTGGAAATTGGTTTTTTTT	HILLINGER ACAGGT-GAGAGCATATAACCTGACCTTGAGCTTCCAAGTTTCCCTCACTGGGCCCCATC CTGGGGGTAGTGAAATGGGACCTCATTCTAGGACTGGCTGTGTCCTGGCTGCTATGACG CCTTGGTTGAGCTTTGTTCTCCCCGGACCTGCACAGTACCTATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
888888888888888888888	Alignment Pred. No.: Score: Percent Si Best Local Query Match DB: US-10-023-	868686	6 6 6 6 6 6 6 6	86868686

⋩	371		371
ą	82295 AGGAA	aggaacagaagagtttgaaaatcaacataaaggcaaaataaagtcaccctaagtctcc	82354
⋩	371		371
ą	82355 ACTT	CTITCCAGGCTIAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGTTTT	82414
 	371		371
ą.	82415 AAGGP	aaggaaaaatagtatctcaatagaattactggtcagagaggtcaaggagggggtctgagtgt	82474
æ	371		371
q	82475 GTTGA	GTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGGCTGCTTTCTCCCCACA	82534
<i>\</i> 2	372	AlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGl	06
a	3	ICCCTATACACAGAGAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAGCGA	CA .
≿ &	390 uValF 82595 GGTAT	uValPheThrThrPheLysGludludetGluLys	401 82653
~	401		401
.g	82654 GCTGC	GCTGCTGGGGGGATAAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCT	82713
λ	401		401
ą	82714 TCTGG	CTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCCCCCTCTTGAGGC	82773
λ	401		401
ą	82774 AGTAT	AGTATCAGTGGTATGTATACACTCCAGGTTGTCCCAGGGAATGGGGCAGTCTTTTCTGTT	82833
⋩	401		401
ą	82834 TGTTI	TGTTTGGTTTTTTTGGGGGGTTTGTTGTTGTTGTTGTTG	82893
~	401		401
ą	82894 GAGAC	GAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCATTGCAGCCTT	82953
λ	401		401
ą	82954 TGCCC	TGCCCCCGGGTTCAAGTGATTCTCCTGCCTCCAGCCTCCTGACTAGCTGGAATTACAGGC	83013
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e e	83014 GCGTG	GCGTGCCACCATGCCTGGCTAATTTTTTTTTTTTTTTTT	83073
λ	401		401
ą	83074 GGGGT	GGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGTGATCTGCCCGC	83133
⋩	401		401
ą	83134 CTTGG	CTIGGCCICCCAAAGIGCIGGGAITATAGGCGIGAGCCACCAIGCCIGGCCCCTTACCAI	83193
λ.	401		401
ą	83194 TCCTT	CCTTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGGGTG	83253
<i>≿</i> :	401		401
ą	83254 TGACT	TGACTGCATCCTGTAATGCCTTGGGCCTTGGGATCAATCA	83313
≿:	401		401
ą	83314 GGTGC	GGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGAGGCCAGCTCTGACCATTTCCTTC	83373
λ;	402	MetThrLysLyslleLysLysLeuGluLysGluThrThrMe	415

qa		Db 84454 CCCAGGAGCACGAGC
	tTyrargSerargTrpGluSerSerasnLysalaLeuLeuGluMetalaGluGlu	84514 CAGGCC 84
	83434 GTACCGGTCCCGGTGGGAGCACCAACAACAAGGCCCTGCTTGAGATGGCTGAGGAGGTGGG 83493	RESULT 34
	CTGTCTGTGATCTGCAGCCAGGGTGGGGTGTGCACTTAGCGCATATCAGGCCCTTTCCT	ID AAS66673 standard; cDNA;
ò	433 433	AAS66673;
	83554 GTATGTTCTACCCATCAGTGACACAGCTAGCATGAGGTAGAGGTGAGATTTGCACACAAT 83613	
	433 433	
qu	83614 GTCCAAGTCCAAAGTTAATGCTGTTCTCTCCCCATGGGAGGTGGTGAGCCCAGTGGTAGG 83673	KW Human; chromosome mapping KW food supplement; medical
	433 433	XX OS Homo sapiens.
	83674 TCTCCAGTGGGAGTGAAGGGAGCAAATGGAAGAAAGAATAAAAGAGCAGAAAAAAAA	XX PN WO200175067-A2.
ò	433 433	XX PD 11-0CT-2001.
	83734 GIGCCAGIGAIGIGCCIGGITIACAIGIAAAGCAGCCCAGGIAGITIGIGAITICACAGC 83793	XX XX
	433 433	XX
_	83794 TIGTAATGTAGAAGAAAAGGAACTAACGATGGAGCAACTGCAAGCCAGACCTTGCTGA 83853	23-AUG-2000;
	433 433	(HYSE-) HYSEQ INC.
	83854 AAGTITITGGGTTTTTTTTGTCTTTTTTGCTGCTGAATGTTTTTAGGTACGTTGTTCATT 83913	
	433 433	DR WPI; 2001-639362/73. DR P-PSDB; ABG02486.
	83914 GAACCTTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAGATGAGACAGGC 83973	
	433	
	83974 TCAAAAGTCAAGTCCTTTGCCAAGGTCACGTGGTAGATAAATGGAGGAATACGTTATCTC 84033	biodiversity.
	433 433	
qq	84034 CAAGCCGTGCCCCTTTTCTGCACCATGCTGCCCCACCTGACAGCCTAGTCATGGCTTCAA 84093	The invention relates to sequences. (I) is useful
	433 433	
	84094 CTAGGACTGTTTCCTAGAGGGGGCCAGCTTTGGACTCGGTCTGCTCTCAGCCTTGTTAAA 84153	in d gene
οχ	433 433	
	84154 GIGTTIGCCGCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGCACGGCACTGAAGGTC 84213	CC polypeptide in tissue, as CC supplement. (II) and its N
	434	
	84214 TCATITCTTTCCCTAGAAACAGTCCGGGATAAAGAACTGGAGGGGCCTGCAGGTAAAAAT 84273	
à t	eGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysAr	
	CCAACGGCTGGAAAGCTGTGCCGGGCACTGCAGACAGAGCGCAATGACCTGAAGAG	
	468 9741CHIASPLEUSEXALSGLYGINGLYSETLEUTHTASSESETGLYFYGGLUARGA 488 	CC electronic format directly CC ftp.wipo.int/pub/published XX
	9ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTy	Seque
	84394 GCCAGAGGGCTGGGGCTCAAGCACCCAGCTCCCCAGGGTCACAGAAGCGCCTTGCTA 84453	
	508 rProGlyalaProSerThrGlualaSerGlyGlnThrGlyProGlnGluBroThrSerAl 528	Score: 542.50 Percent Similarity: 55.61% Best Local Similarity: 40.91%

Length:
Matches:
Conservative:
Mismatches:

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octide (I) and polypeptide (II)
brobes, polymerase chain
chromosome and gene mapping,
polymucleotides are also used
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traits to assess biodiversity
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present novel human diagnostic
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fication, but was obtained in
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GTCCATCTGGAGGCTGACCCCAAA 1167
ArgProGluGlyProGlyAlaGlnAlaProSerSerProArg 501
                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; forensic; genetic disorder; ss.
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ication of mutations
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|TCCACA 1209
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186 487	126 AA	Oy 502ValThrGluAlaProCysT ::: Db 66 GGAATGAAGTAAAATGCT	RESULT 36 ABL10155 ID ABL10155 standard; cDNA; 1843 B	XX AC ABL10155;	XX DT 26-MAR-2002 (first entry) XX	Drosophila melanogaster ex	KW Drosophila, developmental biolo KW pharmaceutical, gene; ss.	XX OS Drosophila melanogaster. XX XX			AA 23-MAR-2000; 2000US-0191637P. PR 11-JUL-2000; 2000US-00614150. XX	PA (PEKE) PE CORP NY. XX PI Venter JC, Adams M, Li PWD,	DR WPI; 2001-656860/75.		YXX Claim 1, SEQ ID NO 24947; 21pp	XX CC The invention relates to an iso CC capable of detecting 1000 or mo CC useful in developmental biology				XX SQ Sequence 1843 BP; 591 A; 424 C,	ment Scores: No.:	Score: Percent Similarity: 53.648 Best Local Similarity: 35.808 Query Match:	DB: US-10-023-523-8 (1-530) x ABL10155	Oy 127 GluGluIleArgGlnSerAspG
		184	0 0		219		808	. 259			299		339	511	359	379		331	4 4	9 7	307	459 247		187
		STyrAlaGluLeuLeu : :::::: SAAAGCAGATATGTTG	LysLeuLeuGlnLysLysGln	rcificaacaitcaagac	HisserLysAlaval 	HisAsnArgSerLeu	AACAGGAGTIGG	JLysGluValThrSer	inamenaginacieca Hisasoginatoaso	 CATGAAATACACAAT	sLysLeulleGluGln BAAGCTCACTGACCAG	sAspLeuGlnGlnGln	JAJaGJuGJuArgHis	:::	nargMetCysGluLeu : :SCaCaaaTaTGaaGaa	ThrGluLysPheGlu:::	PhelysGlnGluMet	TTCAAGCAGGAAACG	MetTyrArgSerArg		sinrvalargasplys ::: \actattcgtgataaa	stevCysArgAlaLeuGln ::: GCTGTACAAGGCTCTTCAA		GAATGAACTCAGTGAGAAACTGGGGATTCTGAAAGGGGGGGG
Conservative: 55 Mismatches: 85 Indels: 81 Gaps: 11	4)	AlaalaLeuCysLysLysTyrAlaGluLeuLeu 	SArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGln	GATAT	-GInLeuvalGinGluLysaspHisLeuArgGlyGluHisSerLysAlaval - CAGTGCCACAAGTAAAACATTTATTGAAAGATGAAGACCCGTAGTTT CAGTGCCACAAGTAAAACATTTATTGAAGATGAAGACCCGTAGTAA	gSerlysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeu		ysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSer	ALAI AI GCAGCAGAAAAAAGAAGAAGAAAAAAAAAAAAAA		uargglngluasnMetGluLeuAlagluargLeuLysLysLeulleglugln	uArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln	GAGGGAAGACACLAAATTAATAAAGCGTTCAAALATAAGGAATTACGACAAAAG palatysieuGTnGTnAlaGInGTuMetLeutygGTuAlaGTuGTUAAgHis		GlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeu 	MetLysGlnGlnThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGlu	GlupheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGl		eLysLysLeuGluLysGluThrThrMetTyrArgSerArg		aleuleuGlumetAlaGluuySinrvalArgAspLyS ::: AAAACTATTCGTGATAAA	GlubeuGluGlyEeuGlnValLysTleGlnArgLeuGluLysLeuCysArgAla:	gAsnAspLeuAsnLysArgVal	CTGGGAATTCTGAAAGGG
40.91% Misn 23.78% Inde	x AAS92278 (1-1734)	OGLUGLULYSLEUALAALAL GCTGGAC	Arg	AATCACAT	lnLeuValGlnGluLys GTGCCACAAGTAATAAA	erLysLeuGluSerLeu		lyValGlnArgAlaArg	AIAIGCAGCAGAAAAA alThrIonAcaacaile	:: TTACTTTAACTGAAACT	rgGlnGluAsnMetGlu :: AGCAGGAGAACATGGAA	rgGluGluHisIleAsp	GGGAAGAGCAAATTAAT latysteuGlnGlnAla	::: CCAGACTTCAACAAACA	ysAspPheLeuLeuLys ::::: GAGAGTTTTTATTAAAA	InGluThrHisLeuLys 	snThrLeuSerLysSer	CTACCATGGCAAAAACC	tThrLysLysIleLysLys		erAsnLysAlaLeuLeu	lybeuglnvalbysile ::: ::: TCTTTCAATAAATTG	gAsnAspLeuAsnLysArgVal	ATGAACTCAGTGAGAAA
Fercent Similarity: Best Local Similarity: Query Match: DB:	US-10-023-523-8 (1-530)	167 SerThrProG 981 AGCACAATGG	185G	927 TGTAACTCTGAATCACAT	202 SerG 888 TCAAATTGCA	220 LeuAlaArgS	828 ATAACAAAG-	LysGluGl	GAGGA	CATTTCCA	280 SeriysieuA ::: : 690 GCCAAACTGC	TyrGlube	320 LeuvalAspA	570 CTTGTAGATG	340 GlnArgGlub 510 CAGAGAGAGA	360 MetLysglnG 450 ATGAACAAG		390 GAATTCCAGA	GluLysMe		420 TrpGluserserAsnLysAL 324	440 GluLeuGluG ::: 306 AATTATAAGG	ThrGluAr	246 ATAGAAAGGA
Best Loc Query Ma DB:	US-10-02	oy Db	ð í	g O	දු දු	8	d d	8 1	a 2	op Op	<i>\$</i> ∂	ð í	g &	qq	λ O	රු සි	à	Dþ	& 1	සි (A G	o d ∂	à	g

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n isolated nucleic acid detection reagent or more genes from Drosophila. The invention is blogy and in elucidating cell signalling and righer eukaryotes for the development of and pharmaceutical drugs. The invention and pharmaceutical drugs. The invention and place (ABL16176-ABL30511), expressed DNA is) and the encoded proteins (ABBS7737-a for this parent did not form part of the was obtained in electronic format directly oub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGLUVALGIYASPArgAspHisArgArgProGlnGluLys 146 :::||| |||::: ::||| |||::: aaaagrGGCGCGACCAGAAGTTG 113
AGTGCCTGTGACGCATTCCTGTGCTGACCTGGATTCTTCC 127
                                             gProGluGlyProGlyAlaGlnAlaProSerSerProArg 501
                                                                                    raaagagccccaggagtccatctggaggctgaccccaaa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ection reagent for detecting 1000 or more elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ssed polynucleotide SEQ ID NO 24947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                logy; cell signalling; insecticide;
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(first entry)

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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                         DNA encoding novel human diagnostic protein #2478
                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                   114 GAGGAG-----TTGGTCATGAAATCCCTTGACGAATGC
                                                               LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal
                                                                                                                                                     246 CAAATGGAGTCGCAGCAGGAGGAGAAGGAGCAGGTTCAGCGGGATCTTAACAAGAGCGTC
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cerivity of is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement: (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess brodivering and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human diagnostic coding sequences. AAS6419-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in partner of the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
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Claim 1; SEQ ID NO 2478; 103pp; English.
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standard; cDNA; 2526

AAS66674

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us-10-023-523-8.rng

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16175) and the encoded proteins (ABBS-137-ABB-2072). The sequence data for this parent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                       1661 GGGGATCCGCGTTCTAAATATAGCCACTGCACACGCACGTTCTCTGTTTTCCGATTTTCC 1720
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                                                                                                                                                                                                      2140 ACCAGATTGGCCTGGAGAAACTGATGCAAGGCGCAACGTGCCATAAAGGATCTCACCGATC 2199
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                                                                                                                                                                                                                                                                                337 luArgHisGln----- 340
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         260 isPheGlnValThrLeuAspAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnS 280
                                                                                                                                                                                        304 luGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaL 324
                                                                                                                                                                                                                                      -----GluMetLeuLysGluAlaGluG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 snThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetT 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 lyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------ArgleulyslysleulleGluGlnTyrGluLeuArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 InGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnA
                                                     280 erLysLeuArgGlnGluAsnMetGluLeuAlaGlu-----
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The present invention describes an expressed sequence tag (BST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing tritipotence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GCTGGAGCCCTCCGTGATGTCTCTGAGGAGTTGAGCCGCCAGCTGGAAGACATCCTCAGT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 GCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGCCTCAAGGAATGGGGAGCCTGAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GlyProGlySerSerGlnAlaProArgLySProGluGlyAlaGlnAlaArgThrAlaGln 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 defreecédececrichagaactagregarecece---decreeadaart-egecaceag 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluPro 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATACTGCGTGGACAACAACAGTCAAGGGGCCCAGGTGAGGATGTGGCACACAGGGTGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An expressed sequence tag (EST), the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell.
                                                                                                                                              Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
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Matches:
Conservative:
Mismatches:
                                                                           Bovine embryonic germ (EG) cell cDNA EST #570.
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Gaps:
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79.718
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                                                                                                                                                                                     development; gene; ss.
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                                                                                                                                                                                                                                                            Bos taurus.
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Alignment Scores:
Pred. No.:
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   Pro---ThrProvalvalTyrGlyGluLysGluProSerLysGlyAspProAsnThrGlu 127
                CCAGAGACTCCAGTAGTCAATGGTGAGAAGGAATCTCCAAGGGGGAGCCGGGCCCGGAC 317
                                                 377
                                                                                                                                                                 Human; ss; sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping; blodiversity; genetic disorder.
                               GluileArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLys
                                              GAGATCCGGACCAGTGATGAAGTCGTAGACCGAGACCACCGAAGGCCACAGGANAAGAAA
                                                             LysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThr 165
                                                                    Jones LW;
                                                                                                                                                                                                                                                                                                          Dickson MC,
                                                                                                                                                                                                                                                                                                          Stache-Crain B,
                                                                                                        ACH31687 standard; cDNA; 334 BP.
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                                                                                                                                                  Human bone marrow cDNA #978.
                                                                                                                                    13-OCT-2003 (first entry)
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LABAT I.
STACHE-CRAIN B.
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                                                                                                                                                                                                                                                                                    DICKSON M C.
JONES L W.
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                                                                                                                                                                                                     US2003073623-A1
                                                                                                                                                                                                                                                                                           JONES
                                                                                                                                                                                       Homo sapiens
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(STAC/)
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New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 18899; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensios, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The present sequence for this patent did not form part of the printed specification, but was constant and directly from 19770 at obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 334 BP; 55 A; 82 C; 73 G; 124 T; 0 U; 0 Other;

ID NO 4742; 2537pp + Sequence Listing; English

Claim 1; SEQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDMAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                   230 ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu
                                                                                                     HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys
                                                                                                                                                                                                                                                               250 GluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGln
                                                                                                                                                                                                                                                                                           290 AlaGluArgleuLysLysLeulleGluGlnTyrGluLeuArgGluGluHisIleAspLys
                                                                                                                                                                                                                                                                                                               94 GGGGAGAAAGAAAGATCATCGAACAGTACGCACTGAGGGAAGAGACACATGATAAG
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                GTGTTCACACATAAGGACCTGCAACAGCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA clone (5'-primer) SEQ ID NO:4742.
                                                         Gaps:
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464.00
91.89%
78.38%
17.17%
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27-AUG-1999; 99JP-0030D253.
11-JAN-2000; 2000JP-00118776.
02-YAY-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                AAH07907 standard; cDNA; 710
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Ishii S,
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence of polynucleotide which comprises a 1'-end sequence of pecification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length or primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs represent human amino acid sequences; and AAH1363 represent human amino acid sequences; and AAH362 represent control of the primers are used in the exemplification of the primers are used in the exemplification of the
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			GluGlyAlaGlnGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly	 GAGGCAGCGGGGGAAAGAGGCGGCGGCGAAGAGGGGGACTGAGGCCGGACGGGGGGGG	ProGluGlyAlaGlnAlaArgThrAlaGlnSer	::::: ::: CGGCGACGCGAGCCCGCGGCAGAGTTTGAAATTGGCACAATGGAAGAAGGTGGAATTTGT	GlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThr	 GGGCTAGGGGTGAAAGCAGATATGTTGTGTAACTCTCAATCAA	roAla	CAAGGCTCAAATTGTGGGGGCACAAGTAACAAGCATTCATTGGAAGGATGAA	GluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro	CCA	ThrProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIle	-GAAGCT	ArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAla		LysGlyLeuGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrPro	-TTAGGAAAAGAAGTTTTATTACTGATGCAAGCCCTAAAACACCCCTTTCAACCCA	GluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsn	GAGGAGAAGCTGGCAGCTCTCTGTAAGAAATATGCTGATCTTCTGGAGGAGAAGAAGA	SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAsp 209
			ıGlyP	ACGGG	rAlaG	rggaa	Tens	CTTC	TyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAl	AGAGG	ProG		Glug	- g	Lysh	GAAA	SerT	TCAA	Hisa	PACA	GluL
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Length: Matches: Conservative	Mismatches: Indels: Gaps:	_	AlaAl	GCCGA	ProGl	GAAAT	LeuSe	TGTAA	ProGl	ACAAG	ThrTy	GGCAGTGACTTTATAACAGAAACAGGAATTTGGTGAGC-	ProSe	GCATACTGCACGCAAGAATCAAGAGGAAATCCCTGGGGGA-	AspHi	GATTC	LeuMe	CTGAT	LysTy	AAATA	Lysty
o A c	A L B	(1-710)	rGln	SCGGC		AGTTT	uGlu	GTTG	,4G1,4	11GGC	rArg'	CAGG	sGlu	- IAGAG	pArg	GCAA	rrLeu]	'ATTA	'sLys]	TAAG	uGln]
			ProSe	25255	Lys	CAGAZ	SerG]	GATA	GlnG]	TGTGC	Lysse	GAGAA(GluLy	TCAAG	GlyAE	GGTC	11erk	GTTT	LeuCy	CTCTG	LeuLe
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Alignment Scores: Pred. No.: Score: Percent Similarity	l Sim ch:	-523-8	12	70	3.2	130	20	190	70	250	90	304	110	346	130	394	150	454	170	208	190
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210 HisbeuArgGlyGluHisSerLysAlaValbeuAlaArgSerLysBeuGluSerLeuCys 229
Cardiovascular system antigen, human, mouse, rabbit, goat, horse, cat, chicken, scheep, immunosuppressive, antiarthritic; vasotropic; dog; antirheumatic; antiproliferative, cytostatic, cardiant, neuroprotective, cerebropic, antibacterial, virucide, fungicide, concer, ophthalmological, vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast, liver; cardiovascular disorder; ss, cerebrovascular disorder; ss, fungal infection; viral infection; ocular disorder; bacterial infection; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                                                                                                                                                                                                                  Human cardiovascular system antigen cDNA polynucleotide SEQ ID.No 467
                                                                              230 ArgGluLeuGlnArgHisAsn 236
                                                                                                     688 ANAGAACTICANCGICACAAT 708
                                                                                                                                                 AAS35582 standard; cDNA; 405 BP.
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17-NOV-2000; 2000US-0249244F.
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Rosen CA, Barash SC,

WPI; 2001-451930/48. P-PSDB; AAU22308.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system

Claim 1; SEQ ID NO 467; 674pp; English

cardiovascular system antigen polypeptides of the invention.

cardiovascular system antigens and their associated polynuclectides are
cardiovascular system antigens and their associated polynuclectides are
cardiovascular system antigens and their associated polynuclectides are
cuseful in the diagnosis, treatment and prevention of various types of
disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
chickens or sheep. A pathological condition can be determined by
chickens or sheep. A pathological condition and a cardiovascular
system antigen polynuclectide. The treatable disorders include autoimmune
diseases such as rheumatoid arthritis, hyperproliferative disorders such
as neoplasms of the breast or liver, cardiovascular disorders such as
cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, and disorders such as Alzheimer's disease, infections caused
by bacteria, viruses and fungi, ocular disorders such as corneal
infection, endocrine disorders such as formed and infection,
das glomerulonophritis and respiratory disorders such as asthma and
pleurisy. The polypeptides can also be used to aid wound healing, to
prevent skin aging due to sumburn, to maintain organs before
transplantarion, to regenerate tissues and in chemctaxis. Note: The
specification, but was obtained in electronic format directly from WIPO
specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

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Length: Matches: Conservative: Mismatches:

1.92e-13 350.00 79.09% 75.45%

Percent Similarity: Best Local Similarity:

Alignment Scores: Pred. No.:

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                                                                                                                                   GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln:::||
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The invention relates to human cardiovascular system related polypeptides and the polymucleotides encoding them. The polypeptides, polymucleotides and antibodies to the polypeptides are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular system tissues, proliferative disorders, foetal and developmental abnormalities, heematopoietic disorders, diseases of arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cardiovascular system related polynucleotides and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular tissues and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 467; 262pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC;
                                                   2000US-0246524P.
2000US-0246525P.
2000US-0246526P.
2000US-0246526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-743766/70.
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                                                               08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; procs; ovarian cyst; dysmenorrhoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibiciammatory; gynaecological; reproductive; gene; ss.
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75 AAAGAACGGGGCTGCCAACTGGAAGACATACTGAGCACATACTGTGGGACATAACCAG 134
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diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders and infections. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and polynucleotides may also be used as food additives or preservatives to increase or decrease storage capabilities, fat content or other nutritional components. This sequence represents a human cardiovascular system related polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1315 GGGGGCCCCGGCGAGGATGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                     57 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 AGAGAAGGAACCTCCAAGGGGATTCCAAACACAGAAGAGATTCCGGCAGAGTTGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerArgThrTyrValAlaArgAsnGlyGluPro-GluProThrProVal----ValTyrGl
                                                                                                                                                                           Sequence 405 BP; 123 A; 90 C; 126 G; 63 T; 0 U; 3 Other;
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83
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 yLysGluIleThrLeuLeuMet 160
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75.45%
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                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                      Alignment Scores:
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The invention relates to 2175 novel. human ovarian antigens (ABB41054-ABB9328) and to CDMAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polyputcleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen of covarian antigen polymoleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related of sorders. Such conditions include ovarian cancer and breast cancer, and clisorders. Gut conditions include ovarian cancer and breast cancer, and clisorders (e.g., infertility, disorders of pregnancy, anovulation, disorders (e.g., infertility, disorders of pregnancy, anovulation, clinquamators, infertility, disorders of pregnancy, anovulation, disorders, infertility, disorders of pregnancy, anovulation, clinquamators, infertility, disorders of pregnancy, anovulation, clinquamators, componitions (e.g., mastitis, oophoritis and disorders, infertilismancy conditions (e.g., mastitis, oophoritis and vagnifically), inmune disorders (e.g., congenital and acquired inmunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaminal, cardiovascular disorders of crepiratory disorders, neurological disorders gastrointestinal disorders may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies clearing in dispersent school polypeptides may be used as food additives or to prepare antibodies clearing in disperse the prainted spanet cepares data for this patent did not form part of the printed spanetic day and the number of the printed spanetic day and the prepare antibodies invention. Note: The sequence data for this patent did not form part of the printed spanetic day and the prepare antiboding and in the prepare antibodic clearing the praint of the prainted spanetication, in the praine
                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1238; 2922pp; English
07-JUN-2001; 2001WO-US018569
                                                 07-JUN-2000; 2000US-0209467P
                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                 Rosen CA;
                                                                                                                                                                                                                   2002-147878/19
                                                                                                                                                                                                                                             P-PSDB; ABP42281
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                                                                                                                                                                                                                                                                                                                                                                                       diseases.
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Sequence 725 BP; 263 A; 122 C; 147 G; 176 T; 0 U; 17 Other;

347 LeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGluThrHis 366 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIle 406 TTAAANGAAGCGACAGAATCGAGCCACAAATACGAACAATGAAACAGCANGAAGTACAA 393 367 LeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer 386 AAAAGCAATGAACTGGTTACAACCTTCAGACAAGGAAATGGAAAAGATGACAAAGAAATT 513 LysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAla 426 Length:
Matches:
Conservative:
Mismatches: Indels: US-10-023-523-8 (1-530) x ABQ55358 (1-725) 3.46e-11 318.00 77.05% 60.66% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 454 407 334 394 387 8 g ò g $\stackrel{>}{\delta}$ g

Sequence 981 BP; 195 A; 212 C; 255 G; 214 T; 0 U; 105 Other;

the present invention

Length:
Matches:
Conservative:
Mismatches:
Indels:

9.81e-11 313.00 62.88% 56.06% 11.58%

Percent Similarity: Best Local Similarity:

No. .

Query Match:

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The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce totipotence in one or more cells. Molecules which induced totipotence in a cell line are useful for inducing incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the exemplification of
                                                                                                            LyslleGlnArg-LeuGluLysLeuCysArgAla-LeuGlnThrGluArgAsnAspLeuA 466
                                                                                                                                 LeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnVal
                                                                             573 CTTTGCAAATGGCTGAAGAGGAAAACAGTCCGNGATAAAGAGTNCAAGGNCCTTCAAATA
                                                                                                                                                                                                                                                                                                                                                                                                   Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
development; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An expressed sequence tag (EST), the expression of which, complementary sequence, in a cell identifies the cell as developmentally competent or incompetent cell.
                                                                                                                                                                                                                                                                                                                                                                            Bovine embryonic germ (EG) cell cDNA EST #561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          silertsen KJ, Pfister-Genskow M, Childs L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 16; Page 458-459; 584pp; English
                                                                                                                                                                                                                                                                           ABN74510 standard; cDNA; 981 BP
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                                                                                                                                                                                                          AT 694
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                                                                                                         GCTGNAGCCCTCCGNGATGTNTCTGAGGAGTTGANCCGNCANCTGGATGACATCCTCANN 141
                                                                                                                                                                         AlagluProgluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProglu 108
                                                                                                                                                                                               261
                                                                                                                                                                                                                    Pro---ThrProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGlu 127
                                                                                                                                                                                                                                         262 ccagaracrecagragrennrenneadaagaannerecaagagagageeggeeggee 321
                                                                                                                                                                                                                                                               GluileArg-GlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLysLy 147
                                                                                                                                                                                                                                                                                    322 TAGATCCTGTACCAGNGATGAAGTTTGAGACCGANACCACCCAAAGCCNCNGGATANTAA 381
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                                          GlyProglySerSerGinAlaProArgLysProGluGlyAlaGlnAlaArgThrAlaGln 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing breast cancer comprises determining expression of nucleic amplecules or expression products that are differentially expressed in normal and malignant tissue.
                                                                                                                                                     ACATACTGCGTGGACAACAGNNANNGGGCCCAGGTNAGGATGTGGCANAGGNGAGCCT
                                                                                                                                                                                              GCTGAACCCGAAGATGCANAGAAGNCCNGGACCTATNCCTCANGGANTGAGNAGCCTGAG
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                                                                                     SerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSer
                                                                                                                                ThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluPro
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                                                                                                                                                                                                                                                                                                            sLysAlaLysGlyLeuGlyLysGluileThrLeu 158
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                        (1-530) x ABN74510 (1-981)
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P-PSDB; AAU84350.
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GACCAACAAAATGCTCAAAGCCGAAATGGAAGACCTGGTCAGCTCCAAGGATGACGTGGG 4226
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the invention are differentially expressed in breast tumours characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of indentification of compounds useful for the treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. ABKAS5S1-ABKASS81 represent the human genes of the invention that are differentially expressed in breast cancer tissue
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153
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hishwyHC polypeptide, nucleic acid, or it can diagnosing, preventing or treating e.g. hypertension, urinary incontinence, irrical cramps, premature labor, glaucoma, bronc cc malfunction, or other medical conditions chember polypeptide or nucleic acid is a continued by the above-mentioned diseases or disorder cc smooth muscle myosin heavy chain (hSWMyHC XX	, , , , , , , , , , , , , , , , , , ,	455Cybargardaeudillingchargaeinspide
XX XX New human smooth muscle myosin heavy cha PT nucleic acid, useful for diagnosing, pre PT hypertension, incontinence, menstrual cr XX XX XX XX XX XX XX XX		4971 GCTGGCCACAGAGGCCCAGAAGAAGATGAGAGTGCCGGCAGCAGCAGCGGGGGGGG
Malik F, Beraud C, WPI; 2003-479585/45. P-PSDB; ABU10399.		rLysLyslleLysLys ::::: acagcagccgagcagcagcagcagcagcagcagcagcagc
10-AUG-2001; (CYTO-) CYTOK		372 aLeuTyrThrGlulysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392
13-FEB-2003.		
/partial /note= "No stop codor US2003032018-A1.		335 aGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGl 352
ou/		325
X Homo sapiens. X H Key Location/Qualifiers		nginleuvalaspalalys
KW Human; smooth muscle myosin heavy chain; KW antiasthmatic; hypertensive; hypotensive, KW gynaecological; tocolytic; cardiant; vask w pulmonary disorder; reproductive disorder; KW asthma; hypotension; hypotension; Mypotension; urinas KW irritable bowel syndrome; menstrual cram; KW bronchioconstriction; cardiac malfunction		294 SUPSECULTEGLA
		SAACTGGAAGACGAAAGCAACGTGCCTGGCAGCTGCAGCAAAA
NO O		267 pIleGinLeuGinMetGluGinHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMe 287
Oy 520ThrGlyPro Db 5390 AGAGCAACGAGGCCATGGGCCGCGAGGTGAAC RESULT 47		GAAGACCCCAGCIGGAAGACCIGGAAGACCAGCCAACAACAACAACAACAACAACAAAAAAA
504 UAlaProCysTyrProGlyAl 5330 AGTCCCAGCGCGCA		4227 CAAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGAT 4286 232 uGlnArgHisAsnArgSerLeulysGluGluGlyValGlnArgAlaArgGluGluGluGl 252 4287 GAAGACGCAGCTGGAAGAGTGGAGAGAGAGAGAGAGAGAG

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| AGCTGCAGCGGGAGCTGGATGAGGCCACGG 5389
rGluAjaSerGjyGln------ 519
                                                                                                                                                                                                                                                                                                                                                                      iin; hSMMyHC; inotropic;
iive; uropathic; antiinflammatory;
vascular disorder;
order; immunological disorder;
iinary incontinence;
rramp; premature labor; glaucoma;
ition; gene; ss.
                                                                                                                 ACGCACTCAAGAGCAAGCTCAGGCGAGG 5447
                                                                                -----GingluProThrSerAlaArg 529
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                                                                                                                                                                                                                                                                                                                               (hSMMyHC) variant cDNA #2.
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uscle myosin heavy chain"
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hain (hSMMyHC) polypèptide and reventing or treating e.g. asthma, cramps, premature labor or cardiac

human smooth muscle myosin heavy
WMYHC protein, nucleic acid, or its
ip reventing or treating vascular,
gical disorders. In particular, the
standularor is useful for
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Other;			Glu	CTCAACGTGTC		gAspValSer	pAsnAsnGln	CCGTGGAAGC		AGCAGIACGA	Gludspalaglulysserarginriyrvalal ::: aaagaccaagacaggcticagcaggcigg	rGlyGluLys(TGGAAAAGAAG	ulleArgGlns:	AATACGC	ysAlaLysGl) 	hrProGluGlı	GAAACCAA	rgAsnSerGlr	AGGAACTCGAC	ysAspHisLet	AGGATGACGTC	euCysArgGlu AGATGGAGGAG	າດເງານເງານເງາ	CTGCAAGCCACGGAGGACGCCAA	SerHisPheGlnValThrLeuAsnA	AGGGA	rgGlnGluAsn
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1868 G; 883	Length: Matches: Conservative Mismatches: Indels: Gaps:	5937)	SerbroglyGlnProgluAlaGlyProgluGlyAlaGln	AGCTGCTTCAAGAAGAAACCCGGCAGAAGGCTCAACGTGT aValGlublaGluGlubroGluGarGarGarGluhlabrohraft	 GGBG	ProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 	GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly	::: :: CATCCAGCTCTCCGAACTAGAAGCTGCAGGACTTTGCCAGGACCGTGGAAGCTCT	GlyProGlyGluAspGlyAlaGlnGlýGluProAlaGluPro	אפפאפאן רפאס	GIUASPATAGIULUASPATAGIULVSSEKAKGIDKIYKVALALA : : : : : : : GAAGGGGGCCGCTTAGAGAAAGAGCAAGAAGAAGGTTCAGAAGAAGAGCTGGA	-GlyGluProGluProThrProValValTyrGlyGluLysGlu ::: :::::	cóaccrogrigaritigaacaaccagcaacrogróricaaccrodaaaagaagca	Pro	HGGHGAAAAAC	AspdiuvalGly-AspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe 	uGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy	; 1 1 ; 4 ; 5	SLeuAlaAlaLeuCySLySLySTyrAlaGluLeuLeuGluGluHiSArgAsnSerGlnLy 	decectercetreeercetreaadadecerriddadeceaagagaacreaage	SGInMetLysLeuLeuGInLysLysGInSerGInLeuValGInGluLysAspHisLeuAr	rggaagacctg	gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 	uGlnåraHisAsnàrdSerieniVsGluGlvValGlnardalaardCluGluGluGl	7	resSer	ACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA	pIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMe
1482 C; 1	_	6 (1-	luAla	GAGCTGCTTC		lnalaargīh	euGluAspIl	 rcgaagaaga	lyAlaGlnGl	7557777555	PATAAACTGG	GlyGluPro	rtggacaacc	SerLy	10114666	Argasphisa GGGACAGAGG	euLeuMetG]		ysLysTyrA]	GGGCCCTTG	lnLysLysG]	AAGCCGAAA1	laValLeuA] :: TGGAGAAGTC	בישאין וופין באפין	GAAGACGCAGCTGGAAGAGCTGGAGGACGAG	hr	ACATGCAGG	luGlnHisAe
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|:::||| ::: |||||:: |||||:: 4158 TCTCCAAGCGGGAGGAGGAGGAGGAGGAGAGCAGCTTCA 4817 5117 1878 GAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAGCTTCAGGCCGACTCTGCCATCAAGGG 4937 ::::||| ||||||::: 4998 AGAGCTGGAAGATGCCCGTGCTCCAGAGATGAGATCTTTGCCACAGAGAAGAGAATGA 5057 5457 CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGGAGCAGGTCGAGCA 5516 5636 | |||||||:: :::||| 5636 CAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAGAGGCAGAGGCAGAGGAGG 5695 5178 TAGCCTGTCGGGAAGGAACGCACTCCAGGACGAGAAGGGCCCGCCTGGAGGCCCCGGATCGC 5237 5696 AGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGAGCTGGATGAGGCCACGG 5755 335 aGluGluArgHisGlnArg------GluLysAspPheLeuLeuLysGluAlaValGl 352 294 sLysLeuIleGlu------ GlnTyrGluLeu---------- 302 352 uSerGlnArgMetCysGluLeuMetLysGlnGlnGlnThrHisLeuLysGlnGlnLeuAl 372 372 aleuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLysLysLeuGluLysGl 412 412 uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet---Al 431 455 ----CysArgAlaLeuGlnThrGluArgAsnAspLeu------AsnLysArgValGl 470 nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp------SerGl 484 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGln----- 519 484 yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504 5756 AGAGCAACGAGGCCATGGGCCGAGGTGAACGCACTCAAGAGCAAGCTCAGGCGAGG 5813 520 ------ThrGlyPro-----GlnGluProThrSerAlaArg 529 4818 CGAGTATGAGACGGAACTGGAAGAGGAGAAAGCAACGTGCCCTGGCAGCTGCAGAA 5058 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTCCATGCAGCTACAAGAGGACCTCGCCGCCGC ----LeuAlaGluArgLeuLy ---HisLysAspLeuGlnGl 431 aGluGluLysThrValArgAspLys-----GluLeuGluGly------318 nGlnLeuValAspAlaLys-------ArgGluGluHisIleAspLysValPheLys-----287 tGlu---470

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5065 AGAGCTGGAAGATGCCCGCGCGCCCCAGAGATCTTTGCCACAGGCCAAAGAGAATGA 5124
                     1258 GGAAGAGGAAGAAGAGGTTCCAGAAGGAGATCGAGAACCTCACCAGCAGTACGAGGA 4317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LeuGlnGlnAlaGlnGluMetLeuLysGluAl 335
                                                                                                                                                                                                                                                                   103 ArgAsn------GlyGluProGluProThrProValValTyrGlyGluLysGlu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMe
39 ProGluGly---AlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu
                                                                                     ::: ::|||||||:::
4198 CATCCAGCTCTCCGACTAGAAGAAGCTGCAGGACTTTGCCAGCACCGTGGAAGCTCT
                                                                                                                                                                                                                                 1318 GAAGGCGGCCGCTTATGATAAACTGGAAAAGACCAAGAACAGGCTTCAGCAGGAGCTGGA
                                                                                                                                                                                                                                                                                      119 Pro-------SerLysGlyAspProAsnThrGluGluIleArgGlnSer
                                                                                                                                                                                                                                                                                                                                                          133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1885 CÓAGTATGAGACGGAACTGGAAGACGAGCGAAGCAACGTGCCCTGGCAGCTGCAGAAA
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                                                                 58 GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly
                                                                                                                                                                                                   -----GluAspAlaGluLysSerArgThrTyrValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                   4492 -------GGATGAGAGGACAGAGCTGAGGCAGAAGCCAGGGAGAAG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4774 ACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCCAGTTCGAA-----AGGGA
                                                                                                                                 78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro----
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given in ABR92047 to ABR92164. A higher level of expression of (I) than

normal indicates the presence of cervical cancer. Also described: (I) a

vector (II) containing (I); (2) a host cell (III) containing (I); and (3)

assessing (MI) whether a patient is afflicted with cervical cancer.

comprising comparing the level of expression of a marker in a patient's

sample, and the normal level of expression of the marker in a control non

cervical cancer sample, where a significant increase in the level of

expression of the marker in the patient's sample relative to that in the

control sample is an indication that the patient is afflicted with

cervical cancer. (I) has cytostatic activity, and can be used in gene

therapy and in vaccines. (I) is useful in detecting, characterising,

preventing and treating human cervical cancers. (I) may also be used in

various prognostic and diagnostic assays, pharmacogenomics and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCCAGGACACCCAGGAGCTGCTTCAAGAAGAAACCCGGCAGAAGCTCAA---CGTGTC 4092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 38
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                                                                                                                                   Human, cervical cancer, cervical cancer marker, cancer therapy, detection, gene therapy, vaccine, gene; ss.
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                                                                                                     ID NO:161.
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Gannavarapu M, Glatt K, Hoersch S;
                                                                                                     marker encoding cDNA SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 318-319; 386pp; English.
                                                                                                                                                                                                                                                                                                                      13-JUN-2001; 2001US-0298155P.
13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
                                                                                                                                                                                                                                                                                        12-JUN-2002; 2002WO-US018638
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                                                                                                     Human cervical cancer cell
                                                                     10-SEP-2003 (first entry)
     standard; cDNA;
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P-PSDB; ABR92126.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                      Homo sapiens,
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5125 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTCATGCAGCTACAAGAAGACCTCGCCGCCGC 5184	335 aGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGl 352	5185 TGAGAGGGCTCGCAAACAAGCGGACCTCGAGAAGGAGGAACTGGCAGAGGAGCTGGCCAG 5244	352 uSerGlnArgMetCysGluLeuMetLysGlnGluThrHisleuLysGlnGlnLeuAl 372	aleuTvrThrGluLvsPheGludluPheGlnAsnThrLeuSerLvsSerSerGluValPh		392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 412	5360CGGGTCCGCAAAGCCACAGAGGCCGAGGCGAGG	uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl	5404 GCTGGCCACAGAGCGCAGCACGGCCCAGAAGAATGAGAGTGCCCGGCAGCAGCAGCTCGAGCG 5463	431 aGluGluLysThrValArgAspLysGluLeuGluGly	5464 GCAGAACAAGGAGCTCCGGAGCTCCACGAGATGGAGGGGCCGTCAAGTCCAAGTT 5523	444	5524 CAAGTCCACCATCGCGGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCA 5583	455CysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGl 470	5584 GGAGGCCAGGAGAGAAAACAGGCGGCCACCAAGTCGCTGAAGGAAG	470 nAspLeuSerAlaGlyGlyGlyGlySerLeuThrAspSerGl 484	5644 GGAAATCTT-GCTGCAGGTGGAGGACGCAAAGTGGCCGAGCAGTACAAGGAGCAGG 5702	484 yProGludrgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504	5703 CAGAGAAAGGCAATGCCAGGTCAAGCAGCTCAAGAGGCAGAGGCAGAGGAGG 5762	504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGln519	5763 AGTCCCAGCGCATCAACGCCAACCAGGAAGCTGCAGGGGGGGG	520ThrGlyProGlnGluProThrSerAlaArg 529	5823 AGAGCAACGAGGCCATGGGCCGCGAGGTGAACGCACTCAAGAGCAAGCTCAGGCGAGG 5880		scandard; coms; iloss b	3809;	26-SEP-2003 (first entry)	Human cDNA differentially expressed in lung cancer #14.	Gene therapy, emphysema; ss; gene; chronic obstructive pulmonary disease; respiratory disorder; lung cancer; asthma; human.	sapiens.	US2003065157-A1.	03-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 ArgAsn------GlyGluProGluProThrProValValTyrGlyGluLysGlu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------SerLysGlyAspProAsnThrGluGluIleArgGlnSer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AspGluValGly-AspArgAspHisArgArgProGlnGluLysLysAlaLysGlyLe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 -----GluAspAlaGluLysSerArgThrTyrValAla 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 ProGluGly---AlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SerProGlyGlnProGluAla------GlyProGluGlyAlaGluArgPro 18
                                                                                                                                                                                     The invention relates to a combination comprising cDNAs or their complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for disponsing or treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or asthma. The present sequence represents human cDNA differentially expressed during lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9583 CCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTGGAGCGCCACATCTCCACTCTCAA
New combination comprising cDNAs that are differentially expressed in respiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease, emphysema or asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9403 GAAGGCGGCGCGTATGATAAACTGGAAAAGACCAAGAACAGGCTTCAGCAGGAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro--------
                                                                                                                                                                                                                                                                                                                                                                             Sequence 11065 BP; 2564 A; 3049 C; 3072 G; 2377 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                        Claim 1; Page; 39pp; English,
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X # X #

	Qy 470 nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGl 484 :::::::	Qy 484 yProGludrgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504	OY 504 ualaproCysTyrProGlyalaproSerThrGlualaSerGlyGln519	Oy 520ThrGlyProGlnGluProThrSerAlaArg 529	SUL E85	ADE65060; 29-JAN-2004 (first entry)	DE Farnesyl transferase inhibitor modulated leukemia associated gene #279. XX XX XW ss; cytostatic; farnesyl transferase inhibitor; gene expression; XW quinolinone; leukemia; cancer.	Homo WO20	XX PD 08-MAY-2003. XX PF 30-OCT-2002; 2002WO-US034784.	XX	(ORTH) ORTH	PI Raponi M; XX DR WPI; 2003-513497/48. XX	Determining whether a patient will transferase inhibitor, by analyzin differentially modulated in the pr	Disclosure; SEQ ID NO 279; 346pp; English. The invention relates to a method of determining whether a patient wirespond to treatment with a farnesyl transferase inhibitor (FTI), by	analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-	CC methyl-2-(H)quinolinone, monitoring the therapy of a patient, treating a CC patient with leukemia with FII if the analysis indicates that the patient CC will respond. This sequence corresponds to a gene whose expression may be CC modulated in the presence of FII.	XX SQ Sequence 3320 BP; 1025 A; 838 C; 1016 G; 440 T; 0 U; 1 Other;	Alignment Scores: 3.3e-08 Length: 3320 Pred. No.: 281.50 Matches: 154
172 sLeualaalaLeuCysLysLysTyralaGluLeuLeuGluGluHisArgAsnSerGlnLy 192 	SGInMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr	gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe ::::::::: CAAGAA.CGTCCAJGAGGTGGAAAAAACCAAAAACCAAAAAAAAAAA	uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluGl ::::	ulysarglysgluvalthrSerHisPheglnValthrleuAsnas 267 ACTGCGGCTGAAGTCAACGGCGCTCAAGGGCCAAGTGAAAGGA 889	267 pileginLeuginMetGluGinHisAsnGluArgAsnSerLysLeuArgGluGluAsnMe 287	287 tGlu	294 sLysLeulleGluGlnTyrGluLeu	303 -ArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGl 318	318 nGlnLeuValAspAlaLys324	325	335 aGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGl 352	352 uSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAl 372 	aLeuTyrThrGluLysPheGluGluPheGlnAsmThrLeuSerLysSerSerGluValPh	392 eThrThrPheLyBGlnGluMetGluLyBMetThrLyBLyBlleLyBLyBLeuGluLyBGl 412	412 uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl 431	431 aGluGluLysThrValArgAspLysGluLeuGluGly	444 454 [8197 CAAAICCACCAICGGGGGCTHGAGGGCCAAGATTGCACAGCTAGAGGAGCAGGTCGAGCA 8138 455CysargalaLeuGlnThrGluargasnaspLeuAsnLysargValGl 470

Db 1525 CGAGTATGAGACTGGAACTGGAAGCGAGCAAAGCAACGTGCCCTGGCAGCTGCAGAA 1584 Qy 294 SLysLeulleGluGlnTyrGluLeu 302	303	318 nGlnLeuValAspAlaLys	Db 1765 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTCATGCAGCTACAAGAGGACCTCGCCGCCGC 1824	Qy 335 aGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGl 352	QY 352 uSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAl 372	Oy 372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392	Oy 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl 412 Db 2000CGGGTCGCAAAGCCACACAGGGCGAGCAGCTCAGCAAGAA 2043	OY 412 uThrThrMetTyTargserargTrpGluSerSerasnLysalaLeuLeuGl 429 Db 2044 GCTGGCCACAGAGGCACGGCCCAGAAGAATGAGAGTTCCCGGCAGCAGCAGCAGCACGC 2103	Oy 429 uMetAlaGluGluLysThrValArgAspLysGluLeuGluGly443	Oy 444 454 Db 2164 CAAATCCACCACCGGCGCTGGAGGCCAAGATTGCACAGCTAGAGGAGCAGGTCGAGCA 2223	Oy 455CysArgalaLeuGInThrGluArgAsnAspLeuAsnLysArgValGl 470	Oy 470 nAspLeuSerAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	OY 484 YFroGludrgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504	Oy 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGln519	Oy 520ThrdlyProGingluProThrserAlaArg 529 Db 2463 AGAGCAACGAGCCGCGAGGTGAACGCACTCAAGAGCAAGCTAGGCGAGG 2520	Search completed: June 8, 2004, 07:01:41 Job time : 796.959 secs	
Percent Similarity: 38.33\$ Conservative: 99 Best Local Similarity: 23.33\$ Mismatches: 230 Query Match: 178 BB: Gaps: 26 US-10-023-523-8 (1-530) y and second (1-3320)	erProGlyGlnProGluala::	Oy 19 SerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLys 38	Oy 39 ProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 57	OY 58 GluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly 77 :::				ProSerlysGlyAspProAsnThrGluGluIleArgGlnSer	sGlyLe	152 uGlyLysGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 1172				232 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGl :::: ::: :::	SerHisPheGlnValThrLeuAsnAs 	Oy 267 piledinleudinMetGludinHisAsnqluArgAsnSerLysLeuArgdinGluAsnMe 287	Qy 287 tGlu

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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543 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAAG 602	201	603 CAGAGCCAGCTGGTAGAAGAAGAACCACCTGCGCGGTGAGCACAGGAAGGCCGTCCTG 662	221 AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 240	241 GluGluGlyValGlnArgAlaArgGluGluGluGluLySArgLySGluValThrSerHis 260	723	261 PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280	281 LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeulleGluGlnTyr 300 	301 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnHeu 3	903 GAGCTGCGCGAGGAGCATATCGACAAGGTCTTCAAACACAGAGCTGCAACTGC 321 ValAspAlaLysLeuGlnGlnAlaGlnGlnArgHisGln	963 GTGGATGCCAAGCTCCAGCAGGAGATGCTAAAGGAGGCAGAAGAGGGGCACCAG	341 ArgGluLyshspPhaLeuLeuLysGluAlaValGluSerGlnArdMetCysGluLeuMet 360	361 LysglnglngluThrHisLeuLysglnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380 	381 PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluWetGlu 400	401 LysMetThrLysLyslleLysLysLeuGluLysGluThrThrMetTyrargSerArgTrp 420 	421 GluserSerasnLysalaLeuLeuGlumeralaGluGluLysThrValargAspLysGlu 440 	441 LeugluGlyLeuglnVallysIleGlnArgLeugluLysLeuCysArgAlaLeuGlnThr 460 	461 GluargasnaspleuasniysargyalGlnaspleuSeralaGlyGlyGlnGlySerleu 480 	481 ThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGluAlaProSerSerPro 500	501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520	521 GlyProGlnGluProThrSeralaargala 530 	RESULT 2 AR374688 LOCUS AR374688 4697 bp DNA linear PAT 18-DEC-2003
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	ALIGNMENTS	RESULT 1 AR199536	LOCUS AR199536 4697 bp DNA linear PAT 20-APR-2002 DEFINITION Sequence 17 from patent US 6355451. ACCESSION AR199536		Σ	REFERENCE 1 (bases 1 to 4697) AUTHORS Lees, A.W., Lees, R.S., Law, S.W. and Arjona, A.A. TITLE Low density lipoprotein binding proteins and their use in	diagnosing and treating atheroscierosis JOURNAL Patent: US 6355451-A 17 12-MAR-2002; FEATURES 14697	/organism="unknown" /mol_type="unassigned DNA" ORIGIN	1.79e-124 Length: 2702.00 Matches:	ty: 100.00% arity: 100.00%	100.00% Indels: 6 Gaps:	-10-023-523-8 (1-530) x AR199536 (1-4697) 1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln	3 AAAAGCAGCCCAGGACAAGCAGGACCCGAGGAGGCCCAGGAGCCGAGGCGACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCAG	63 GCGGCTCCTGCAGTAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGGCGGGG 41 GlyalaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 1	61 ArgGinLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly	OD 183 CGCCAACIGGAAGACATACIGAGCACATACIGIGGACAATAACCAAGGGGGCCCCCGGC 242 Qy 81 GluAspGlyAlaGluGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100 Dh 243 GaCGARGCGCAACAAGAGCCCGCARGAACAAGAAGAAGAACACACAAGAAAAAAAA	101 ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer	121 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 14	363 AGGGGGGGTCCAAACACAGAAGAGGTCCGGCAGAGTGACGAGGTCGGGAGGCCGAGACCAT 42 141 ArgargproglnGlulysLysLysBlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 16	423 CGAAGGCCACAGAGAAAAAAAGCCAAGGGTTTGGGGAAGGAGATCACGTTGCTGATG 161 GlnThrLeuasnThrLeusserThrProGluGluiysLeualaalaLeucysLystyr [DD 483 CAGACATTGAATACTCTGAGTACCCCAGAGGAGAAGCTGGCTG

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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their
diagnosing and treating atherosclerosis
Patent: US 6605588-A 17 12-AUG-2003;
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261 PheGlnValThrLeuAsnAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer	GAGCTGCGCGAGGAGCATATCGACAAGTCTTCAAACACAAGGACCTACAACAGCTG ValaspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln	1013 CGGGAGAGGGATTITCICCTGAAGAGGCAGIAGAGTCCCAGAGGATGIGIGAGGCIGAIG 361 LysGlnGlnGluThrHisLeuLysGlnGlnClneuAlaLeuTyrThrGluLysPheGluGlu 1083 AAGCAGCAAGAGACCCACCTGAAGCAACGAGCTTGCCCTATACACAGAGAAGTTTGAGGAG	Oy 381 PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 400	Db	441 LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr 	461 GluArgAsnAspleuAsniysArgValGlnAspleuSerAlaGlyGlyGlyGlrieu 	481 InrappserdiyProGluargArgFroGluGlyFroGlyAlaGlnAlaFroSerSeFro 50 1443 ACTGACAGTGGCCTCAGAGAGGCCAGAGGGCCTCGGGCTCAAGCACCCCAGCTCCCC 15	501 ArgvalintGlualarrocystyrFroGlyA	Oy 521 GLYPROGLINGLUPFOINTSERALAARGALA 530 	RESULT 4 AXX339574 LOCUS DETINITION Sequence 17 from Patent WO0164874.	ACCESSION AX239574 VERSION AX239574.1 GI:15797259 KEYWORDS GORDE Home sapiens (human)		AUTHORS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A. TITLE Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis JOURNAL Patent: WO 0164874.A 17 07-SEP-2001; Boston Heart Foundation, Inc. (US)
REFERENCE 1 (bases 1 to 4697) AUTHORS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A. TITLE Low density lipoprotein binding proteins and their use in JOURNAL Batent: US 652923-A 17 14-0CT-2003; FEATURES Location/Qualifiers Source //organism="unknown" //mol_type="genomic DNA"	Alignment Scores: 1.79e-124 Length: 4697 Score: 2702.00 Matches: 530 Forcent Similarity: 100.00\$ Conservative: 0 Dest Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	US-10-023-523-8 (1-530) x AR409323 (1-4697) Qy	21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 	41 GlyAladinAlaArgThrAladinSerGlyAlatenArgAspValSerGluGlubeuSer 123 GGGGCTCAAGCCAGACGGCTCAGTCTGGGGCCCTTCGTGATCTCTGAGGAGCTGAGG 61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAshAsnGlnGlyGlyProGly	DD 183 CGCCAACIGGAAGACAIACIGAGCACAIACIGIGGGACAAIAACCAGGGGGGCCCCCGGC 242 Qy 81 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100 DD 243 GAGGATGGGGCACAGGGTGAACCCGAAGATGCAGAGAAGATCCCGGACCTAT 302	Oy 101 ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer 120	Oy 121 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 	Oy 141 ArgargProGlnGluLysLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 160	Oy 161 GINThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLyr 180	Oy 181 AlaGluLeuLeuGluGluHisArgÀsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 200	Qy 201 GlnSerGlnLeuvalGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 221 AlaargSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 240	241 GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis

Oy 201 GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220 Db 603 CAGAGCCAGCTGCAAGAAGACCACCTGCGCGGTGAGCACAGCAAGGCCGTCCTG 662 Qy 221 AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 240 Db 663 GCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCGCACACCGCTCCTCTCAGG 722 Qy 241 GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis 260 Db 723 GAAGAAGGTTGCAGCGCCCCGGGAGCAGCCCAACCGCTCCTCAAG 722 Qy 261 PheGlnValThrLeuAspAlaArgGluGluGluGluGluLysArgLysGluValThrSerHis 260 Db 783 TTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGACCACATGAGCGCAACTCC 842 Qy 281 LysLeuArgGluGluMasmMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 300 By AAGCTGCCCCAAGAACTTCAGCTGAACGACACACACAATGACCAATTCAGCAATTGACACACAC	321 ValAsphlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln 3	Oy 361 LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380 1083 AAGCAGCAAGAACCACCTGAAGCAACCATGCCCTATACACAGAAAGTTGAGGAG Oy 381 PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 400 1143 TTCCAGAACACACTTTCCAAAAGCAGGAGGTATTCACCACATTCAAGCAGGAGATGGAA 1202	Oy 401 LysMetThrLysLysIeLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp 420 Db 1203 AAGATGACTAAGAAGATCAAGAGAGAAAGAAACCACCATGTCCGGTCCGGTGG 1262 Oy 421 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu 440 Db 1263 GAGGAGCAGCAAGGCCTGCTTGAGTGGTGTLTTTTTTTTTT	SAAGC SAGTG SAGTG SG1yA	Oy 501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520
FEATURES Location/Qualifiers 14697 /mol type="unassigned DNA" /mol type="unassigned DNA" /db xref="taxon:9606" /a1595 /a. taxt=1 /protein product" /codon start=1 /protein id="CAC88297.1" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:115797250" /db xref="gl:1157972700" /db xref="gl:1157972700" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:115797270" /db xref="gl:11579770" /db xref="gl:11579770" /db xref="gl:11579770" /db xref="gl:11579770" /db xref="gl:11579770" /db xref="gl:1157970" db xref="gl:115790" /db xref="gl:115790" /db xref="gl:115790" /db xref="gl:115790" /db xref="gl:115790" /db xref="gl:115790"	9	0-0 0-4	GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAsyvalSerGluGluLeuSer GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAsyvalSerGluGluLeuSer GGGGCTCAAGCCAGAACGCTCGGGGCCTTCGTGATGTTCTCTGAGAGTGAGA ArgGlnLeuGluAsp11eLeuSerThrTyrCysValaspAsnAsnGlnGlyGlyProGly GGCCAACTGGAAGACATACTGAGAGCACATACTGTGAGACAATAACCAGGGGGGGCCCCGGC	GluaspolyAlaGlnGlyGluProAlaGluProGluaspAlaGluLysseraghrryy 10 GAGGATGGGCACAGGCTGACCGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTAT 30 GAGGATGGGGCACAGGCTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTAT 30 ValAlaArgAsnGlyGluProGluProThrProValVaTtyrGlyGluLysGluProSer 12	141 Argaegeartccaacacacacacacacacacacacacacacacacac

161 GINTHILEUASNTHILEUSETTHIPFOGIUGIULYSLEUAJAAIALEUCYSIY 183 CAGACATTGAATACTCTGAGTACCCAGAGGAGAAGTGGCTGCTCTGTGCAA 181 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuGl 181 AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuGl 181 AlaGluCHill	CAGAGCCAGCTGGAAGAAGGACCACCTGCGGGGGTGAGCACACGCAAGGCGGTCCTG ALAATGSELVSLEUGIUSErLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys	Qy 241 GludluGlyValGinArgAlaArgGluGluGluLySArgLySGluValThrSerHis 260 Db 723 GAAGAAGTGTGCAGCGGCCCGGGAGGAGGAGGAGGAGGAGGTGACCTCGCAC 782 Qy 261 PheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280 280 Db 783 TTCCAGGTGACACTGAATGACATTCAGCTGCAGATGAGACACATCC 842 280	Oy 281 LysleuargGlnGluAsnMetGluLeualaGluArgLeuLysLysLeuIleGluGlnTyr 300	321 Valaspalarysteudinglandiadlumetreurysglualaglugluarghisgln 3 321 Valaspalarysteudinglualagluglumetreurysglualaglugluarghisgln 3 341 ArgGlulysaspPheLeurysglualayalgluserGlnArgmetCysGluLeumet 3 341 ArgGlulysaspPheLeurysglualayalgluserGlnArgmetCysGluLeumet 3 1023 cGsGaAGAAGTTTTCTCCTGAAAGAGGCAGTAGAGCAGAGGATGTGTGAGCTGATG 1	361	1143 TTCCAGAACACACTTTCCAAAAGCAGGGAGGTATTCACCACATTCAAGCAGAGAAGGAAAGCAGAAAGCAGAAAACCACCATTCAAGCAGGAGATGGAA 401 LysMetThrLysLysllelysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp 1203 AAGATGACTAAGAAGCAGAGAAAACCACCATGTACCGGTGGGGAGAGGAGGAAAACCACCATGTACCCGGTGGGGGGGG	Oy 421 GluSerSerAsnLysalaLeuLeuGluMetalaGluGluLysThrValArgAspLysGlu 440 1263 GAGAGCAGCAACAAGGCCTTGGTTGAGATGGCTGAGGAGAAAACGTCCGGGATAAAGAA 1322 Oy 441 LeuGluGlyLeuGlnVallysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr 460 Db 1323 CTGGAGGGCTGCGGTAAAAAATCCAACGGCTGGAGAAGCTGTGCGGGCACTGCAGACA 1382	Qy 461 GluargasnaspLeuAsnlysargValGlnaspLeuSerAlaGlyGlyGlrglnGlySerLeu 480 Db 1383 GAGGCAATGACCTGAAGGTACAGGACCTGAGTGCTGGTGCTGCTGCTGCTCCTC 1442 Qy 481 ThrAspSerGlyProGluArgArgProGluArgArgProGluArgarglyProGlyAlaGlnAlaProSerSerPro 500 Db 1443 ACTGACAGTGGCCCTGAGAGGCCTGAGGCCTCAAGCACCCAGCTCCCC 1502	Oy 501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr 520
ACCESSION BD056450 VERSION BD056450.1 GI:22602056 KENWORDS JP 20015066983-A/8. SOURCE Aequorea victoria ORGANISM Aequorea victoria CRGANISM Aequorea victoria REFERENCE Aequorea. Aequorea in the second and are also and a	AUTHORS Lees, A.B., Lees, A.B., Lew, B.W. and Allond, A.A. TITLE Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis JOURNAL Patent: JP 2001506983-A 8 29-MAY-2001; COMMENT PN JP 2001506983-A 8 29-MAY-2001; PD 29-MAY-2001 PD 29-MAY-2001	PF 26-NOV-1991 US 199854810 PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC AGIK38/04, AGIK38/17, AGIK39/00, AGIK48/00, AGIK49/00, AGIK51/08, PC CO7H21/00, PC CO7K7/00, CO7K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC Strandedness: Single; CC Topology: Linear;	FEATURES Location/Qualifiers. FEATURES 14697 Source 17697 /organism="Aequorea victoria" /mol_type="genomic DNA" /db_xref="taxon:6100"	Scores: 1.79e-124 2702.00 2702.00 milarity: 100.00\$ Similarity: 100.00\$ h: 6	US-10-023-523-8 (1-530) x BD056450 (1-4697) QY	Oy 21 AlahlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 40	61 ArgGinLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 8 [11] [11] [11] [11] [11] [11] [11] [1		Db 363 AAGGGGGATCCAAACACAGAAGACTCCGGCAGAGTCGGAGACCGT 422 Qy 141 ArgArgProdinGluLysLysAlaLysGlyLeuGlyLysGluIleThrLeuleuWet 160

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AlaGluLeuLeuGluGluHisargasmSerGlnLysGlnMetLysLeuLeuGlnLysLys 200 	<u>អេជី</u> គិធ	RESULT 7 AX239603 LOCUS DEFINITION	AX239603 1638 bp DNA linear PAT 26-SEP-2001 Sequence 46 from Patent WO0164874.

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GAQAPSSSPRVTEAPCYPGAPSTEASGGTGPQEPTSARA"
                                                                                                 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis

Patent: WO 0164874-A 46 07-SEP-2001;

Boston Heart Foundation, Inc. (US)
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Catarrhini, Hominidae, Homo.
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321 ValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGln 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     667 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAG
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                                                                                                                                                                                                                                                           ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
                                                                                                                                                                                                                                                                                                          307 CGCCAACTGGAAGACATACTGAGCACATACTGTGGACAATAACCAGGGGGGCCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607 CAGACATIGAATACTCTGAGTACCCCAGAGGAGAGAGGTGGCTGCTGTGCAAGAAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1207 AAGCAGCAAGAACCCACCTGAAGCAACAACTTGCCCTATACACAGAGAAGTTTGAGGAG
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                                       GCGGCTCCTGCAGTAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAG
                                                                                                                                                                                247 GGGGCTCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 gadgardogccacaggrgagccgcrgaacccgaagargcagagagrcccggaccrar
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                                                                                                             41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer
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Shataki.H., Nogami,S. and Satoh,S.
Shirataki.H., Nogami,S. and Satoh,S.
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1 (bases 1 to 1993)

Nogami, S., Satch, S., Nakano, M., Shimizu, H., Fukushima, H., Maruyama, A., Terano, A. and Shirataki, H., Fukushima, H., Taxilin; a novel syntaxin-binding protein that is involved in Cat-dependent exceytosis in neuroendocrine cells Genes Cells 8 (1), 17-28 (2003)
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Homo sapiens mRNA; cDNA DKFZp45110918 (from clone DKFZp45110918);
ALB32636
ALB32636.2 GI:30268324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Genome Project.

This clone (DKFZp45110918) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4880)
Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
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Submitted (17-UTN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
On Apr 30, 2003 this sequence version replaced gi:21733212.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. wiemann@dkfz-heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the CDNA sequencing consortium of the
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DH10B; sites Not1 + Sal1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 4851) [ Kochrer.K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
                                                     sapiens (human)
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GAGCTGCGCGAGGAGCATATCGACAAAGTCTTCAAACACAAAGGACCTACAACAACAGCTG
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Berlin-Charlottenburg, GERWANY, Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/pc/DNA/.
Location/Qualifiers
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FQVTLNDIQLQMEQHNERNSKLRQENMELAERLKKLIEQYELREBHIDKVFKHKDLQQ
QLVDAKLQQAQEMLKEAEERHQREKDFLLKEAVESQRMCELMKQQETHLKQQLALYTE
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Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. Wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Halnicol-Heine-University, Duesseldorf(Germany) within the CDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp451K215) is available at the RZPD in Berlin. Please contact
the RZPD: Account Centern Heubensyng (14059)
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/clone_lib="451 (synonym: hlcc1). Vector pSport1; host
DH10B; sites Not1 + Sal1"
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Conservative:
Mismatches:
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/db_xref="taxon:9611"
/clone="DKFZp451K215"
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C PRI 13-MAY-2003 DKFZp451K215);

HSW803646 4851 bp mRNA linear Homo sapiens mRNA; cDNA DKFZp451K215 (from clone I complete cds.

TTCCAGAACACATTCCAAAAGCAGCAGGTATTCACCACATTCAAGCAGGAATGGAA TTCCAGAACACACTTTCCAAAAGCAGGCAGGTATTCACCACATTCAAGCAGGAATGGAA LysMetThrlysLysLysLeugluLysGluThrThrMetTyrArgSerArgTrp [Hilli]	421 GluserSerAsnLysAlaLeuLeuGluMerAlaGluGluLysThrValArgAspLysGlu 440	1531	TGAAGCACCCAGCTCCCCC rGlualaSerGlyGlnThr AGAAGCATCAGGCCAGCT	Oy 521 GlyProGlnGluProThrSerAlaArgAla 530 	RESULT 11 HSM803947 HSM803947 HSM803947 HSM803947 S023 bp mRNA linear PRI 17-JUN-2003 DEFINITION HOMO Sapiens mRNA; cDNA DKFZp451J0118 (from clone DKFZp451J0118). DEFINITION AL832637 VRPSION AL8326372 GI:30268326	Homo sapiens (human) Homo sapiens (human) Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae (bases 1 to 5023)	AUTHORS Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H. W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. TITLE Direct Submission JOORNAL Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr. 1, D-85764	Neuherberg, GERMANY COMMENT On Apr 30, 2003 this sequence version replaced gi:21733213. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Cherry, Family Banall s wiemann@dkfr-heidelberg.de; Research Center (DREZ); Email s wiemann@dkfr-heidelberg.de;	Sequenced by Embh (Eutropean Morecural Protogy Laboration of the Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Profoct. This clone (DKFZp451J0118) is available at the RZPD in Berlin.	Please content the RZPD: Ressourcenzentrum, reuthierwy v, 1905, Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de Futther information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.	E	/db_xref="RZPD:DKFZp451dU118" /db_xref="Laxon:9606" /map="1p34.2-36.11" /clone="DKFZp451J0118"	/tissue type="human spinal cord" //clone_lib="451 (synonym: hlcc1). Vector pSport1; host DH10B; sites NotI + SalI" //dev_stage="adult" gene 15023
21 AlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGlu 40 211 GCGGCTCCTGCAGTAGAAGCTCCCGGCAGCAGGCTCCTCGGAAGCCGGAG 270 211 GCGGCTCCTGCAGTAGAAGCAGAAGCCCGGCAGCAGCTCCTCGGAAGCCGGAG 270 41 GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 60 21 GCGCTTCAGAGAACCAGACCTCTCAGAGACTGAGAGACTGAGAGAGA	### ### ##############################	ACCTAT 450 Proser 120 CCCTCC 510	LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140	TGATG 630 198TYR 180 690	AlaGlubeuLeuGludluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 200	GINSETGINEQUVALGINGLULYSASPHISHEUMAGGIYOLUHISSELLYSALLEG 220 [SerHis 260 CGCAC 930	AACTCC 990	SlnTyr CAGTAT	301 GluLeuargGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnLeu 320	Hisgln 340 CACCAG 1170	341 ArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMet 360 	361 LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380

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Db 870 GCTGAACTGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTACAGAAAAG 929 201 GInSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220 110 GInSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220 1110 111 11	281 LysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTryr 1170 AAGCTGCGCCAAGAAACATGGAGCTGGCTGAGAGCTCAAGAAGCTGATTGAGCAGTAT 301 GluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGluCeu 1230 GAGCTGCGGCGAGGAGCATTGGACAAGTTTTGAAAGAAGAACAAAGAGGGCTGAGTGCGGAGGAGGAGTATGGACAAAGTTTTGAAAGAAGAAGAAGAAGAGGGGGGGG	Db 1350 CGGGGAGAAGGATTTCTCCTGAAAGGGGAGAGGGGGGGGG	441 LeuGludyLeuGlnvallySileGlnvalLeuGsargaranachanachanachanachanachanachanachana	AR199533 4722 bp DNA linear PAT 20-APR-2002
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	320 LeuvalAspalaLysLeuGlnGlnAlaGluMetLeutysGluAlaGluCluArgHis	Oy 380 GluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet 399	1426 GAGCTGGAAGGCCTGCAGGTGAAATCCAGCGGC 460 ThrGluArgAsnAspLeuAsnLysArgValGlnA 1486 ACAGAGCGCAATGACCTGAACAAGGGGTGCAGG 480 LeuThrAspSerGlyProGluArgArgPro 1546 GTCTCCGACAGGGTCCTGAGCGAGGGCGAGG 1546 GTCTCCGACAGGGTCCTGAGCGAGGCCAGGG 490GluGlyProGlyAlaGlnAlaProSerSerP	Db 1606 GTCGAGGCCCCAAGTACCCAACTCCCAAGGCCCACAGGCTTCCTGCTGC 1665 Qy 509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla 528 Db 1666 GCAGGTGCACCCAGGAGGCATCAGGCCAGAGGCCCCAGGAGCCCACCACTGCC 1725 Qy 529 Argala 530 Db 1726 ACTGCC 1731	RESULT 13 AR374685 AR374685 4722 bp DNA linear PAT 18-DEC-2003 LOCUS DEFINITION Sequence 14 from patent US 6605588. ACCESSION AR374685 GI:40077500
DEFINITION Sequence 14 from patent US 6355451. ACCESSION AR199533 GI:20249607 KEYWORDS SOURCE ORGANISM Unknown. ORGANISM Unknown. AUTHORS Lees, A.M. Lees, R.S., Law, S.W. and Arjona, A.A. AUTHORS Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis JOURNAL Decation/Qualifiers SOURCE //ORGANISM="unknown" // ACTOR // ACTOR // ACTOR // Mol_type="unassigned DNA"	ignment ed. No.: ore: rcent Si st Local ery Matc	SProGlu SCCGGAG ULEUSER ULEUSER GCTGAGC YProGlY CCCGGGT	JThrTyr 10 GCCTAT 40 sGlubro 11 GAGACC 46	4. C. C. C. C. C. C. C. C. C. C. C. C. C.	salaval ::: GGCCATC gSerLeu

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Unclassified.

1 (bases 1 to 4722)

Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.

Low density lipoprotein binding proteins and the:

diagnosing and treating atherosclerosis

diagnosing and treating atherosclerosis

Location/Qualifiers

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Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Location/Qualifiers
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density liprotein binding proteins and their
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                                                                                                                                               BD056447 Innear PAT 27-AUG-2002 Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis,
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                                                                                                                                                                                                                                                            BD056447.1 GI:22602053
JP 2001506983-A/5.
Aequorea victoria
Aequorea victoria
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
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Matches:
Conservative:
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Indels:
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Organism="Aequorea victoria"
|mol_type="genomic DNA"
|db_xref="taxon:6100"
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Best Local Similarity:
529 ArgAla
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DB:
                                                                                                     RESULT 16
BD056447
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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g ò 셤 ò 엄 RESULT 17

g ò

BC060227

REFERENCE AUTHORS

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KFEEFQNTLSKSSEVFTTFKQEMERNTKKIKKLEKETTMYRSRWESSNKALLENAEEK
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KEQGVESPGAQPASSPRATDAPCCSGAPSTGTAGQTGPGEPTPATA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ArgGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80
        through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
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10
10
36
16
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                   organism="Mus musculus"
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                                              Location/Qualifiers
1. .4702
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2382.00
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Best Local Similarity:
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2 (A)
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Zeeberg, B., Butchow, K.H., Scheefer, C.K., Schuler, G.D., Altschul, S.F., Jordan, H., Mooret, T. Marchan, C.M., Hopkins, R.F., Jordan, H., Mooret, Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Hulyk, S.W., Villalon, D.K., Mullahy, S.J., Gunzarne, P.H., Richards, S., Sanchez, A., Whiting, M., Sodergren, R.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Koung, A., Shevchenko, Y., Butcerfield, Y.S., Kzzywinski, M., Salska, U., Shevchenko, Y., Butcerfield, Y.S., Kzzywinski, M.I., Salska, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length human and manned manned more and mercential analysis of more than 15,000 full-length
                            1606 GTCGAGGGCCCGGGGGCTCAAGTACCCAACTCTCCAAGGCCACAGACGCTTCCTGCTGC 1665
                                                                                                                                                                                                                                                1666 GCAGGTGCACCCAGCACAGAGGCATCAGGCCAGACAGGGCCCCAGGAGCCCACAGGAGCCCAGGACATGCC 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC060227
Mus musculus cDNA clone MGC:77972 IMAGE:30357541, complete cds.
BC060227
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                                                                                                        ---GluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
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Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,Y., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-OCT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                             509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla
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broc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
LeuThrAspSerGlyProGluArgArgPro-
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Mus musculus
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TITLE
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PUBMED REFERENCE

JOURNAL

TITLE

REMARK COMMENT

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		TyralaGluLeuLeuGluGluHisargasnSerGlnLysGlnMetLysLeuLeuGlnLys	 1876 ACTGCC
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		LeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgKisAsnArgSerLeu	AX578043.1 AX578043.1 Homo sapiens
HisPheGinValThirleuAnAsplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinLeuGlindisAnSplieGinChandachartrachachachartrachachartrachachachartrachachachartrachachachartrachachachartrachachachartrachachachartrachachachartrachachachachartrachachachachartrachachachachartrachachachachartrachachachachartrachachachachartrachachachachachachachachartrachachachachachachachachachachachachacha		LysGluGluGlyGlyGluBhArgAlaArgGluGluGluGluLysArgLysGluValThrSer 	Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;
Seritysfeukrgdingluksmketgluteuklagiteulystysteullegludin 199		HisPheGlnValThrLeuasnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgasn 	
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CTAGGORDACCOARCTCOARCCCACACACTCOARCCCACACTCCACCACACTCCACCACCACCTCCACCACCAC		TyrgluLeuArggluGluHisTleAspLysValPheLysHisLysAspLeuGlnGlnGlnGll. 	/mol_type="unas /db_xref="taxon /note="Homo sap
Collaboration Collaboratio		LeuValAsphlaLysteuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHis 	Scores: 7.39e-77 1727.00
		GINArgGlubysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeu 	τy:
		MetlysginginginththisleulysginginleualaleutyrthrgiulysPhegiu 	-10-023-523-8 (1-530) x AX578043 (1
		GluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet	1791 AATTCACAGAAGCAGATGAAGCTCCTACA
TrgGluserSerSerAsmicantana Control of the control		GAGIICCAGAACACACIIICCAAAAAGCAGIGAICAICCACGIICAAAACAGGAGGIG GluLysMetThrLysLysIleLysLysLeuGluLysGluThrThrMetTyrArgSerArg 	209 Asphistenzeguyotunisseriy 1731 GACCTGCGCGGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
		O TrpGluSerSerAsnLysalaLeuLeuGluMeralaGluGluLysThrValArgAspLys 4	229 CYSATGOTHURGUSITATGATSASTAT
Comparison		5 TGGGAAAGCACAACAAGGGTCTGCTGGAGATGGCTGAAGAGAAACCGTCCGGGACAAA 0 GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln	249 GluGluGluGluLysargLy
This class pleads and year year of the control of		AAGCTGGAGGCCTGCAGGTGAAATCCAGCGGCTGGAGGAGCTGTGCCGAGCACTGCAG	269
		ThrGluargasnaspleuasniysargvalGlnaspleuSeralaGlyGlyGlnGlySer 	1551
GluGlyProGlyAlaGlnAlaFroSerSerProArgValThrGluAlaProCysTyr 508		LeuthraspserglyProgluargargPro	1491 CTGGCTGAGAGGCTCAA 309 LysValPheLysHisLy
ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla 528		GluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr	1431
		ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla	1371

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GCCAGACAGGGCCTGGAGAGCCCACCCCTGCC 1875
                                                                                            linear PAT 08-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHisGlnArgGluLysAspPheLeuLeulys 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rSerHisPheGlnValThrLeuAsnAsp11e 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uGlnTyrGluLeuArgGluGluHisIleAsp 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nGlnLeuValAspAlaLysLeuGlnGlnAla 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nLysLysGlnSerGlnLeuValGlnGluLys 208
                                                                                                                                                                          Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        con, R., Call, K., Theilhaber, J., lell, S. E. and Rawadi, G., and methods of use ct. 2002;
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/cell_line="Namalva" /tissue_type="Burkitt lymphoma"	Alignment Scores: 6.18e-75 Length: 1793 Pred. No.: 6.18e-75 Length: 339 Score: 1688.00 Matches: 3 Percent Similarity: 99.12% Mismatches: 3 Query Match: 9.12% Indels: 1 DB: Gaps: 0	US-10-023-523-8 (1-530) x HUMENWBCGF (1-1793)	1791 ATTCACAGAAGCAGATGAAGCTCCTACAGAAAAGCAGAGCCAGCTGGTGCAAGAAAGCAGCAGCAGCTGGTGCAAGAAAGCAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	Db 1731 GACCACCTGCGCGCGCAGCACCC-GTCCTGGCCGCAGCAGCTTGAGGCTTA 1673 Oy 229 CysargGluLeuGlnArgHisAsnArgSerLeuLygGluGluClyValGlnArgAlaArg 248	Db 1672 TGCCGTGAGCTGCACGGCACACTCCCTCAAGGAAGAAGAGGCGCAGGGGCCCGG 1613 Oy 249 GluGluGluLyaArgLyaGluValThrSerHisPheGlnValThrLeuAsnAspIle 268	Db 1612 dAGGAGGAGAAGCGCAAGGAGGTGACCTCCCACGTGACACTGAATGACATT 1553 Qy 269 GInLeuGlnMetGluclnHisAsnGluArgAsnSerLysLeuArgGluGluAsnMetGlu 288	Db 1552 CAGCTGCAGATGGACACACACACACACTCCAAGCTGCGCCAAGAGAACATGGAG 1493 Qy 289 LeuAlaGluhrgLeulysLysLeulleGluGluHrgGluLeuArgGluGluHis1leAsp 308	rarcgac	Db 1432 AAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGGCGC 1373 Qy 329 GlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLys 348 Db 1372 CAGGACATAAAGGAGCAAAAAGAGCAGCAGCAGCAGGAGAAAGGATTTCTCCTGAAA 1313	349	369	Qy 389 SerGluvalPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIJeLysLys 408	409	Oy 429 GluMetalaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIle 448	Qy 449 GlnargleuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArg 468	469	n 0
Qy 349 GlualavalGluserGlnargMetCysGluLeuMetLysGlnGlnGluTbxHisLeuLys 368 	Qy 369 GlnGlnLeualaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSer 388 Db 1251 CAACAGCTTGCCCTATACACAGAGAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGC 1192 Qy 389 SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysLyslleLysLys 408 Db 1191 AGCGAGGTATTCACCACATTCAAGGAGATGGAAAAGATGACAAAGAAGATCAAGAAAG 1132	Qy 409 LeuGlulysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeu 428	429 GlumeralagluglulysThrValArgAspLysGluLeugluglyLeugluValLysIlle 4	Oy 449 GlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArg 468	Qy 469 ValGlnAspLeuSerAlaGlyGlyGlyGsrLeuThrAspSerGlyProGluArgArg 488	Qy 489 ProGludlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaProCysTyr 508	Oy 509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla 528	Qy 529 Argala 530 Db 771 AGGGCC 766	RESULT 19 HUMHWWGCGF/c LOCUS HUMHWWBCGF 1793 bp mRNA linear PRI 25-MAY-1995 DEPINITION HUMAN high molecular weight B cell growth factor mRNA sequence. ACCESSION L15344	VERSION L15344.1 GI:832913 KEYWORDS B-cell growth factor; interleukin 14. SOURCE Homo sapiens (human) ORGANISM Homo sapiens	Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1793) AUTHORS Ambrus, J.L. Jr., Pippin, J., Joseph, A., Xu, C., Blumenthal, D.,	Tamayo,A., Claypool,K., McCourt,D., Srikiatchatochorn,A. and Ford,R.J. TITLE Identifiation of a CDNA for a human high-molecular-weight B-cell growth factor	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (13), 6330-6334 (1993) MEDLINE 93317675 FURMED 8327514 REFERENCE 2 (bases 1 to 1793)	AUTHORS Ambrus, J.L.Jr. TITLE Direct Submission JOURNAL Submitted (JOB-MAY-1993) Julian L. Ambrus, Jr., Department of JOURNAL Medicine, Washington University School of Medicine, St. Louis, MO	63110, USA COMMENT On May 25, 1995 this sequence version replaced gi:347805. Original source text: Homo sapiens cDNA to mRNA. Iocation/Oulifiers	rce	

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Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wayman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
Submitted (08-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Gambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                                                                                         .----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The cord of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: 239_013
Sequencing vector: Plasmid; nd; 100% of reads
Sequencing vector: Plasmid; nd; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 180713 bases at least Q30
Consensus quality: 1808040 bases at least Q30
Consensus quality: 181059 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 181147; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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1 76950: gap of 100 bp
1 181547: contig of 104597 bp in length.
Location/Qualifiers
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15698: gap of 100 bp
17443: contig of 1745 bp in length
17543: app of 100 bp
39808: contig of 22265 bp in length
39908: gap of 100 bp
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'note="assembly_fragment"
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/organism="Mus musculus'
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vector_side:right"
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Mus musculus clone RP23-239013, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                              509 ProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGluProThrSerAla 528
                                                                                                  892 CCAGAGGGGCCTGGGGCTCAAGCACCCAGCTCCCCCAGGGTCACAGAAGCGCCTTGCTAC 833
                                                                                                                                                                                                                832 ccadeadecacceaecacacacacatcadeccadactregecercaagacecaccreeded 773
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-239013 Unpublished
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                               529 ArgAla 530
                                                                                                                                                                                                                                                                                                                                        772 AGGGCC 767
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111689	. 111	Y 144 146 b 111809 GATAAGTGGATATTAGCCCAAAACCTAGGATACCCAAGATATAAGATACAATTTGCTAAA 111868	Y 144 144 b 111869 CACATGAAACTCAAGAAAATGAAGACTGAAGTGTGGACACTATGCCCCTCCTTAGAAGT 111928	Y 144 144 b 111929 GGGAACAAAACCCCTTGGAATGAGTTACAGAGACAAAGTTTGGAGCTGAGATGAAAGGA 111988	y 144 144 b 111989 TGGTCCATGTAGAGACTTCCATATCCAGGATCCACCCATAATCAGCATCCAAACGCTG 112048	Y 144 144 b 112049 ACCCCATTCATACACTAGCAAGTTTTATTGAAAGGACCCAGATGTAGCTGTCTCTTGT 112108	y 144 144 b 112109 GAGACTATGCCGGGGCCTAGCAAACACAGAAGTGGATGCTCACAGTCAGCTAATGGATGG	Y 144 144 b illi69 atcacaggcccccaatgaagaagtactaaaagtacccaaggagctaaagggatctgca 112228	y 144 144 b 112229 ACCCTATAGGAACAACATTATGAACTAACCAGTACCCGGAGCTCTTGACTCTAGCT 112288	Y 144 144 b 112289 GCATATGTATCAAAAGATGGCCTAGTCGGCCATCACTGGAAAGAGAGAG	Y 144 144 1 12349 GCAAACTTTATATGCCCCAGTACAGGGGAACGCCAGGGCCAAAAAGGGGGAGTGGGTGG	144	o 112409 TAGGGGGATTGGGGGTAGGGGAACTTTTGGTATAGCATTGGAAATGTAAATG 112468	112469 AGCTAAATCCCTAATAAAAAAAAAAAAAAAAAAATGTAAATGTAAATGTAAATTCTAA 112528	112529 TAAAAAATTTAGAAAATACCCCTAAAAAAAAAAAATAGAATCTTACAGAAAAAAAA	/ 145GluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLe 158	158 uleuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLy	112649 GCTGATACAGACACTGAACACGCTGAGTACCCCAGAGGAGGAAGCTGGCTG	178 SILYSTYALAGLULeulevüldülülisArgAsnSerölnLysölnMetLysileuleuöl 198 	198
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		luArgProSerGln 20 :: AAAGACCCAGACAG 110801		uSer 	3lyGlyProgl	hr 17	luPr 	rgAs	E			ATGCAAATCAAAA 111328 144	AATTCAGGTGACA 111388	IGCA	144 TTGGACACAGTAC 111508		GTCCCAACCGGTA 111568	GCCAGAAGCTGGA 111628	! !	TACALCIACACAA 111688 144
Conservative: 35 Mismatches: 89 Indels: 505 Gaps: 6	-181547)	Lysserserproglyginproglualaglyprogluglyalagingluargprosergin 		요_요	ArgGlnLeuGluAspileLeuSer-ThrTyrCysValAspAsnAsnGln 	YGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgT :::	rValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysG 	erlysglyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAs GTAAGSGGACGCTGTTACAGAGAATCCGAACAAATGCAAAAAAAAA	PHISAEGARGPEOGIN	The state of the s	10000000000000000000000000000000000000	CAGAGAAGCACCTGAAAAAATGTTCAACATCCTTAATCATCAGGGAAATGCAAATC	CAACCCTGAGATTCCACCTCACCAGGTCAGAATGGCTAAGATCAAAAATTCAGGTGACA	GCAGATGCTGGCGTGGATGTGGAGAAAGAGGAACACTCCTCCATTGTTGGTGGGAT	GGCTTGTACAACCACTCTGGAAATCAGTCTGGTGGTTCCTCCAGAAAATTGGACACAGTAC		TACTIGGAGGATICCCGCAATACCTCTCCTGGGGATATATATCCAGAGATGTCCCAACCC	AGAAGGACACATGCTCCACTATGTTCATAGCAGCCTTATTATAATAGCCAGAAGCTGGA		ANT GGALACAGAAAATG1GG
. 39.59% 53.74%	x AC108815 (1-	SSerSerProglyGlnProgluAla ::: 	AlaAlaProAlaValGluAlaGluGly ACAGCTCCTGGGGGGAAGCTGAAGGT	yAlaGlnAlaArgThrAlaGlnSerGly ::: ::: GCTCGAGCTAAAGCGCGTAGACTGGG	euGluAspileLeuSer-Th TGGAAGACATTCTGAGTAAA	YGluAspGlyAlaGlnGlyGluProAl	aArgAsnGlyGluProGluPr CAGGAATGGAAGCCTGAATC	GlyAspProAsnThrGluGl:	ArgProGlnAGGCAACAAGAA			SCACCTGAAAAATGTTCAA	AGATTCCACCTCACACCAG	TGGCGTGGATGTGGAGAAA	CAACCACTCTGGAAATCAG		GATCCCGCAATACCTCTCC	ACATGCTCCACTATGTTCA		
Percent Similarity: Best Local Similarity: Query Match: DB:	10-023-523-8 (1-530)	1 Lysserse :: 110742 AAGAGCAA	21 AlaAlaPr 110802 ACAGCTCC	66	61 ArgGlnLe 110919 CGGCAGTT	80	100 rValAlaA 	119 oS 11089 CT	# <u>7</u> 0	144	14 6	111269 CAGAGAAG	111329 CAACCCTG		144 111449 GGCTTGTAC	144	111509 TACTGGAGG	111569 AGAAGGACA	144	
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AARGRGGGAEEATEAGRGGRRRSPRQKFEIGTMEEAG
HGGSNCGGTSNKAEJEEDBGSDFTTENRLUSPAYCT
PDS ECNNRKSKYLGKEVULIMQALMTLSTPEEKLAALC
KKOQOIVKEKYHLGSEHSKAILARSKLESLCRELQRH
SATAHPOITLDEIQADIHNAKLRQENIELGEKL
ELQQQLVDAKLQGTYQLIKEADEKHGRENFLIKEAT
SLYMDKFEEPGTTMAKSNELFTTFRQEMEKMTKKIKKL
TAREKTYRDKEYKALQIKLERLEKLCRALQTBENEINB
NLATPVMQPCTALDSHKELNTSSKRALGAHLGAEPKSQ
                                                   . Hayashi,K., Saito,K., Yamamoto,J.,
J.A., Nagai,K. and Otsuki,T.
sngth cDNA and their use
10010gy (JP)
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ICAGAGTGCAACAGGAAGAAGAAAACT 453
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aniata; Vertebrata; Euteleostomi;
Itarrhini; Hominidae; Homo.
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2045 bp DNA linear PAT 17-JAN-2003 full-length cDNA and use thereof.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 202191363-A 11877 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMAISU,
KEIICHI NAGAI, TETSUJI OTSUKI
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PN JP 2002191363-A/11877
PP 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SATTO,
PI SATTO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATK PI KEIICHI NAGAI, TETSUJI OTSUKI
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC CLINI/19, C12N1/21, C12N5/
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T CDS [52] ([635])
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Primer for synthesizing
BD157034
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JP 2002191363-A/11877.
                                                                                          CAAAAGCCCCCGTCCA 1603
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                                                                 GluGlulysbeuAlaAlabeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsn 189
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                                                                                                                               SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAsp 209
                                                                                                                                                        HisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys 229
                                                                                                                                                                                                                       ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu 249
                                                                                                                                                                                                                                                                                        GluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGln 269
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                                                                                       270 LeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeu
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Db 1348 CGGTTAGAGAAGCTGTGCAGGGCTG Qy 470 Gln	SULT 23 SULT 23 CUS CUS FINITION CESSION RESION YWORDS URCE ORGANISM	BUKATYOCH; MECAZOA; Mammalia; Butheria; Isogai, T., Ota, T., H Nishikawa, T., Nagai, Wagatsuma, M., Takahas Sugawara, M., Takahas Ono, Y., Takahas Ono, Y., Takahas Ishii, S., Kawai, Y., Nakamura, Y., Nagahar Nisho human cDNA sequ	REFERENCE 2 (Dases 1 to 2045) AUTHORS Isogai, T. and Otsuki, T. TITLE Direct Submission JOURNAL Submitted (16-FEB-2000) Ta) Genomics Laboratory; 1532-2 COMMENT (E-mail:genomics@hri.co.jp. NEDO human cDNA sequencing International Trade and International Research Associscent Construction, 5- & 3-end Helix Research Institute (8	ecc.) and Dep University Of Loca Loca 1 Org /And /And /Ab /Ab /Ab /Ab /Ab	CDS 52163 pc / codon start=1 / codon start=1 / protein id="BAA92 / db_xref="GI-7023" / translation="MATTT
TTATAACAGAGAATTTGGTCAGC		ArgellueGinarghisasardagserleuuysGiluchusyvaltorargalargelu 249 Agagaacttcagcgrcacaataagaccttaaagaagaaaatargcagaccaccagag 747 Agagaacttcagcgrcacaataagaccgttaaagaagaagaaatargcagaccaccagag 747 GluGluGluLysargLysGluValThrSerHisPheGlnValThrLeuAsnaspIleGln 269 GluGluGluLysargLysGluValThrSerHisPheGlnValThrLeuAsnaspIleGln 269 GluGluGluGluSargLysGluValThrCaGartraccttagargaaftcaa 807 LeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeu 289	AlaGluArgleuLysLysLeuIleGluGlnTyrGluLeuArgGluGluHisIleAspLys 309 :::	AlaValGluSerGlnArgMetCysGluLeuWetLysGlnGluThrHisLeuLysGln 369	GAACTGTTACAACCTTCAGACAGAAATGAAAAGATGACAAAGAAAATTAAAAACTG 1227 GluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGlu 429
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) Takao Isogai, Helix Research Institute,
532-3 Yana, Kisarazu, Chiba 292-0812, Japan
o.jp, Tel:81-438-52-3975, Fax:814-388-52-3986)
cing project supported by Ministry off
d Industry of Japan; cDNA full insert
secriation for Biotechnology; cDNA library
end one pass sequencing and clone selection:
te (supported by Japan Key Technology Center
f Virology, Institute of Medical Science,
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PDGQDSECNRNKEKTLGKEVILLMQALNTLSTPEEKLAALC
WKILOKKQAQIYTKEKTHLGKEVILLMQALNTLSTPEEKLAALC
STEKKBATAHFOITLDEIQAQLEQHDIHNAKLRQENIELGEK
KYEKKELQQQIVDAKLQOTTQLIKBADBKACREBEFLIKEAT
KQQLSLYMDKFEEFQTTWAKSNELFTTFRQEMEKMTKKIKKL
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TCTTCAAACAGAATGAGCTCAATGAGAAGGTG 1407
                                                                                                          CATCAAAGCGGCCATCAAAGCGGCGAACAGGGATTTA 1467
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                                                        -----Aspleu 472
                                                                                                                                                                  uThr-----AspSerGlyProGluArgArgProGlu 490
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tes; Catarrhini; Hominidae; Homo.
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Sharatori,A., Sudo,H.,
Kaku,Y., Kodaira,H., Kondo,H.,
Chiba,Y., Ishida,S., Murakawa,K.,
Asnabe,S., Kimura,K., Murakawi,K.,
Asnabe,S., Yamamoto,J., Wakamatsu,A.,
Masuho,Y., Ninomiya,K. and Iwayanagi,T.
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4625 bp mRNA linear PRI 30-AUG-2003
Homo sapiens mRNA; cDNA DKFZp451B226 (from clone DKFZp451B226).
BX647633
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1408 GAAGTCCTGAAAGAGCAGGTATCCATCAAAGCGGCCATCAAAGCGGCGAACAGGGATTTÄ 1467
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                                                           Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemannsdAfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heinne-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
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GCGACAGBATCGAGGCACAAATACGAATGAAACAGCAGGAAGTACAACTAAAACAG
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Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A. Fobo, G., Han, M. and Wiemann, S.
The German Human cDNA Consortium
868 GGGGAGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAGCACATTGATAAG
                                                                                                    330 GluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 GAGGAGAAGCTGGCAGCTCTCTGTAAGAAATATGCTGATCTTCTGGAGGAGGAGGAGGAGT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAsp 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisleuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCys 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGlu 249
                                                                                                                                                                                                                                                                                               CAA-----GGCTCAAATTGTGGTGGCACAAGTAACAAGCATTCATTGGAAGAGGATGAA 303
                                                                                                                                                                                                                                                                                                                                SerSerGlnAlaProArgLys-----ProGluGlyAlaGlnAlaArgThrAlaGlnSer 49
                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
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                                                                                                                                                                                                                                                                                                                                                                                                                                   70 TyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 CGAACAGATCCCCTGATGGTCAGCAAGATTCAGAGTGCAACAGGAACAAAGAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TTAGGAAAAAGAAGTTTTATTACTGATGCAAGCCCTAAAACACCCTTTCAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 GluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 GCATACTGCACGCAAGAATCAAGAGGAAATCCCTGGGGGA------GAAGCT
                                                                                                                                                                                                                                                                                                                                                                130 CGGCGACGCAGCCCGCGCAGAAGTTTGAAATTGCCACAATGGAAGAAGCTGGAATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                    GlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThr
                                                                                                                                                                                                                                                                  GluGlyAlaGluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 GGCAGTGACTTTATAACAGAGAACAGGAATTTGGTGAGC----
                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                               Length:
Matches:
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1285.00
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                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                               Alignment Scores:
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2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		: 1.12e-53 Length: 1265.50 Matches: LY: 61.31% Conservative: arity: 46.39% Mismatches: 46.84% Indels: 9 Gaps:	18 ProSerGlnAlaAlaProAlaValGluAlaGlu	GluGiyalaGlnalaArgThr	ASDASHGINGIYGIYPTOGIYGIUASPGIYAIAGINGIYGIUPTOAIAGIUPTOGIUASP .::	TyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAsp	LysGluIleThrLeuleuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeu 17	Metlysleuleuglnlyslysglnserglnleuvalglnglulysasphisleuarggly :::

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JeuvalaspalaLysLeuGlnGlnAlaglnGluMetLeuLys 333
                                                                                                                                                                                                                                                                                                                                                                                                      TTGAGAACTGTAACAAGCTCTGTTGGACATGATTGAAGAG 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hrGluArgAsnAspLeuAsnLysArgValGlnAspLeuSer 473
||||||||||:::|||:::|||
AAGAGAGAAACGAACTCCACAAAAAATCAGAGAACGCAGAA 1479
iisPhedinValThrLeuAsnAspiledinLeuGinMetGlu 273
                                                                                                                                                             YrGluLeuArgGluGluHisIleAspLysValpheLysHis 313
                                                                                                                                                                                                                                                                                                                                             373
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                                                                                                         293
                                                                                                                       luLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLys 453
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                                                                                                                                                                                                                                                                                                                                            let LysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeu
                                                                                                         erlysteuArgGinGluAsnMetGluLeuAlaGluArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hrGlyProGlnGluProThrSerAla 528
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LOCUS

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

npublished

AUTHORS TITLE JOURNAL REFERENCE

AUTHORS

REFERENCE

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* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

28688 28787; gap of 100 bp
28788 30488; contig of 1701 bp in length
30489 30588; app of 100 bp
101010 110209; gap of 100 bp
Center clone name: 44 A 4

Center clone name: 44 A 4

Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 237099 bases at least Q40

Consensus quality: 237099 bases at least Q20

Consensus quality: 240394 bases at least Q20

Insert size: 210000; agarcse-fp

Insert size: 240848; sum-of-contigs
Quality coverage: 12.5 in Q20 bases; sum-of-contigs
Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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f 100 bp
g of 21687 bp in length
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gap of 100 bp
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gap of 100 bp
contig of 12158 bp in length
gap of 100 bp
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contig of 28855 bp in length
gap of 100 bp bp in length.
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of 4473 bp in length
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113807. .120823
'notes"arr
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142967. .147439
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147540. .161221
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-44A4"
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28788. .30488
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'note="assembly_
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E Birren, B., Nusbaun, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Bouthgalter, B., Cooke, P., Cooke, P., Cooke, P., Cooke, P., Cooke, P., Cooke, P., Cooke, P., FitzGerald, M., Gage, D., Galagan, J., Faros, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gord, S., Graham, L., Johnson, R., Hagos, B., Horton, L., Hulme, W., Ilev, T., Johnson, R., Jones, C., Kamat, A., Karasas, A., Kalls, C., Landers, T., Levinhe, R., Lindblad, Toh, K., Liu, G., MacLean, C., MacOnald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Mayer, T., Maylor, J., Nguyen, C., Nicoh, R., Mathews, C., Norman, C., Nor, M., C., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seanan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Scojanovic, M., Talamas, J., Lammer, A., Milson, B., Wille, M., Wilson, B., Wille, M., Milson, B., Wille, M., Wilson, B., Wil
        AC110537 24-AUG-2002
Mus musculus clone RP23-44A4, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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All repeats were identified using RepeatMasker:
Smtt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                              ACI10537
AC110537.5 GI:22475046
HTG, HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-44A4
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Db 87202 AGAGGAGAAGCTGCTGTAAGAAATATGCTGATCTCTGGAAGAAAGCAGGAA 87143	Db 87022 CAGGGAACTTCAGCGTCATAATAAGACCTTAAAGAAGAAGAACATGCAGCAGCAGCAGGAAGA 86963 Qy 249 uGluGluLySArgLySGluValThrSerHisPheGlnValThrLeuAsnaSpl1eG1 269	86842 GGGAGAAGTTGAAGACTTATTGAGCAGTATCCACTAAGGGAAGACATATAGATAA 309 sValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGl 86782 AGTATTCAACAAGAAATGCACAACAAGCTTGTGGATGCCAAACTTCAGCAACAACAACAACAACAACAACAAACA	349 GlualaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLys 86662 GAAGCAACAGATCCAGGCACAAATATGAACAATGAACAACGAAGAAGTACAACTAAAA 369 GlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSer	B6542	469 ValGlnAspLeuSeralaGlyGlnGlySerLeuThrAspSerGlyProGluhrgarg 488 489 ValGlnAspLeuSeralaGlyGlnGlySerLeuThrAspSerGlyProGluhrgarg 488 489 ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504 489 ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504 480 ProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504 486290 CCTGAAAGAAGAGCAGATCTCTATCAAAGCAGATGGGGACTTGGTGTCACCTGCAACGCA 862 505 AlaProCysTyrProGly 510 86230 GCCCTGTGCTGTCTGGA 86213 SULT 29 M807623 4647 bp mRNA linear PRI 30-AUG-200
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193 629 213 719 233 779

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1080 GAAGCGGAGGAGCGACAAACGAGAAAAGGAATATTTGCTGAACCAGGCAGCAGAGTGG 1139
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                                                                                                 CCCGTCAGCAATAAGGAGCAAAA-----TTGGAAAAGAAATCCTAAAAGGATTAGGC
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                                                                                                                                                                                                      174 AlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGln
                                                                                                                                                                                                                                                                  MetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspH1sLeuArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 LysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLys
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                                                                                                                                                                                                                                                                                                                                                                  Berlin-Charlottenburg, GERMANY; Email: clone@rrpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.
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                                                                                                                                                                                                                                 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZP451R216) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerveg 6, 14059
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                                                                                                   Chordata, Craniata, Vertebrata; Euteleostomi;
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460B. .4613
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BX647477
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                                                                                                                                   1 (bases 1 to 4647)
Koahrer K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.
Fobo, G., Han, M. and Wiemann, S.
The German Human cDNA Consortium
                                                                                                                                                                                                                      Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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Conservative:
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                                                                                                                      Mammalia; Eutheria;
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                                                                                      AlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg
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muscle-derived protein encoded by GenBank Accession Number
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/protein_id="AAL3399.1"
/db_xref="GI:L7026374"
/translation="MEINHPDQLSVEHPTPPGDSSSLNQNGPGKQDGERCSTSGQAPE
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Benson, K.F.
Benson, K.F.
Submitssion
Submitted (21-SEP-2001) Medical Genetics, University of Washington, 1705 Pacific Street NE, Seattle, WA 98195, USA
Location/Qualifiers
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LCRELQRHNKTLKEETLQRAREEBEKRKEITSHFQTTLTDIQTQIEQQSERNMKLCQE
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NTELAEKLKSIIDQYELREEHLDKIFKHRELQQKLVDAKLEEAQELMQEAEERHRREK
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Ttkkmkklekdtatwkarfencnkalldmibekalrakeyecfvmkiorlenlcralg
Berkelykkireakmsekedovortseefpepsusenbevdaeeansfokauenlata
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                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                         1 (bases 1 to 2435)
Benson, K. P. and Chada, K.
Molecular characterization of the mouse In(10)17Rk inversion a identification of a novel muscle-specific gene at the proximal
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chromosome="10"
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/sex="female"
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Mammalia; Eutheria; Rodentia;
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'dev_stage="adult"
. . . 2435
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/strain="C57BL/6J"
                                                                                                                               Mus musculus (house mouse)
                                                                                            AF422244.1 GI:17026373
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                                       GluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGln
                                                       GAGCACAACAGGGGCGTCCTTGCTCGAAGCAAACTCGAGAGTCTGTGTCGGGAGCTACAG
                                                                                                                                         GinHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeu
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  CTGAAGCTCCTACTGAAACAGCAGGCGCAGACCCAGAGAAGAAGGACCAGTTGCAGAGT
                                                                                                                   ArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluLys
                                                                                                                                                                                               ArglysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGlu
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FTI LHHPETTEDOPTEROLVANNOPOSGSDVTHQHPETARLINHPSL PADSGS FR PPVGA
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/db_xref="GI:17026376"
/translation="MEINHPDQLSVEHPPPGDSSSINQNGPGKQDGERCSTSGQAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ValValTyrGlyGluLysGluProSerLysGlyAspProAsnThrGluGluIle----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GACTITATTACAAAGAACAGAAATTTGGTGAGCTCAGTATTCTGTACACAGGAGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 IleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAla
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Mismatches:
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                                                                                         Mammalish Surchila; Sciurognachi; Miridae; Muthae; Mus.

I (Bases 1 to 1226)
Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Shemman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casvant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninch, P., Praneg, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Gazcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Boutferd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutferd, G.G., Blakesley, R.W., Touchman, W., Green, E.D.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-CCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 131 Row: i Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gagabs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/mol_type="mRNA"
/strain="FVB/N"
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Strausberg, R.
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TITLE

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276 AsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLys

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LeuileGluGlnTyrCluLeuArgGluGluHisIleAspLysValPheLySHisLysAsp 879 criaridadcagrangcacraaaggaagagcarrangaraaggaagaaggaa LeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAla TTGCAACAACAGCTTGTGGATGCCAAACTTCAGCAAACAACACAGCTGATAAAAGAAGCT

296

/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone_lib="NCI_CGAP_Mam6"

/clone_lib="NCI_CC/lab_host="DH10B"

/db_xref="taxon:10090" /clone="IMAGE:4947346"

FEATURES

316

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Db 327 CCCTGGGGGAGAAGCTCGAACAGATCCCCTGATGGTCAGCAAGATTC 374 Qy 140 sArgArgProdInGluLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMe 160 375 AGAGTGCAACAAAAAAAAAAAACTTTAGGAAAAGAAAGAAATTTATTATTACTGAT 428 Qy 160 tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTy 180	20 ualaArgSerLysLeuGusSerLeuCysArgGlubeuGlnArgHisAsnArgSerLeuLy 20 ualaArgSerLysLeuGluSerLeuCysArgGlubeuGlnArgHisAsnArgSerLeuLy 609 GGCAAGAAGCAAGCTAGAATCTCTTTGCAGAGAATTCCAGCTCACAATAAGACGTTAAA 240 GGCAAGAAGCAAGCTAGAATCTCTTTGCAGAGAATTCCAGACAACAGACGATAAGAAGATTAAGAAGATTAAGAAGACGTAAAGACGTAAAGAGAAAATAAGAAGAAAGA	320 uValaspalaiysLeuGinGinalaGinGiumetLeuLysGlualaGiuargHisGl 34 320 uValaspalaiysLeuGinGinalaGiumetLeuLysGlualaGiuGiuargHisGl 34 320 uValaspalaiysLeuGacaAacGacaCaCaCaCaCaCaCaCaCaCaCaCaCaCaCaCaCa	RESULT 36 BD006992 LOCUS BD006992 LOCUS BD006992 BETNITION Mcdulators of BRCA1 activity. ACCESSION BD006992.1 G1:18635363 VERYORD SOURCE Unidentified ORGANISM Unidentified Unclassified. REFERENCE LUbinfield,B.V. Porakisu,P., Rigenferuta,C. and Buon,T.T. AUTHORS Lubinfield,B.V. Porakisu,P., Rigenferuta,C. and Buon,T.T. AUTHORS JOURNAL PAREMACEUTICALS INC ONIX PHARMACEUTICALS INC
336 GluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArg 355 115	RESULT 35 AR072731 LOCUS AR072731 AR072731 ACCESSION AR072733 ACCESSION AR072731 TERMORDS COURCE ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE AUTHORS Rubinfeld, B., Polakis, P.G., Lingenfelter, C. and Vuong, T.T. TITLE AUTHORS Rodiators of BRCA1 activity JOURNAL Location/Qualifiers 1.1191 Authors Source //organism="unknown" /mol_type="unassigned DNA"		Db 111 TGGCACATGGAAGCTGGAATTTGTGGGGTGAAAGCAGATATGTTGTGTAA 170 Qy 60 rArgGlnLeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl 80 171 CTCTCAATCAAATGATATTCTTCAACATCAAGGCTCAAATTGTGGGGGGGGCAAG Qy 80 yGluAspGlyAlaGlnGlyGluProAlaGluArgAlaGluAspAlaGluLySSerArgThrTy 100 225 TAACAAGCATTGAAAGAATGAAGAATGAAGAATTT 284 Qy 100 rValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLySGluProSe 120

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	549	609 GGCAAGAAGCAAGCTAGAATCTCTTTGCAGAACTTCAGCGTCACAATAAGACGTTAAA 668	y 240 sGluGluGlyValGlnArgAlaArgGluGluGluGluGlucJuysArgLysGluValThrSerHi 260	y 260 sPheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSe 280	y 280 rLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTy 300	y 300 rGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLe 320 	320	Y 340 nArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMe 360	y 360 tlysglngluthrHisLeuLysglnglnLeuAlaLeuTyrThrGluLysPheglugl 380 	y 380 uPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGl 400	y 400 ulysMetThrLysLysleLysLysLeuGluLysGlu 412 		322 322.1 GI:21732875 sapiens (human)	Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 4154)		Neuherberg, GERMANY COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the	Heinrich-Heine-University, Duesseldorf/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp451A175) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059	ග ස	<pre>source 1 4154 /organism="Homo sapiens" /mol_type="mRNA"</pre>
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;	COMMENT OS Unidentified PN JP 2001502893-A/3 PD 06-MAR-2001	06-AUG-1997 JP 1998812659 04-SEP-1996 US 60/025601 BONY LUBINFELD, PAUL, PORAKISU CAROL RIGENFERUTA, TERIRIN T	;	Ablk3//02 CC Strandedness: Double; CC Topology: Linear; FF Key	300	/mol_type="genomic DNA" /db_xref="taxon:32644" ORIGIN	Alignment Scores: Pred. No.: 1.49e-43 Length: 1191 Score: 1047.50 Matches: 230 Percent Similarity: 69.01% Conservative: 55	initatity: 55.03% mismacches: 38.77% Indels: 6 Gaps:	US-10-023-523-8 (1-530) x BD006992 (1-1191) QY 3 SerbroGlyGlnProGluAlaGlyProGlu-GlyAlaGlnGluArgProSerGlnAlaAl 22 Dh 12 Trofford Annary Control Anna Control	aProklavalGluAlaGluGlyProGlySerSerGlnAlaProkrgLysProGl	55GUGACHUIGAGGUUGGACGGACGGACGGGACGCAGCCUGGGCAGAAGITIGAAAI 110 40 uGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSe 60	rargGlnLeuGluApplleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGl	80 yGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTy 100 :::	100 rValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSe 120	120 rLysglyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHi 140	140 sArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMe 160 :::	160 tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTy 180	180 ralagluleuleugludiuHisargasnSerGlnLysGlnMetLysLeuleuglnLysLy 200	200 sGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLe 220

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421 ATGATGAAGGGAAGGAGGAGGACAAAAGAAAAAGGAATATTTGCTGAACCAGGCA 480
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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therefor
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| AAGGACACACACATGGAAAGCCCGATTTGAGAACTGTAACAAAGCTCTGTTGGACATG
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                                                                                     LeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGlu
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LUDWIG INSTITUTE FOR CANCER RESEARCH
Location/Qualifiers
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WO0073801.
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KEYWORDS SOURCE ORGANISM		mo sapiens mo sapiens karyota, Me	(human)	a; Craniata; V	ertebrata; E	
REFERENCE AUTHORS	T X X	mmalla; Eur ogai,T., St mamoto,J.I.	ineria; Frimac ugiyama,T., Ot ., Isono,Y., H , Seki,N., Yos	s; catarrilli uki,T., Wakame o,Y., Otsuka,F ikawa,T., Otsu	A., S. lagai, I., Na	
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OW 377 yesPediuGlubhedinAsmThrieuSerLysSerSerGluValPheThrihrPhelysG 1977 OW 1818 AGGAGAGGGGGTTCCAAAACACACTTCCAAAACACGGGGGGGTTTCACCACATTCACG 1877 OW 187 InGluwMecGluLyWWerTh 403 DD 1878 AGGAGATCGAAAACACATTTCCAAAACAGCGGGGGGTTTCACCACATTCACG 1877 RESULT 40 AKO95939 LACUTS AKO95939 LACUTS AKO95939 AKO95939 AKO95930 GI21756551 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95939 AKO95999 AKO9599 AKO9599 AKO9599 AKO9599 AKO9599 AKO9599 AKO9599 AKO9599 AKO95999 AKO95999 AKO95999 AKO95999 AKO95999 AKO95999 AKO9599 AKO95999	Alignment Scores: Pred. No.: Pred. No.: 820.50 Matches: Score: 820.50 Matches: Score: 820.50 Matches: 84.1 Mismatches: 84.1 Mismatches: 84.1 Mismatches: 85.41 Mismatches: 86.83 Mismatches: 87.7 Mismatches: 88.7 Mismatc
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61808 ATCAGACCATGCCATTCCCAAGGACATGGGTCGGCAGGAGACCGGGATGAAGTGCCTTGTT 61749 61688 GCATATCGACAAAAGTCTTCAAACATAAGGACCTGCAGCAGCAGCTAGTGGACGCCAAGCT 61629 61748 TCCTAGAGTTGGGGCTTTCTTGAAAGGGAACTCCTGACTCCATAAATTACCTTTTCTGCA 61689 61569 61450 61449 TGTCCAGACAGCAGTCTGAGAGCAGGTAGCCTCAGTGGGTCCAGTGCTTGTGGCTAAAGA 61390 61270 60790 GCTGTATTGATATGCATATGAGTGTTTTGCATGGATGTATATTTTTCCCCCACTTGTGTTC 60731 61330 61269 CCTAAAGCAGCAGGT-GAGACGGGAACCTGACCTGCAGTTTCCAGGATGCTTTCACAAGG 61211 61151 61090 CIGTGTAGCCCTGGCTGTCCTGAAACTTGCTTTGTACACCAGGCTGGCCTGGAACACAGA 61031 60851 50850 CTCCCAGAIGCAIGAGGCGIIAGCIACCAGGICIAGCICAAIICIGICIACIIIIAIIII 60791 61030 GATTTGCCTGTCTTAGCCTCCTAAGTAATGGGATTAAATGTAGGCATGTGCCATCATGCC 60971 345 366 -- 305 346 346 371 371 uGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPh 61628 CCAGCAGGCCCAGGAGATGCTGAAGGAGGCAGAGGAGCGCCACCAGCGAGAGAAGGAGTT 61568 TGT-GAGGCTCAGGCCCCAGGGCTGTGGGGGCTGGAAGGAAGTGGGCTGGGTTCTGGC 51389 AGGTCAGACATACCCTCAGGGCTTCTGACAGGTTCTGGGGTCCTGTCTTGGAAATAGCT 61329 CCTGAAGGAAGCGGTGGAGTCCCAGAGGATGTGCGAGCTGATGAAGCAGCAGGAGCCCA 61210 GCCCATCTGCAGGGCAGTGGAGACAGGACTGTCATAGCCTGGCTTTGTGCCAGCTGGCCT 60970 AGGCATTTTTGTTGTTGTTGAAGAACAGGTCTCTGAGTTTTAGCTGTGGCTACAACTAAC 50910 CCAGAACTTACCTTGTAGACCAGGCTCTCTGGTGGCCTTGAACTTGTGACAGTCCTCTGA 347 -LeulysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHi 61150 GTTGGTGTCGGCCAAGTCTTTTATTTATGTGTGTTTTTGTTTTCCCCAAAGACAAAGTTTCT

	401	15	ογ 401 401	Db 15112 GGAAGCTCCCATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCC 1517	401	14152 Qy 401 401	Db 15232 TCTTTTCTGTTTGGTTTTTTTGGGGGGTTTGTTGTTGTTG	b 15292 TGTTTGAGARGACTCACCTATTGCCCAGGTGGAGTGCAGTGGCATGATCTCAGCTC 1535:	14272 Qy 401 401		Db 15412 GAATTACAGGGGGGGCGCCACCATGCCTGGCTAATTTTTCTTTTTTTT	Oy 401	52 Qy 401	DD 15532 GATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGGGTTATAGGCGGGAGCAACAACAAGTGGCTGGGGGGGG	Db 15592 CCCCTTACCATTCCTTGTTATTGGTGGAGACCTCTGACTTCCTGGTGGTGGTGGTGGTGGT	369 1 1662 PROPERTY AND 1662 PROPERTY OF THE P	32 Oy 401		369 402		Db 15892	32 Db 15	386 Db 16012 TIGGACACAAATGICCAAAGITAAIGCIGITCICCCCAIGGGAGGIGGIGAG 16071
							LeuclnGinAlacinGluvetLeuvsGluAlaciucroHischnargcluvysasp 544		TTTGTGAGGCTCAGGCTCCAGGGTTGGGGGGTGTGGGAGGGA	345 TTCCTT 1433	345			14	369	ن ن	4	10 1				 4 4	386

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	16012 TIGCACACAATGICCAAAGITAATGCIGTICICCCCCATGGGAGGIGGIGAGC	Db 16072 CCAGTGGTAGGTCTCCCAGTGGAGTGAAGGGAGCAAATGGAAAGGAATAAAAGGAATAAAAAGGAATAAAAAGAATGAAATGGAAATGGAAATGAAAAGGAATAAAAAGAATAAAAAGAATAAAAAA	Qy 433 433	16132 GAAAAAAACGGGTGCCAGTGATGTGCCTGGTTTACATGTAAAGCAGCCCAGGTAGTTTGT	Db 16192 GATTTCACAGCTTGTAATGTAGAAAGAAACTAACGATGGAGCAGCAAGCCA 16251	Qy 433 433	Db 16252 GACCTTGCTGAAAGTTTTTTGGGTTTTTTTTGTCTTTTTTGCTGCTGAATGTTTTTAGGTA 16311	Qy 433 433	Db 16312 CGTTGTTCATTGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAG 16371	433	Db 16372 ATGAGACAGGCTCAAAAGTCAAGGTCCAAGGTCACGTGGTAGATAAATGGAGGAA 16431	3.3.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	1000-1000-1000-1000-1000-1000-1000-100	16492 CATIGGOTTICAACTAGGACTTGTTTTTTTTTTTTGGACTTGGACTTGGACTTCTCTCAA	13.	16552 GCCTTGTTAAAGTGTTTGCCGCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGGCACGG	Ov 434InsthrValAroAsoInsGluGlvLeu		445 GlnValLvsIleGlnArqLeuGluLvsLeuCvsArqAlaLeuGlnThrGluArqAsnAsp	16672 CAGGTAAAAATCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGAGACACAGAGCGCAATGAC	Oy 465 LeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGly 484	Db 16732 CTGAACAAGAGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGTGCC 16791	Oy 485 ProGludrgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGlu 504	Db 16792 CCTGAGAGGCCCAGAGGCCCTGGGGCTCAAGCACCCCGGGCTCCACAGAA 16851	Oy 505 AlaproCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu 524	Qy 525 ProThrSerAlaArgAla 530	912 C		LOCUS BD060509 529 bp UNA linear FAI 27-AUG-20UZ DEFINITION Secreted expressed sequence tags (SESTS). ACCESSION BD060509	VERSION BD060509.1 GI:22606115 KEYWORDS JP 2001518793-A/869.	7 A G
14873 GGTCTGAGTGTTGACCAGAGTGCCTCCCAGAGAACCCAGTCTTATCTGTGGGGCTGCT 14932	370GlnLeuAlaLeuTyrThrGluiysPheGluGluPheGlnAsnThrLeuSer 386	387 LysSerSerGluValPheThrThrPheLysGlnGluMetGluLys	C) 100 101 101 101 101 101 101 101 101 10	GGCCAGGCATGGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCT		GGAAGCTCCCATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCC	401	1.1.2. CC.1.7.1.1.0.3.0.4.7.3.1.4.7.3.1.0.1.3.3.4.7.3.4.1.0.1.0.4.3.0.4.1.0.4.7.0.4.7.3.4.4.7.4.7.4.4.7.4.7.4.4.7.4.7.4.7	TCTTTTCTGTTTGTTTTTTTTTTTTGGGGGGTTTGTTGTT	401	15292 TGTTTGAGATGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTC 15351	401 401	15352 ATTGCAGCCTTTGCCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGACTAGCTG 15411	401	15412 GAATTACAGGCGTGCCACCATGCCTGGCTAATTTTTTTTT	401 401	15472 TTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGT 15531	401 401	15532 GATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGG 15591	401 401	15592 CCCCTTACCATTCCTTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGAGGTGGC 15651	401	15652 ACAGAGGCATTGACTGCATCCTGTAATGCCTTGCGCCTTGGGATCAATCA	TIGGAGACACAGGIGCAGTICCCCACCTICGAGACACCTTICGAGACGCCAGCTCTGA		CCATTTCCTTCTGTCTGTCACATAACCTAGATGACTAAGAAGATCAAGAAGCTGGAGAAA	412 GlufhrThrMetTrvArgSerArgTrpGluSerSerAshLysAlaLeuLeuGluWetAla 431 	432 GluGlu 433	15892 GAGGAGGTGGTCTGTGATCTGCAGCCAGGGTGGGGGGTGTGCACTTAGCGCATATCA 15951	433	GGCCCIIICCIGIAIGIICIACCCAICACACACACAIGAGGIAGGGIGAGAI

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Tubaes I to 3554)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Mooree, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Boughland, N.A., Peters, G.J., Morley, K.C., Hale, S., Garcia, A.M., Gask, S.A., McEwan, P.J., Hulyk, S.W., Worlley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Brock, J., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Samilus, D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

11. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 78 Row: p Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc mgc@nhgrilnin.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R., W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masielllo,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cons. Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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db_xref="taxon:9606"

clone="IMAGE:5534975"

/tissue_type="Uterus, leiomyosarcoma"

(clone_lib="NtH MGC_71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/organism="Homo sapiens"
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                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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KEYWORDS
SOURCE
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AUTHORS
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PUBMED
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI TOTAL TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC C12N15/12, C12NS/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness: Double; CC Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca Topology: Linear; Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 dedecticaadecadaacdectcadtererdedececritereadarererdadeaderdade 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GlyalaGlnalaargThralaGlnSerGlyalaLeuArgAspValSerGluGluLeuSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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                                      Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1998 UP 1998543070
LO-APR-1997 US 08/837312
KENNETH JACOSS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, TD MRRERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LysglyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC046565 3554 bp mRNA linear PRI 30-SEP-;
Homo sapiens taxilin, mRNA (cDNA clone IMAGE:5534975), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysserSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln
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                                                                                                                                                            Jacobs,K., Mccoy,J.M., Lavallie,B.R., Racie,L.A., Merberg,D., Treacy,M., Spaulding,V. and Agostino,M.J. Secreted expressed sequence tags (sESTs) Patent: JP 2001518793-A 869 16-OCT-2001; PROFFICS INSTITUTE INC.

PN JP 2001518793-A/869
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Mismatches:
Indels:
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Matches:
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713.00
99.28%
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BC046565.1
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Best Local Similarity:
Query Match:
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AUTHORS Satou, Y. and Satoh, N. TITLE Direct Submission JOURNAL Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department of Zoology; Sakyo-ku, Kyoto, Kyoto 606-8802, Japan (E-mail:satoh@ascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095, Fax:81-75-705-1113) COMMENT Glona intestinalis CDNA Project (URL: http://ghost.zool.kyoto-u.ac.jp/indexrl.html). FEATURES Location/Qualifiers source / 1. 2181 / Organism="Ciona intestinalis" / mol. type="mRNA" / mol. type="mRNA" / db xrefe"taxon:7719" / clone="cits018c13"	Alignment Scores: Pred. No.: Score: Score: 682.00 Matches: 166 Percent Similarity: 53.85* Conservative: 93 Best Local Similarity: 34.51* Query Match: 35.24* Thdels: 79 DB:	US-10-023-523-8 (1-530) x AK117024 (1-2181) QY 29 GlyProGlySerSerGln-AlaProArglySProGluGlyAlaGlnAlaArgThrAlaGl 48	48 nSerGlyAlaLeu	Oy 81 UASpGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrVa 101	271	Db 318 GAAACCCCGTATAAAGCTGGGTAAAGACTTAAGTATGATGATGAT 362 Qy 161 nThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTytAl 181	Qy 201 nSerGinLeuValGInGluLysAspHisLeuArgGlydluHisSerLysAlaValLeuAl 221 Bb 483 GGCACAAACACTGAAGGATTCTTTACAAGCTGAGCATAATAAGGCAGTTCTCGC 542 Qy 221 aArgSerLysLeuGluSerLeuCysArgGluLeuGluArgHisAsnArgSerLeuLysGl 241 Db 543 AAAAGGAAAACATTGGCCAGGGAATTGCAGAAAAAAGCAAACTTATCAAGGA 602	Qy 241 uGluGlyValGlnArgAlaArgGluGluGluLlysArgLysGluValThrSerHisPh 261
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Human DNA sequence from clone RP4-622LS on chromosome lp34.2-36.11,
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where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: SMLS SWLSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at the primary accession http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contiss of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at.

This sequence is the entire insert of clone RP4-622L5 This sequence was finished as follows unless otherwise noted: all regions were covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-622L5 is from the library data is sequenced by the group of Pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2417 of consensus"
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note="TIGGER1 repeat: matches 1117. .1501 of consensus"
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/note="TIGGER1 repeat: matches 2259.
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/note="TIGGER1 repeat: matches 1957.
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VECTOR: pCYPAC2.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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/note="12 copies 2
20865. .20922
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clone="RP4-622L5"
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note="TIGGER1
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2094021043 /note="u copies 26 mer 74% conserved" /note="u copies 26 mer 74% conserved" 2116821234 /note="u copies 26 mer 74% conserved" /note="match: GSS: Bm:AQ317905" /note="match: GSS: Bm:AQ317905" /note="match: GSS: Bm:AQ31256" /note="match: GSS: Bm:AQ732256" /note="match: GSS: Bm:AQ316964" /note="match: GSS: Bm:AQ376964" /note="match: GSS: Bm:AQ376964"	/note="Limec repeat: matches 15462095 of consensus" 3976139882 /note="Limec repeat: matches 14291546 of consensus" complement (4325443726) /note="match: GSS: Em:AQ146371" /s55546686 /note="match: GSS: Em:AQ146371" /s55546468 /note="match: GSS: Em:AQ040362" /note="match: GSS: Em:AQ040362" /note="match: GSS: Em:AQ040362" /note="match: A8982 /note: A8982	######################################		6888: 8818: 818: 818: 818: 818: 8518: 8518: 8518:
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371	· 43	83314 GGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGGGCCAGCTCTGACCATTTCCTTC 83373
82235 AGTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGAGGT 82294	i i	APATTATION TO THE TOTAL
371	∂ <i>†</i>	
82295 AGGAACAGAAGTTTGAAAATCAACATAAAGGCAAAATAAAAGTCACCTAAGTCTCCT 82354	20 d	1G1 C1G1 C4CN1 C4CN1 C4CN1 C4CN1 C4CN1 C4CN1 C4CN1 C4CN1 C7CN1 C4CN1 C4CN1 C4CN1 C7CN1 C4C
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82355 ACTITCCAGGCITAGCATTITGGATTATATCCTTCCAAATATATAGCTTTGCTTT	g :	01.ACCGG1.CGG1.GGGAGAGCAGCAACCAACCT.GC1.GGGAT.GGC1.GGG
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82415 AAGGAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAGTGT 82474	<u>a</u>	CIGICIOIGAICIGCAGCCAGGGIGGGGGIGIGCACITAGCGCAIAICAGGCCCITICCI
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82475 GTTGACCAGAGTGCCTCCCAGAGAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCCACA 82534	ସ୍ପ	GTATGTTCTACCCATCAGTGACACAGCTAGCATGAGGTAGAGGTGAGATTTGCACACAT
372AlaleuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGl 390	ð t	433
82535 GCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACATTTCCAAAAGGAGGGA 82594	20 6	1970-1991-1991-1991-1991-1991-1991-1991-
390 uValPheThrThrPheLysGlnGluMetGluLy8	ਨੇ ਜ਼ਿੰ ·	433
82595 GGTATTCACCACATTCAAGCAGGAGGTGGA-AAAGGTAACTGTGGTCCAGGCCAGG	<i>ŏ</i>	
401 401	qq	83734 GIGCCAGIGAIGIGCCIGGITIACAIGIAAAGCAGCCCAGGIAGIITGIGATITICACAGC 83793
82654 GCTGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCT	λŏ	433 433
401	- q <u>u</u>	83794 TTGTAATGTAGAAGAAAGGAACTAACGATGGAGCAGCAACTGCAAGCCAGACCTTGCTGA 83853
82714 TCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCCCCTCTTGAGGC 82773	ò	
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82894 GAGACTCACCTATTGCCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCATTGCAGCCTT 82953	<u>а</u>	TCAAAAGTCAAGTCCTTTGCCAAGGTCACGTGGTAGATAAATGGAGGAGAATACTTATCTC
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83014 GCGTGCCACCATGCCTGGCTAATTTTTTTTTTTTTTTTT	8	433 433
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83074 GGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGTGATCTGCCCGC 83133	8	
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401	\$ A	COPACGGCTGGAGAGGCTGTGCCGGGGCACTGCAGACAGACAG
83194 TCCTTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGGGGTGGCACAGAGGCCAT 83253	8	ovalGlnAspLeuSerAlaGlvGlvGlpGlvSerLeuThrAspSerGlvProGluArgAr
401 401	3 A -	GGTACAGSACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGAG
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Secritarian Secritarian	Best Local Similarity: 100.00% Mis Query Match: 24.65% In DB: Ga	OS-10-023-523-8 (1-530) x BC029686 (1-349) 8	421	2 OY 441 OY 441 OY 461	Db 181 GAGGGCATGACCTGAACAAGGGGTA Oy 481 ThraspserdlyProGluArgArgProC Db 241 ACTGACAGGGCCTGAGAGGGGCCA	301	Oy 521 GlyProGinGlubroInrSerAlaArg 		ACCESSION AY047502 VERSION AY047502.1 GI:15010371 KEYWORDS FLI_CDNA. SOURCE DESCONIIA melanogaster (fri	ORGANISM Drosophila melanogaster ORGANISM Eukaryota; Metazoa; Arthropod Neopetar; Endopterayota; Dipte	REFERENCE AUTHORS	Yu,C., Lewas,S.E., Rubin,G.M. TITLE Direct Submission JOURNAL Submitted (19-JUL-2001) Berkel Lawrence Berkeley National Laf Sequence submitted by: Berkeley Droscophila Genome Pro	Lawrence Berkeley National Berkeley, CA 94720 This clone was sequence as sequence clones from Drosof Science 2000). The sequence	for sequence accuracy, present within 100 kb in the genome. Treflect accurately this partic artifacts associated with the have not been detected in our	
C C C C C C C C C C C C C C C C C C C		5 2 8		mRNA linear PRI 20-MAY 57, mRNA, partial cds.	raniata, Vertebrata, Butel starrhini, Hominidae, Homo	NY-2002) National Institutes of Health, Mammalian (MGC), Cancer Genomics Office, National Cancer anter Drive, Room 11A03, Bethesda, MD 20892-2590,	URL: http://mgc.nci.nih.gov p desk	Mmail.nin.gov int: ATCC pparation: Life Technologies, Inc. "ayed by: The I.M.A.G.E. Consortium (LLNL) yy: Baylor College of Medicine Human Genome	er -HGSC /www.hgsc.bcm.tmc.edu/cdna/ 	Lumc.cau A.M., Lu, X., Hulyk, S.W., Hale, S.M., Garcia, A.M., Lu, X., Martin, R.G., Muzny, D.M., S, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., bbs, R.A.	on: MGC clone distribution information can be four A.G.E. Consortium/LIANL at: http://image.llnl.gov.te: 42 Row: j Column: 8.nn/qualifiers	sm="Homo sapiens" pe="mRNA" ff="texon:9606" "IMAGE:4993857" ; type="placenta, choriocarcinoma"]ib="NIH MGC 10"	<pre>st="DH10B" Vector: pCMV-SPORT6" start=1 t="Unknown (protein for IMAGE:4993857)"</pre>	.n.id="AAH29686.1" f="d1:20987362" ation="KOYKKIKKLEKETTMYRSRWESSNKALLEMAEEKTVRDKELEC EKLCHALQTRENDINKRVQDLSAGGGGSLTDSGPERRPEGFGAQAPSSEF ogapsteasgggtgpgeptsaaa"	ie-24 Length: 3495 00 Marches: 130

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as part of a high-throughput process to ophila Gene Collection 1 (Rubin et al., eee has been subjected to integrity checks esence of a polyA tail and contiguity me. Thus we believe the sequence to articular cDNA clone. However, there are the generation of cDNA clones that may our initial analyses such as internal taminating genomic DNA, retained introns to of unspliced precursor RNAs, and ors that result in single base changes. Bout this sequence, including its location sequences, please visit our Web site edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong, L., Agbayani, A., Carlson, J., Lt, V., Farfan, D., Frise, E., George, R., P., Liso, G., Mungall, C.J., M., Park, S., Phouanenavong, S., Wan, K., I. and Celniker, S.
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aboratory, Berkeley, CA 94720, USA
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tera; Brachycera; Muscomorpha;
Drosophila.
Mismatches:
Indels:
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Laboratory
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406 AAGTICCAAAGCICCCIGAACGAIGICCAAAAGICGCIGGCCAAGAACAACAACAAGAGAGAAC 465
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 ThrGluArgAsnAspleuAsnLysArgValGlnAsp 471
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QESAATESKAELEAAGDASNVKNEKEQTVDIATDTQELVGDGDAITAKSLVDISEVPP
LIDANAN"
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KEALGWRQKYEKANAMVI DLATEKSLQTQHSERLQKQIQQLQKLLRALQLERTTLHKC
LRDHEI EI PALPQLPPEPEPVNVKPVSAENVKMEMMSRNCAELKQTLANLQNQMKLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHUDSEKNVSRLTAELRVLQROMESQOREKEOVORDLNKSVLMRDKLOEVCREOQRÍÍ
KSVKNESLLQIKVEEERRKESOTKFOSSLNDVOKSLAKNNERNÍKLRDÝNIEMTKKLK
LLAEQYQTREGHLEKLNEQVQLEAQLHQAKLQKCQVEAAMEKEILSKENQIGLEKLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MEKLSKAKKVAREEKQRDQKLEELVMKSLDECPSAEEKVKLLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 GluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgProGlnGluLys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 LysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeu 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 SerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGlu 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 CCCTCCGCCGAGGAGAAGGTGAAACTT--------CTGCTGCAACGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GlnMetLysLeuLeuGlnLys 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 LeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeu 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 CTGATGCGAGACAGCTGCAGGAGGTGTGCCGCGAACAGCAGCAGCATCATAAAGTCCGTA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSer 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AAGAACGAGAGCCTGCTGCAAATCAAAGTGGAGGAGGAGCGGCGCAAGGAGAGCCAGACA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 HisPheGlnValThrLeuAsnAsplleGlnLeuGlnMetGluGlnHisAsnGluArgAsn 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GAGAAGCTAAGCAAGGCGAAAAAGTGGCGCGCGAGGAGAAAGCAGCGCGACCAGAAGTTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal
                                                                                                                                                                                                                                    note="alignment with genomic scaffold AE003753"
db_xref="FLYBASE:FBgn0039379"
                                                         /organism="Drosophila melanogaster"
|mol_type="mRNA"
|strain="y; on bw sp"
|Ab_ref="taxon:7227"
|map="96F5-96F5"
|clone="GH01188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                              /product="GH01188p"
/protein_id="AAK77234.1"
/b_xref="G1:15010372"
/db_xref="FLYBASE:FBGn0039379"
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cdna@fruitfly.berkeley.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       note="Longest ORF"
                                                                                                                                                                                                             gene="CG5886"
                                                                                                                                                                                                                                                                                                  gene="CG5886"
                                                                                                                                                                                                                                                                                                                                           codon_start=1
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597.50
63.64%
35.80%
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Muric, Merzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alabrace, Merzker, M.Lee., Abramzon, S., Anguiano, D., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Bara, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barstead, M., Benhmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, F., Brown, M., Bryant, N., Buhay, C., Burch, P., Burch, F., Burch, F., Gardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chaver, D., Chaver, D., Chen, G., Chen, R., Chen, Y., Chen, T., Chen, C., Coyle, M., Cree, A., D'Souza, L., Delgdo, J., Danson, S., Deramo, C., Doyle, M., Cree, A., D'Souza, L., Delgdo, O., Denson, S., Deramo, C., Durpin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Frorbes, L., Foster, M., Gebregeorgis, B., Geer, K., Gill, R., Gardia, M., Guerra, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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280 SerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLysLeuIleGluGln 299
                                                                                                                                                                              300 TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 CTGCACCAGGCCAAGCTGCAAAAATGCCAGGTGGAGGCTGCCATGGAAAAGGAGATATTG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 GlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeu 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 AGCAAGGAAAACCAGATTGGCCTGGAGAAACTGATGCAAGCGCAACGTGCCATAAAGGAT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                     320 LeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 MetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysMetThrLysLysLeLysLysLeuGluLysGluThrThrMetTyrArgSerArg
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             Hernandez, R., Hawes, A., Henderson, N., Hernandez, J., Hawas, A., Haddun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kally, S., Kally, S., Kally, S., Kally, S., Kalna, Z., Lopez, J., Lordon, R., Johnson, R., Johnson, R., Johnson, R., Lous, J., Lau, J., Lu, X., Man, J., Loulseged, H., Lozado, R.J., Lu, X., Man, J., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahinday, R., Martinez, E., Mangum, B., Mahinday, M., Martin, R., Martinez, E., Mangum, R., Mandun, P., Moreis, S., Mondeas, M., Martinez, E., Mangum, B., Mandua, P., Martin, R., Martinez, E., Mangum, B., Moris, K., Martin, R., Martinez, E., Mangum, R., Martin, M., Martinez, E., Mangum, B., Morris, K., Morris, S., Mundasa, M., Norris, S., Mordea, M., Norris, S., Mordea, M., Norris, S., Mordes, M., Norris, S., Mordes, M., Norris, S., Mandexel-mech, O., Okwuchu, G., Olarnpunsagoon, A., Pals, S., Paul, H., Perez, A., Perez, L., Pfannsch, C., Pluges, F., Pluges, P., Poloper, P., Poludexer, A., Perez, J., Prants, E., Pulz, S., Reilly, M., Ren, Y., Reuter, M., Richards, S., Raigs, F., Reilly, M., Ren, Y., Robe, M., Rose, M., Rose, M., Rose, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Storg, R., Strong, R., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Strong, M., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Willams, G., Millams, G., Willams, G., Millams,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (109-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23321701.
The sequence in this sasembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Direct Submission

Submitted (19-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 245095)

Rat Genome Sequencing Consortium.
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Center clone name: CH230-171G2
Center clone name: CH230-171G2
Assembly program: Phrap; version 0.990329
Consensus quality: 153773 bases at least Q40
Consensus quality: 160170 bases at least Q30
Consensus quality: 164659 bases at least Q20
Estimated insert size: 160182; sum-of-contigs estimation
    Hawes, A., Henderson, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
Harvey, Y., Havlak, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
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AUTHORS
TITLE
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COMMENT

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140839 GIGCAGCGAGCCCGIGAGGAGGAGAGAGCGCAAAGAGGTGACTICACACTICCAGGTG 140898
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces are not in the pieces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GlnArgHisAsnArgSerLeuLysGluGluGly 243
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Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnVal
                                                                                                                                                                                                                                                                      69762: contig of 69762 bp in length 69862: gap of unknown length 73689; contig of 1827 bp in length 73789; gap of unknown length 88447: contig of 14658 bp in length 184613: contig of 14658 bp in length 124713: gap of unknown length 179270: contig of 54575 bp in length 179270: contig of 54575 bp in length 179370: gap of unknown length 22456: contig of 45126 bp in length 228136: contig of 45126 bp in length 228136: contig of 45128 bp in length 228136: contig of 1829 bp in length 23826: gap of unknown length 238366: gap of unknown length 238366: gap of unknown length 238565: gap of unknown length 238565: gap of unknown length 238565: gap of unknown length 238565: gap of unknown length
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Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-171G2"
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401	141979 GCCFTGAACTCAAAGATTTGCCTGCCTCCTGAAGAAATTAAAGAATTAAAGAATTAAAGAAATAATAAGAAAGAATAAAAGAAAAGAATAAAAGAAAAAA	<u>a</u> è
143059 AATGGTGGGGTTTTTTCCCTGGAACTCTTGGTGTAGACCAGA		ζ
401	141919 AAGACAGCGTTTCTCTGTGTGAGCTCTGGCTGTCCTGGAACTTGCTTTGTAGACCAGGTTG 141978 Qy	qa
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142939 AGAAAGGGCTCCCTCCTCCCACAGGGGACAGTGTCTGTI	369	δ δ
401	141799 TITCACAAGGGCCCATCTTCAGGGGAGGGAAGACACACGACTCTCGTCTTAGACTGGCTT 141858 QY	Dβ
142879 CCACTTCTTTAGAGCTGAGCTGCCCTTGACAGCCTCTTCATG	398	ò
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376 ulysphediddluphedinanintleusettsetot 142759 GAAGTTTGAGGAATTCCAGAACACACTTTCCAAAAGCAGTGA		8 8
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370	141559 CCGGTACTCGCCTGTCCAGACAGACTGGAGAACAAGTAGCCTCAGTGGGTTCAGGGCT 141618 Qy	qa
142639 GCACAGCTTTGCTTGTGTGTATTAGGAAATGGTGTCTCGGT	345	ò
369	141499 CIGGGIICIGACITAGCICAGICIAGIICIICAGGAIGGGAGGGITITGCCTGCCCAGI 141558 Qy	qa
142579 IGCTGAAGTCTTACCAAGGCTCACTTTGCAGAATCTTCTGT	345 345 Db	ò
142514 CCATCAAIGIAIGIIIAGIICIGIIIIGIIIICIIIITITITITITITITITITITI	[GGAGAAGGAGTTTGTGAGGCTCAGGCCTGGGGGCTGCCGTGGGGGCTAGAAGAAGGAAG	; A
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142459 TAAGAGAATTGAACCCAAGTCCACAGCCAGTGATCTTAGCTG	321 lAspalaLysLeuGlnGlnAlaglnGluMetLeuLysGluAlaGluGluArgHisGlnAr 341	8
369		qa
142399 CATTIGIGIICCIGCIACCTICAGAGGICAGAAGAGIIACAG	306HislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuVa 321	δ
	141259 TGTTTCCTAGAGTTGGGGGCTTTCTTGAAAGGGAGCTCCTGACAAGCATTAATAGCATTAA 141318	qa
142339 TTTTTCTTTTCTTTACTATTATGCATTTGAGTATTTTGCAT	302 305 305 305 305 305 305 305 305	λõ
	141199 TGAGTTAGCAGGAGGCTTCCCAAGGCCATGGGGATGAGAATGAGACTGGACGAAGTGCCT 141258	qq
269 - 2007 GTOCTOTORACTICCCAGATIGCATGAGGCCTTAGGCTAGCTAGCTTCTTAGGTTAGG	305 305	ò
142219 TATAACTAACCCAGAATGCACCTTGTACACCAGGCTCAGGTI	GTAGAATATTTAGTTCTAGAGGTATGTCCTTGTCCTAGCTCGACATCTGACTGT 141198) E
369	141079 ACTGGGGCAGCAGCAGCATTTTCTTGCTCTTCAAAGATGGTGTCTGGAACCAGCAT 141138 QY	ପୁର
142159 ACCATGCTAGGCATTTTTATTGTTGTTTTGTTTGAAAAGGTCT		δŏ
369	141019 GAGGAGGTGAGGGAAGGTGGTGGCCAGCAGCAGACTGTGAGGCTGTAGTGTGCCGGGG 141078 OY	ਰੂ ਹ
142099 GGGTTCGGTCCCCAGCTCCGAAAAAAGACCCCAAAAAAAA	305	ò
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142039 CCACCGGGGCTGGGGATTTAGCTCAGTGGTAGAGCGCTTACCT	284 GlnGluAsnWetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuArg 303	δ

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143118	AATGGTGGGGTTTTTTCCCTGGAACTCTTGGTGTAGACCAGACTGGTCTTGAACTCTTAA	143059	ф
401		401	ò
143058) TTGATTTCTTTATTTTATGCTGGAATTAAAATAGAGAATATGCATTTTGCTACTAGGCTTC	142999	Q
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142998	AGAAAGGGGCTCCCTCTCCTCCCACAGGGACAGTGTCTGTTTTTTTT	142939	οg
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142938) CCACTICITIAGAGCIGAGCIGCCCTIGACAGCCICTICAIGIAICAGGAAGAGGIGGIT	142879	QQ
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142818	GAAGTTTGAGGAATTCCAGAACACTTTCCAAAAGCAGTGAAGTGTTCACCACGTTCAA	142759	qu
396	ulyspheGluGluPheGlnAsnThrLeuSerLysSerSerGluValFheThrThrPheLy	376	ઠે
142758	CIGAGGGIGCIGICICAICITIGCIICIGIGCCICICACCACCAGCICGCCCIGIAIAAAAAAAA	142699	qq
376	GInLeuAlaLeuTyrThrGl	370	ò
142698	GCACAGCTTTGCTTGTGTATTAGGAAATGGTGTCTCGGTGGAGTGGGTTATGTCCGA	142639	Dp
369		369	ò
142638	TGCTGAAGTCTTACCAAGGCTCACTTTGCAGGAATCTTCTGTGGGACACATCCCTGCTGT	142579	g
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142578	CCATCAATGTATGTTTAGTTCTGTTTTTGTTTTTTTTTT	142519	qq
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142518	TAAGAGAATTGAACCCAAGTCCACAGCCAGTGATCTTAGCTGCTGGCCATCCCTTCAGCC	142459	q
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142458	CATITIGIGITICCTGCTACCTTCAGAGGTCAGAAGAGTTACAGACATITGTGGCCTCCATG	142399	qq
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142398	TITITCTITITCTITACIAITAIGCAITTGAGIAITTIGCAIGGAIGIAIAICIGIGCC 1	142339	QC
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142338	GTCCTCTGACTCCCCAGATGCATGAGGCCTTAGCTACCATGTCTAGCTTGATTTCTGTTAA 1	142279	qq
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42218	ACCATGCTAGGCATTTTTATTGTTGTTTTGTTTGAAAAGGTCTCTGACTTTAGCTCTGGC 1	142159	do
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Sequence 3 Sequence

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Sequence 640, App Sequence 20, Appl

Sequence 3,

Sequence 130, App Sequence 1065, Ap Sequence 735, App

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Sequence 249, Sequence 30, Sequence 248

Appli

Sequence 17, Appl

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Sequence 119, App Sequence 119, App Sequence 119, App

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Sequence Sequence

Sequence:

Run on:

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Sequence 119, App

Appl

Sequence 2

Sequence 93, Appl Sequence 93, Appl Sequence 548, App

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Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

COUNTRY: USA

ZIP: MA

COUNTRY: USA

ZIP: 10110-264

COMPUTER: TEBABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: TEBM Compatible

OMPRATING SYSTEM: DOS

CURRENT APPLICATION DATA:

PILING DATE: 26-No. 6355451-1997

PRILING DATE: 03-JUN-1997

FILING DATE: 03-JUN-1997
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
ATREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08979608A; Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
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-MODEL-frame+ p2n.model -DEV-x1h
-Q=CQGN2_1/VESPC_3ROO1/USIO023523/runat_08062004_063749_29963/app_query.fasta_1.1422
-Q=CQGN2_1/VESPC_3ROO1/USIO023523/runat_08062004_063749_29963/app_query.fasta_1.1422
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPECL=0
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-NDSV_TRAGEDUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPPOP=6 -FGAPPOP=10 -YGAPEXT=0.5 -FGAPPOP=6
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Sequence 17, Appl
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Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
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Sequence 5, Appl
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                                                                                                                                June 8, 2004, 06:37:58; Search time 113.29 Seconds (without alignments) 2596.205 Million cell updates/sec
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1 KSSPGQPEAGPEGAQERPSQ.....APSTEASGQTGPQEPTSARA 530
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                           protein - nucleic search, using frame_plus_p2n model
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US-09-517-849-17
US-09-616-289-46
US-09-979-608A-14
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US-09-516-289-14
PCT-US94-01101-1
US-08-968-751-5
US-09-618-289-51
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Maximum Match 1008
Listing first 50 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database :

Result

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722 260 782 280 842

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1503 AGGTCACAGAAGCGCCTTGCTACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACT 1562
                                       AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys
                                                                      GCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGCTCCCTCAAG
                                                                                                     GluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSerHis
                                                                                                                          963 GTGGATGCCAAGCTCCAGCAGGCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAG
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Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
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REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION HUMBER: 10797-002001 (formerly 3983/59818)
TELEFHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID 0.7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4697 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr
                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 60/031,930 FILING DATE: 27-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 3...1592
7: SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-08-979-608A-17
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Query Match:
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 Law, Simon W.
Arjona, Anibal A.
OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES:
TREATING ATHEROSCLEROSIS
                                                                                                                         COMPTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
PRIOR APPLICATION DATA:
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PILLING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: WPOE'S, LOUIS
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION OF 17/642-8906
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence
LOCATION: 3...1592
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                       STRET: 225 Franklin Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4697 base pairs
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                                                         NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & F
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Best Local Similarity:
Query Match:
DB:
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183 CGCCAACTGGAAGACATACTGAGCACATACTGTGGACAATAACCAGGGGGGCCCCGGC 24	OY 81 GluAspGryAlaGluGlyGluProAlaGluProGluAspAlaGluLysserArgThrTyr 100	Oy 101 ValalaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer 120	Qy 121 LysGlyAspProAsnThxGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 Db 363 AAGGGGATCCAAACACAGAAGCAGAATCCGGCAGAGTGACGAGACCGAGACCAT 422	Qy 141 ArgArgProGlnGluLysLysAlaLysGlyLeuGlyLysGlulleThrLeuLeuMet 160	Qy 161 GlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaalaLeuCysLysLysTyr 180 Db 483 CAGACATTGAATACTCTGAGTACCCCAGAGGAGAAGCTGGCTG	Qy 181 AlaGluLeuLeuGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLys 200	Oy 201 GlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeu 220	Qy 221 AlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLys 240	Qy 241 GluGluGlaPyalGlnArgAlaArgGluGluGluGluLysArgLysGluValThrserHis 260	Oy 261 PheGlmValThrLeuAsnaspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSer 280	Oy 281 LysLeuArgGlnGluAsmMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyr 300	OY 301 GlubeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeu 320		Qy 341 ArgGluLysAspPheLeuLeuLysGluAlaYalGluSerGlnArgMetCysGluLeuMet 360	Oy 361 LysGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380 	Oy 381 PheGlnAsnThrLeuSerLygSerSerGluValPheThrThrPheLygGlnGluMetGlu 400	Qy 401 LysMetThrLysLysLysLeuGluLysGluThrThrMetTyrargSerArgTrp 420	Qy 421 GluserSerAsnLysalaLeuLeuGluMeralaGluGluLysThrValargAspLysGlu 440
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Db 1383 GAGCGCAATGACCTGAACAAGGGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTC 1442	Qy 481 ThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro 500	InThr 	GlyProglnGluProThrSerAlaArgAla 530 	RESULT 3 US-09-616-289-17 . Sequence 17 bonlication HS/Assisse	; Cadamic 1, Application OS/0301005 ; Patent No. 6632223 ; GENERAL INFORMATION: ; APPLICANT: Lees Ann N.	ָ נ נ	; TITLE OF INVENTION: ATHEROSCIEROSIS; FILE REFERENCE: 10797-004001; CURRENT APPLICATION WHERE: 19709/616, 289	FRIOR APPLICATION NUMBER: US 09/517,849 FRIOR FILING DATE: 2000-03-02 FRIOR FILING DATE: 2000-03-02 FRIOR PREDICATION NUMBER: US 08/979,608	FRIOR APPLICATION WUMBER: US 60/031,930 ; PRIOR FILING DATE: 1996-11-27 ; PRIOR FILING DATE: 1996-11-27 ; PRIOR PEPLICATION WUMBER: US 60/048,547 ; PRIOR PETING DATE: 1907-05-03	NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 17 ; FACTH. 4697	; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS	; LOCATION: (3)(1592) US-09-616-289-17	Alignment Scores: Pred. No.: 5056-228 Length: 4697 Score: 2702.00 Matches: 530 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches:	100.00\$ Indels: 4 Gaps:	OS-10-023-323-8 (1-330) X OS-09-618-289-1/ (1-469/) QY	0G]rd	GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer 	61 ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly

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288 100 120 408 140 468 160 528 180 588 200 648 220 708 240 768 260 828 280 888 300 948

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949 GAGCTGCGCGAGGAGCATATCGACAAAGTCTTCAAACACAAAGGACCTACAACAGCAGCTG 1008
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                LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis
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GlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSer
                                                                         ArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly
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                                       1323 CTGGAGGGCCTGCAGGTAAAAATCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACA 1382
                                                                                                                1443 ACTGACAGTGGCCCTGAGAGGAGGCCAGAGGGCCTGGGGCTCAAGCACCCGAGCTCCCCC 1502
                                                                                                                                                                                                                                                    520
                                                                                             480
                                                                                                                                                                      ThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro 500
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon M.
APPLICANT: Lees, Annibal A.
TITLE OF INVENTION: OVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROYERING AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCILENCES:
TITLE OF INVENTION: ATHEROSCILENCES:
TITLE OF INVENTION: ATHEROSCILENCES:
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
COFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AAAAGCAGCCCAGGACAACCGGAAAGCAGGACCCCAAGAGCCCAGGAGCGGCCCAGCCAG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysSerSerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGln 20
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                                                                                                                                                                                                                                                ArgValThrGluAlaProCosTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr
                                                                                             GluArgAsnAspleuAsnLysArgValGlnAspLeuSerAlaGlyGlnGlySerLeu
                    LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                      1563 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1592
                                                                                                                                                                                                                                                                                                                               521 GlyProGlnGluProThrSerAlaArgAla 530
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2693.00
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1).
US-09-616-289-46
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Pred. No.:
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LENGTH: 1638
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US-09-616-289-46
                                                                                                                                   1383
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280 SerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGln 299
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Best Local Similarity:
                                                                  US-08-979-608A-14
                                                                                                     Alignment Scores:
FEATURE
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                AAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACCATGTACCGGTCCCGGTGG 1308
                                                                                 1309 dadadcadcaacaacccccccccrccrrdadarddcrcaddaaaaacagrccggaraaadaa 1368
                                                                                                                                                                                                                        1488
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                                                                                                                                                   1369 chádaddochfocaddnaaaanccaacdddagaaaadchdccddccachdcadan 1428
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Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
RINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                 440
                                                                                                                    460
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                                                                                                                                                                                                                                                         ThraspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro 500
                                                                                                                                                                                                                    1429 GAGCGCAATGACCTGAACAAGAGGGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTC
                                                                                                                                                                                                                                                                                                                              501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThr
                                              421 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGlu
                                                                                                                    LeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThr
                                                                                                                                                                                       461 GluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDNIEKT 105A

CUNTER READABLE FORM:
MEDIUM TYPE: Diskette

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastsEQ for Windows Version 2.0

CURRNY APPLICATION DATA:

RILING DATE: 26-No. 6355451-1997

FILING DATE: 03-UN-1997

APPLICATION NUMBER: US 60/048,547

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     1609 GGGCCTCAAGAGCCCACCTCCGCCAGGGCC 1638
                                                                                                                                                                                                                                                                                                                                                                                                521 GlyProGlnGluProThrSerAlaArgAla 530
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08979608A Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lees, Ann M.
Lees, Robert S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-979-608A-14
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101 ValAlaArgAsnGlyGluProGluPro --- ThrProValValTyrGlyGluLysGluPro 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCAGTTGGAAGACATACTCAGTACATACTGTGTGGACAACAACAACCAGGGGCCCCCGGGT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 HisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeu 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 CACCGGAGGCCACAGGAAAAAAAAAAAGGAAGGGTCTGGGAAAGGAGATCACGCTGCTG 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TyrAlaGluLeuGeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLys 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 AAGCAGACCAGCTGGTGGAGGAGGACCACCTGCGTGGCGAGGCGAGGCAAGGCCATC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 LysGluGluGlyValGlnArgAlaArgGluGluGluGluLysArgLysGluValThrSer 259
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112
125
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                               Indels:
NAME/KEY: Coding Sequence
LOCATION: 61...1731
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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2465.50
92.99%
90.77%
91.25%
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Length:
Matches:
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LOCATION: 61...1731
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                LENGTH: 4722 base pairs
        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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2465.50
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Best Local Similarity:
Query Match:
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                                                                            TACGAGCTGCGAGAGAGACATCGACAAAGTCTTCAAACACAAGGATCTGCAGCAGCAG 1065
                                                                                                                                       CTGGTGGACGCCAAGCTCCAGCAGGCCCAGGAGTGCTGAAGGAGCAGAGGAGCGCAC 1125
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                                                TyrGluLeuArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGln 319
                                                                                                           LeuValAspAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHis 339
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                                                                                                                                                                                                                                  MetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGlu 379
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Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
TREATING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                      TrpGluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 439
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Patent No. 6605588
GENERAL INFORMATION:
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Lees, Robert S.
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APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
FILING DATE: 02-Mar-2000
FILING DATE: 26-NOV-1997
ATORNEY/AGENT, INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965 Conservative: Mismatches: Indels: REFERENCE/DOCKET NUMBER: 10797-003001 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 x US-09-517-849-14 (1-4722)

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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN HINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN HINDING
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-004001
CURRENT PEPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1090-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-11-26
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PRIOR FILING DATE: 1997-11-26
PRIOR PELICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LEGTH+ A722
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Matches:
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                                                                                                                                          Sequence 14, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
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ORGANISM: Oryctolagus cuniculus
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US-09-616-289-14
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                                      TyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLys
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	140 HisArgArgFroGinGluLysLysLysLysClyLeuGlyLyGglulleThrLeuLeu 159 140 HisArgArgFroGinGluLysLysLysLysClyLeuGlyLyGglulleThrLeuLeu 159 526 CACCGGGGCCACACGAAAAGAAGGACGCCAAGGGTTCTGGAAAAGAAGATCACGTGCTG 585 160 MetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLys 179	180 TyralagluLeuLeuglugluHisArgAsnSerGlnLysGlnMetLysLeuLeuglnLys 199 	200 LysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaVal 219 	220 LeualaargSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeu 239 	240 LysqludludlyValGlnArgalaArgdluGludludludlubysArgLysGluValThrSer 259 	260 HispheGlnValThrLeuAsnAspIleGlnLeuGlnMetGluGlnHisAsnGluArgAsn 279 	280 SerlysLeuArgdinGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGln 299 	300 TyrGluLeuargGluGluHisIleaspLysValPheLysHisLysAspLeuGlnGlnGln 319 	320 LeuvalaspalalysLeuglnGlnalaGlnGluMetLeulysGluAlaGluArgHis 339 	340 GInArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeu 359 	360 MethysglnglngluthrhisLeulysglnglnteualaleuTyrThrglutysPheglu 379 	380 GlupheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMet 399	400 GlulysmetThtlyslysllelyslysleuGlulysGluThtThtmetTyrargSerarg 419 	420 TrpGluSerSerAsnLysalaLeuLeuGluMerAlaGluGluLysThrValargAspLys 439 	440 GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGln 459 	0 ThrG1

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939 CAACCGAGCACAGAAGCATCAGGCCAGACTGG-CCTCAAGAGCCCACCTCCGCCAGGGCC
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,751
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                            APPLICANT: Rubinfeld, Bonnee
APPLICANT: Rubinfeld, Bonnee
APPLICANT: Polakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Vuong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRCA1 AC:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaccuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
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                                             RESULT 9
US-08-968-751-5
; Sequence 5. Application US/08968751
; Patent No. 5948643
; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-9758
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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       Conservative:
Mismatches:
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       97.66%
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// Patent No. 6632923

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          GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Arjona, Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ITILE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ITILE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-07-49
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
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INFORMATION:
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	14873 GGTCTGAGTGTTGACCAGAGTGCCTCCCAGAGAACCCAGTCTTATCTGTGGGCTGCT 14932	셤	15952 GGCCCTTTCCTGTATGTTCTACCCATCAGTGACACGCTAGCATGAGGTAGAGGTGAGAT 16011
	370GinLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSer 386	රු ජි	433
	14933 TICTCCCCACAGCTTGCCCTATACACAGAGAGTTTGAGGAGTTCCAGAACACACAC	}	
		ት ብ	433
	TETTO COCCONCTINE COCCONCTINE CONTRACT	ò	
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	471179977799991797144444777145777997777777777	ζ	433 433
	15112 GGAAGCTCCCATCTGGGGTGTCTCAAGGGCAGGGCTGTTAAGGAAAGTTCAAAAGTTAAGTAAAGAAAG	qu	16192 GATTTCACAGCTTGTAATGTAGAAGAAAGAACTAACGATGGAGCAGCAACTGCAAGCCA 16251
	7/11/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/	6	433 433
	CCTCTTGAGGCAGTATCAGTATGTATACACTCCAAGTTGTCCCAAGGGAATTGGGAAA	ద	16252 GACCTIGCTGAAAGTTTTTTGGGTTTTTTTTTGCTGCTGCTGAATGTTTTTAGGTA 16311
		ò	433
	TCTTTTCTGTTTTGGTTTTTTTTGGGGGGGTTTGTTGTTG	QQ	16312 CGTTGTTCATTGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAG 16371
	:	δ	433
	15292 TGTTTGAGATGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCCAGCTC 15351	QQ	16372 ATGAGACAGGCTCAAAAGTCCATTGCCAAGGTCACGTGGTAGATAAATGGAGAA 16431
	401 401	ò	433
	15352 AITGCAGCCTTIGCCCCCCGGGITCAAGIGATTCICCTGCCTCAGCCTCGTGACTAGCTG 15411	DP	16432 TACGTTATCTCCAAGCCGTGCCCCTTTTCTGCACCAIGCTGCCCCACCTGACAGCCTAGT 16491
	401 401	ò	
	15412 GAATTACAGGCGCGTGCCACCATGCCTGGCTAATTTTTTTT	DP.	16492 CATGGCTTCAACTAGGACTGTTTCCTAAAGGGGGCCAGCTTTGGACTCGGTCTGCTCTCA 16551
	401 401	λõ	
	15472 TTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGT 15531	අු	16552 GCCTIGITAAAGIGITIGCCGCCAAGIGGIGAIGGIAAGIGGGAGGITGAIGGGGCACGG 16611
	401 401	ò	
	15532 GATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGG 15591	đ	16612 CACTGAAGGICTCAITTCTTTCCCTAGAAACAGTCCGGGATAAAGAACTGGAGGGCCTG 16671
	401	λο i	445 GlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAsp 464
	15592 CCCCTTACCATTCCTTGTTATTGGTGGACACCTCTGACTTCCTGGTGGTGGTGGC 15651	g O	
	401	à i	LeuAsniysArgValGlnAspLeuSerAlaGlyGlnGlySerLeuThrAspSerGly
	15652 ACAGAGGGCATTGACTGCATCCTGTAATGCCTTGCGCCTTGGGATCAATCA	do e	CTGAACAAGAGGGTACAGGACCTGAGTGCTGGCCAGGGCTCCCTCACTGACAGTGGC
	401	ò	485 ProGluArgArgProGluGlyProGlyAlaGluAlaProSerSerProArgValThrGlu 504

326 548

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429 GCTGGGGGGGAGAAGCTAAAGAAGCTCATCGAACAGTACGCACTGAGGGAAGAGCACATTGA
                                                                                                                                              489 TAAGGTGTTCAAACATAAGGAACTGCAACAGCAGCTTGNTGGATGCCCCAAAACTGCAAN
                                                                                       308 pLysValPheLysHisLysAspLeuGlnGlnGln-LeuValAspAla---LysLeuGln-
                                                                                                                                                                                                                                         327 GlnAlaGlnGluMetLeu-LysGluAlaGluGluArgHisGlnArgGluLys 343
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Liu, Pu
APPLICANT: Liu, Pu
APPLICANT: Siciliano, Michael J.
APPLICANT: Clarkon, David
TITLE OF INVENTION: Markers for Detection of Chromosome
TITLE OF INVENTION: Rearrangements
UNDMERS OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
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CURENT APPLICATION DATA:
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATONNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 315-00869COB
TELECOMMUNICATION INFORMATION:
TELEFRENCE/POCKET NUMBER: 2115-00869COB
TELEFRENCE/POCKET NUMBER: 2115-00869COB
TELEFRENCE/POCKET NUMBER: 2115-00869COB
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TELEFRENCE
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INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
TISSUE TYPE: subtype (inv16)
POSTIION IN GENOME:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUNKESSEE: Harness, Dickey & Pierce, STREET: P.O. Box 828 CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08533306A
Patent No. 5837457
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STRANDEDNESS: double
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Sest Local Similari
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Pred. No.:
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JS-08-533-306A-5
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                                                                                                                16852 GCGCCTTGCTACCCAGGAGCACCGAGCACAGAGCATCAGGCCAGACTGGGCCTCAAGAG 16911
      16792 CCTGAGAGGACCAGAGGGCCTGGGGCTCAAGCACCCAGCTCCCCCAGGGTCACAGAA 16851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 GTTCAGAAGCAAATGAAGATCCTGCAGAAGCAAGCAAGCCCAGATTGTGAAAGAGAAAGTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sArgGluLeuGlnArgHisAsn--ArgSerLeuLysGluGluGlyValGlnArgAlaArg 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGluGlu-LysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIl 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 TCAAGCCCAGCTGGAGCAGGAGGAGCATGACATCCACAAACTCCGCAAACTCCGAAAACATTGA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 SerGiniysGinMetiysLeuLeuGiniysLysGinSerGinLeuValGinGluLysAsp 209
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                                                            AlaProCysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyProGlnGlu
                                                                                                                                                                                                                                                                                                                                Sequence 1333, Application US/09833381
Patent No. 6672186
GRNERAL INFORMATION:
APPLICANT: Robison.
TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT PAPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR PLING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                16912 cccaccrcccccaccc 16929
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                         525 ProThrSerAlaArgAla 530
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652.50
83.66%
71.29%
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                         RESULT 11
US-09-833-381-1333
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:::	303 -ArgGluGluHisIleAspiysValPhelysHisLyaAspLeuGluGluHisli	318 nGlnieuValAspAlaLys	1671 GAAGAAAGCCAAGAGCTTGGAAGCAGA	335 aGluGluarghisGinargGlubyshappheleuleulyschuararaigh 		Qy 372 aLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPh 392	Oy 392 eThrThrPheLysGlnGluMetGluLysMetThrLysLysLysLysLeuGluLysGl 412 :::	Qy 412 uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMetAl 431	431 2010	Oy 444 LeuGlnVallysileGlnArgleuGluLysLeu 454	455CysargalaLeuGlnThrGluargasnAspLeuAsnLysargValGl	Qy 470 nAspLeuSerAladlyGlnGlySerLeuThrAspSerGl 484	Oy 484 yProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGl 504	Qy 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 518	RESULT 13 US-08-742-923A-5 ; Sequence 5, Application US/08742923A ; Patent No. 5865611	; GENERAL INFORMATION: ; APPLICANT: Collins, Francis S. ; APPLICANT: Siciliano, Michael J.	; APPLICANT CLARGON, DATA ; TITLE OF INVENTION: Markers for Detection of Chromosome 16; TITLE OF INVENTION: Rearrangements; TITLE OF SEQUENCES: 14; CORRESPONDENCES: 14	SSEE: F
DB: US-10-023-523-8 (1-530) x US-08-533-306A-5 (1-2680)	3 SerProGlyGlnBro :: 582 GCTCCAGGACACCCAGGA	19 S 639 T	39 684	58	Qy 78 GlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluPro91	92	864 GAAGGCGCCCCTTATGATAAACTGGAAAAGACCAAGÀACAGGCTTCAGCAGGAGCTGGA 92 103 ArgasnGlygluProgluProthrProvalvalTyrGlygluLysGlu 11	Db 924 CGACCTGGTTGTTGATTTGGACAGCGGCAACTGGTGTCCAACCTGGAAAAGAAGCA 983 Qy 119 Pro		Db 1038GGATGAGAGGACAGAGGCAGAAGAGCCAGAGAGAGAGAGA	Db 1078GAAACCAA 1085 Qy 172 sLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192	Db 1086 GGCCCTGTCCTGGGCCCTTGAAGAGCCTTGGAAGCCAAAGAAGTGGAAGTGGAGGG 1145 Qy 192 sGlnMetLysLeuLeuGlnLysLySGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212	1146 GACCAACAAATGCTCAAAGCCGAAATGGAAGACCTGGTCAGCTCCAAGGATGACGTGGG 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe ::::::	1206 CAAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGGCCCTGGAGACCCAGATGGAGGAGT	Se Se AAGGG	Oy 267 pIleGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMe 287		Qy 294 sLysLeulleGluGlnTyrGluLeu302

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1491 GAAGAAGCTGGAAGGGGACCTGAAAGACCTGGAGCTTCAGGCCGACTCTGCCATCAAGGG 1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGACGCAGCTGGAAGAGCTGGAGGACGAG-----CTGCAAGCCTCGGAGGCCCCAA 1319
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                                              ArgAsn------GlyGluProGluProThrProValValTyrGlyGluLysGlu 118
1791 TAGCCTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGCTGGAGGCCCGGATCGC
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                                                                    984 GAGGAAATTTGATCAGTTGTTAGCCGAGGAGAAAAACATCTCCTTCCAAATACGC----
                                                                                                                                                                                                                                                                                                         sLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy
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|GGAAGAGGGGAAGAAGAGGTTCCAGAAGGAGATCGAGAACCTCACCCAGCAGTACGAGGA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GluAspAlaGluLysSerArgThrTyrValAla 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo TISSUE TYPE: Subtype (inv16)
POSITION IN GENOME:
                                                                                                        SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/7/*
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                    2115-00869DVC
                                                                                                                                                                       FILING DATE: No. 5869611ember 1, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
REFRENCE/DOCKET NUMBER: 211:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2680 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SerProGlyGlnPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA to mRNA
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38.90%
22.99%
10.31%
   CITY: Bloomfield Hills STATE: MI
                                                                       ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CD
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Best Local Similarity:
                                                           USA
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US-08-742-923A-5
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                                                           COUNTRY:
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MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
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38.90%
22.99%
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Best Local Similarity:
    STRANDEDNESS:
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                                                                                         uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuGluMet---Al
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                                                                                                                                                                                                                                                                           ----CysArgAlaLeuGlnThrGluArgAsnAspLeu-----AsnLysArgValGl
                              eThrThrPheLysGlnGluMetGluLysMetThrLysLysIleLysLysLeuGluLysGl
                                                             --CGGGTCCGCAAAGCCACACAGCAGCCGAGCAGCTCAGCAACGA
                                                                                                                                                                                                                  -----LeuGlnValLysIleGlnArgLeuGluLysLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08533306A
Patent No. 5837457
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Siciliano, Michael J.
APPLICANT: Collins, Francis S.
APPLICANT: Or INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 uAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 518
                                                                                                                                                   431 aGluGluLysThrValArgAspLys-----GluLeuGluGly----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
ATTORNEY/ADDAME:
                                                                                                                                                                                                                                                                                                                                      nAspLeuSerAlaGlyGlyGlnGlySerLeuThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
A1TORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
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INFORNATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
TYPE: nucleic acid
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|011 GGAAGAGGGAAGAAGAGTTCCAGAAGGAGATCGAGAACCTCACCCCAGCAGTACGAGA 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ArgAsn------GlyGluProGluProThrProValValTyrGlyGluLysGlu 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GluAlaGlyProGluGlyAlaGlnGluArgPro
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ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 1
IISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
IISSUE TYPE: subtype (inv16)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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	SASTITCAAG 18	Db 1818 AGAGCTGGAAGATGCCTGCCAGAGATGAGATCTTTGCCACAGCCAAAGAGAATGA 1877 Qy 325	Db 1878 GAAGAAAGCCAAGAGCTTGGAAGCAGACCTCATGCAGCTACAAGAGGACCTCGCCGCCGC 1937 Ov 335 aGluGluAzgHisGlnArgGluLysAspPheLeuLeuLysGluAlaValGl 352	1938 TGAGAGGCTCGCAAACAAGGGGACCTCGAGAA	98 TAGCCTGTCGGGAAGGAACGCACTCCAGGACGAGAAGCGCCGGCTGGAGGCCCGGGATCGC	2058 CCAGCTGCAGGAGCTGCAGGAGCAGCCAGCCAACATGCAGGCCATGAGCGAC	2113CGGGTCCGCAAAGCCACACAGGCGAGGCGAAGCAGCAAA	Oy 412 uThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuLeuLeuLeuLumetA1 431 	Qy 431 aGluGluLysThrValArgAspLysGluLeuGluGly	Oy 444 454	Oy 455CysargAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgValGl 470	470	Db 2397 GGAAATCTT-GCTGCAGGTGGAGGACGAGCGCAAGATGGCCGAGCAGTACAAGGACAGG 2455	2456 CAGAGA	2516 AGTCCCAGCGCATCAACGCCAACCGCAGGAAGCTGCAGCGGGA 25	RESULT 16 US-08-056-200-93 ; Sequence 93, Application US/08056200 ; Patent No. 5616500	WATION: Steiner Lee, Se Kim, In	APPLICANT: Caludy Social ; APPLICANT: Park, Sang-Chul ; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and ; TITLE OF INVENTION: Mehods of Using Same ; TITLE OF CONTRAINTON: 117	; NUMBER OF SEQUENCES: 11, ; CORRESPONDENCE ADDRESSES: ; ADDRESSES: Knobbe, Martens, Olson & Bear ; STREET: 620 Newport Center Drive, Sixteenth Floor
118-10-023-523-8 (1-530) x US-08-742-923A-3 (1-2887)	3 SerproglyglnProglualaglyProgluglyAlagluArgPro 1 ::	Qy 19 SerGinalaAlaProAlaValGluAlaGluGlyProGlySerSerGinAlaProArglys 38 	Oy 39 ProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGlu 57	Qy 58 GluLeuSerargGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGly 77 :: :: :: ::: :: Db 951 CATCCAGCTCTCCGACTCGAAGAAGAAGAAGAAGACTGCAGGACTTTGCCAGCACGGAGGAGCTCT 1010	Oy 78 GlybroGlyGluAspGlyAlaGlnGlyGluProAlaGluDro91	Oy 92	Oy 103 ArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGlu 118	119	1191 GAGGAATTTGATCAGTTGTTAGCCGAGGAAAAAAAAAAA		Db 1285GAAACCAA 1292 Oy 172 sLeuAlaAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192	1293 GGCCTGTCCCTGGGCCCTTGAAGGCCTTGGAAGCCAAAGAGAACTCGAGCG 13	Oy 192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysApH1sLeuAr 212	Oy 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232 	Oy 232 uGlnArgHisAsnArgSerLeuLysGluGlyValGlnArgAlaArgGluGluGluGl 252 ph 1473 gaagaggaggaggaggaggaggaggaggaCTGCAAGGCCTGGAAGGCCAA 1526	252	267	287	294

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                                  gThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGl
                                                                                                                1381 GCAGCAGCTGAGGCGCGAGGAGGAGGAGGCGCGAGCAGCAGCAGCTGAGGCGCGAGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaArgihrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeu 63
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959
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CURRENT APPLICATION DATA:
1.25
CURLENTION NUMBER: US/08/056,200
FILING DATE: .30-APR-1993
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GlyGlnProGluAlaGlyProGluGly.
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              IBM PC compatible
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                       OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Newport Beach
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STRANDEDNESS: sing
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Query Match:
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MOLECULE TYPE:
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ANTI-SENSE: N
FEATURE:
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FEATURE:
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CCATION: 16452511 FEATURE: NAME/KEY: CDS LCCATION: 25128070 US-08-800-644-93 Alignment Scores: 1.18e-13 Length: 9551 Score: 274.00 Matches: 140 Percent Similarity: 40.73 Mismatches: 235 Dest Local Similarity: 40.73 Mismatches: 235 Us-10-023-523-8 (1-530) x US-08-800-644-93 (1-9551)	Oy. 5 GlyGlnProGlualaGlyProGluGlyAlaGlnGluArgProSerGln 20	Qy 21 AlaAlaProAla 24 ::	Oy 25ValGlualaGluGlyProGlySerSerGlnalaBroArgLysProGluGlyAlaGln 43	Qy 44 AlaArgThrAlaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeu 63	Qy 64 GluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGly 83	Qy 84 AlaGlnGly-GluProAlaGluProGluAspAlaGluLysSerAr 98	Oy 98 gThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGl 118 :::	Qy 118 uProSerLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValG1 136 :::	Oy 136 yaspargasphisargargProGlnGluLysLysAlaLysGlyLeuGlyLysGluIl 156 :::::	Qy 156 eThrLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLe 176	Oy 176 uCysLysLysTyralaGluLeuLeu-GluGluHisArgAsnSerGlnLysGlnMetLysL 196	Oy 196 euLeuGlnLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisS 216	Oy 216 erLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisA 236	Oy 236 snargSerbeuLysGluGluGluGlnArgAlaArgGluGluGluGluL 253	253
427 euleuGluMetAlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValL 447	507 ysTyrProGlyAlaProSerThrGluAlaSerGlyGlnThrGlyPro 522	SULT 17 -08-800-644-93 Sequence 93, Application US/08800644	FACELL NO. 35307.108. APPLICANT: Steinert, Peter M. APPLICANT: Lee, Seung-Chul	APPLICANT: Kim, In-Gyu APPLICANT: Chung, So-Chul APPLICANT: Park, Sang-Chul TITLE OF INVENTION: Trichobyalin and Transglutaminase-3 and	TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCES: 117 CORRESPONDENCE ADDRESS: ADDRESSEE: Knobbe, Martens, Olson & Bear	STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach STATE: CA COUNTRY: U.S.A.	ZIP: 92660 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/800,644	FILING DATE: 14-FEB-1997 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/056,200	FILING DATE: 30-APR-1993 ATTORNEY/AGENT INFORMATION: NAME: Fedrick, Michael F. REGISTRATION NUMBER: 36,799	REFERENCE/DOCKET NUMBER: NIH054.001A TELECOMMUNICATION INFORMATION: TELEPHONE: (714) 760-0404 TELEPHONE: (714) 760-9502	INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS: LENGTH: 9551 base pairs TYPE: nucleic acid	ESS: line PE: C	ANTI-SENSE: NO FEATURE: NAME/KEY: CDS LCATION: 1507. 1644	

us-10-023-523-8.rni

CITY: PALO ALTO STATE: CALIFORNIA COUNTY: USA ZIP: 94304 COMPUTER READABLE PORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,655 - FILING DATE: HERRHITH CLASSIFTCATION DATA: APPLICATION NUMBER: 37,071 REGISTRATION NUMBER: 37,071 RECIPENCE/DOCKET NUMBER: 37,071 RECIPENCE/COCKET NUMBE	ignment Scores: ed. No.: ore: rore: str. Similarity: st Local Similari ery Match: : -10-023-523-8 (1-	239 LeuiysGluGluGlyValGlnArgAlaArgGluGluGluGluGluLySargLySGluValint	GindinaladindiumetleuLysGluala 3 CAGCAANCGACACACAGATAACAGAAANCGACACAGATAACAGAAGCT 1
	ysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaL	Db 4442 GGCTGAAGCGCGAGCATGAGGAAGA 4468 Qy 467 ysArgvalGlnAspLeuseraladlyGlydlnGlySerLeuThrAspSerGlyProGluA 487	RESULT 18 (US-09-023-655-548/C) Sequence 548, Application US/09023655) Patent No. 6607879) GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Gusan G. Stuart APPLICANT: Jeffrey J. Sellhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS: STREET: 3174 PORTER DRIVE

54 AspValSerGluGluLeu	Db 3081AAAGCTCAAGAAGAAGAGTTTGACATCAGTCAGCAGAACAG 3122 Qy 74 AsnAsnGlnGlyGlyProglyGluAspGlyAlaGlnGlyGluPro 88	3123	Qy 89 AlaGluProGluAspAlaGluLysSerArgThrTyrValAlaArgAsnGlyGluProGlu 108 Db 3183 GGCACGCATCGAGGACGAGTAGAGGCGGACGCACAC 3230	109 ProThrProValValTyrGlyGluLysGluProSerLysGlyAspProAsnThr-GluGl	3231 CCGGGC 128 ulleArgGlnSer- ::: 3282 GATCAGTGAGGGG	Qy 140 sArgArgProGlnGluLysLysLysLysGlyLeuGlyLysGlulleThrLeuLeuMe 160 :::	Oy 160 tGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTy 180	Oy 180 rAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLe 196	OY 196 uLeuGlnLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSe 216	Oy 216 rLysalaValLeuAlaArgSerLysLeuGluSerLeuCysArg230 ::: ::: :::	Oy 231GluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGl 245	OY 245 nArgAlaArg 248 :: Db 3675 GCGAGCCAAGAATGCGAATTGGCTAGGCAACTGGAAGAAAGGAAAGAAA		Db 3735 ACTGATTTGGCAGCTGACCCGGGGCAAGCTCTCCTATACCCAGCAGATGGACGCCTCAA 3794 Qy 249GluGluGluGluLy8ArgLy8GluValThrSerHisPheGlnValTh 264	3795	Db 3855 CCGCATGACTGCCGCCTGCTGCGGGAACAGTACGAAGAAATGGAGGCCAAGGCCGA 3914 OV 279	3915 GCTGCAGCGTGTCCAAGGCCAACTCAGAGGCCAGTGGAGGACCAAGTATGA	Qy 284GingluasnMetGluLeualadluargLeuLysLysLeuIleGluGl 299	Qy 299 nTyrGluLeuArgGluGluHisIleAspLysVal
376 GluiysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPhe 395 	396 LysGlnGluMet 399 :::	LESULT 19	NS-08-938-105-2. Application US/08938105 Patent No. 6353151	GENERAL INFORMATION: APPLICANT: Letimand, Leslie A. APPLICANT: Vikstrom, Karen L. TITLE OF INVENTION: TRANSCENIC MODEL FOR HEAPT FAILURE	ESS: dan Ross P.C. coln St., Suite 3500	STATE: CO COUNTRY: U.S.A.	, =	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/938,105 FILING DATE:	CLASS.FLATION: NAME: Crook, Wannell M. REGISTRATION WHERE: 31,071 REGISTRATION WHERE: 31,071		SEQUENCE CHARACTERISTICS: LENGTH: 5661 base pairs TYPE: nucleic acid carbannece. cind	2 · · >	NAME/KEY: CDS LOCATION: 15661 -08-938-105-2	1.67e-13 Length: 268.50 Matches:	rcent Similarity: 36.22% Conservative: 82 est Local Similarity: 24.57% Mismatches: 214 ery Match: 9.94% Indels: 236 3: Gaps: 31	-10-023-523-8 (1-530) x US-08-938-105-2 (1-5661)	3 SerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAla 22	Glnala	/sProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArg

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Henderson, Robert A
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     Yasir A.W
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; ORGANISM: Homo sapien
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                 1155 TGCG------GCCGCCGCAGCCTGGACAAAAAGCAGAAACTTCGACAAGATCCT 4205
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                                                                                                                         ----TGGAAGCAGAAGTATGAGGAGTCCCAGTCAGAGCTGGAGTCTTCCCA 4259
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 -PheLysHisLys-----AspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGl 327
                                                                                                uLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLe 367
                                                                                                                                                367 uLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLy 387
                                                                                                                                                                                                  sSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLyslle-- 406
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                                               nAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLe
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Patent No. 6426072
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Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
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Fan, Liqun
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APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Hosken, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GluValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGly 153
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APPLICANT: MCNGIII, PATRICIA D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455211
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFFWARE: FastSEQ for Windows Version 3.0
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Kalos, Michael D.

λŏ	243GlyvalGlnArgAlaArgGluGluGluGluLysArgLys 255	; APPLICANT: ; APPLICANT: ; TITLE OF INV
qq	5519 GGAGTACGATGACGTGAGGAGGACGAAGGGAGAGAGAGAG	; TITLE OF INV ; FILE REFEREN
ý	256GluvalThrSerHisPheGlnValThr264	CURRENT APPL
ΩP	5579 CTTGGAACTAAGGAGCCAGCTGCAGATCAGCAACAACAACCGGACCCTGGAACTGCAGGGGCT 5638	, NUMBER OF SE ; SOFTWARE: Fa
δλ		; SEQ ID NO 119 ; LENGTH: 894
qq	адаааттссаааа	, TYPE: DNA , ORGANISM: H
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qa	5699 GCAGGCTITAGAGGCATCTAATAGGATTCAGGAATCAAAGAATCAGTGTACTCAGGTGGT 5758	Alignment Score Pred. No.:
ò	LeuValAspAl	Score: Percent Similar
qa		Duery Match:
ò	323 aLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLy 343	UB:
g G	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
δλ	GlnArgMetCysGluLeuMetLysGlnGl	
qq	5850	DP 4895 G
ò	363 nGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAs 383	Oy 60 S
qq	5868 -GAAACCAGGGTGAAACAGCGCCTGGAGTGTGAGAAACAGCAAATTCAGAA 5917	Db 4955 C
. &	383 nThrieuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetTh 403	Oy 80 G
Db		Db 4973 d
λò	403 rLysbysjjelyslysleugjuLysgjuThrThrMetTyrArgSerArgTrpGluSerSe 423	Qy 99 T
ДQ	::: ::: :::	DP 5033 G
ζ	423 rAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 439	Qy. 119 F
QD	5985ACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 5048 G
ò	440GlubeuGluGlyJeuGlnValLysIjeGlnArgLeuGluLysLeuCysArg 456	Oy 134 G
qq	:::	DD 5108
λŏ	457	Qy 154 I
qq	6080 GCTGGAGGATTCTACCAGGGAGACACTCACAGTTAGAAACAGAACGCTCCCGATATCA 6139	Db 5159 (
δλ	466 nLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGl 486	Oy 173 t
q	6140 GAGGGAGATTGATAAAACTCAG 6160	Db 5219 1
ò	486 uArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaPr 506	Oy 192 E
Q C	6161 ACAGCCCCATATGGGTCCCATCGAGAGACCCAGACTGA 6199	Db 5279 (
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οp	 6200 GTGT 6203) 6223 qq
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, Pate,	nt No. 6482597 RAL INFORMATION:	Qy 228 1
APP	, APPLICANT: Wang, Tongtong APPLICANT: Fah, Light Annual Manna	Db 5459 (
. HEE	DICANT: HOSKem, wancy of	

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INVEXTION: COMPOUNDS AND METHODS FOR THERAPY INVEXTION: COMPOUNDS AND METHODS FOR THERAPY SHENCE: 210121.455C6
APPLICATION NUMBER: US/09/480,884A
FILING DATE: 2001-08-27
FREQ ID NOS: 330
FREQ ID NOS: 330
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ð.	243GlyValGlnArgAlaArgGluGluGluGluLysArgLys 255	; APPLICANT: Hosken, Nanc
В	5519 GGAGTACGATGACCTGAGGAGGAGGAGGGAAGCGGACAGGTGATAAAAATGCAACCAT 5578	; TITLE OF INVENTION: COI
ò	256GluValThrSerHisPheGlnValThr	; FILE REFERENCE: 210121 ; CURRENT APPLICATION NUM
qq	5579 CTTGGAACTAAGGAGCCAGCTGCAGATCAGCAACAACGGGACCCTGGAACTGCAGGGGCT 5638	CURRENT FILING DATE: 20
ò	265 -LeuAsnAspIleGlnLeuGlnMetGluGlnHisAenGluArgAsnSerLysLeuArgG1 284 ::: :: ::::	; SOFTWARE: FASTSEQ for W
ДQ	5639 GATTAATGATTTACAGAGAGAGAGAAAATTTGAGACAGGAAATTGAGAAATTCCAAAA 5698	; LENGTH: 8948 ; TYPE: DNA
ò	284 nGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuAr 303	ORGANISM: Homo sapien US-09-542-615A-119
Q	5699 GCAGGCTTTACAGGCATCTAATAGGATTCAGGAATCAAAGAATCAGTGTACTCAGGTGGT 5758	Sco
ò	luHisIleAspLysValPheLysHisLysAspLe	
ପୁପ	5759 ACAGGAAAGAGAGACCTTCTGGTGAAAATCAAAGTCCTGGAGCAACAAGACAAGGC 5812	it Similarity:
ò	323 aLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLy 343	Query Match: 9.0
QQ	5813 AAGGCTGCAGAGGCTGCAGGATGAGCTGAATCGTGCA5849	-10-023-523-8 (1-530)
δλ	343 sAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGl 363	luglvAlag
do ,	5850AAATCAACTCTAGAGGCA	4895
VO.	nGluThrHisleuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAs	Qy 60 SerArgGlnLeu
đ		Db 4955 CTA
ď	383 nThrLeuSerIysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetTh 403	Qy 80 GlyGluAsp0
QΩ	5918 TGACCTGAATCAGTGGÄÄĞACTCAATATTCGCGCAAGGA 5956	 -
λΌ	rLysLysIleLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSerSe ::: :::	Qy 99 ThrTyrValAla
qq	5957 GGAGGCTATTAGGAAGATAGAATCGGAA	Db 5033 GCT
<i>λ</i> ο	423 rAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys 439	Qy 119 ProSerLysGly
qo	5985AGAĞAÀAĞAGTGAGAĞAĞAĞAĞAĞAĞAĞAĞAĞAĞAĞAĞAĞT	
ò		
qq	6020 GAGTGAGATCGAAGACTCCAAGCAGAGATCAAGAGATTGAAGAGAGGGGCGTAA 6079	\$108
ò	457	154
Ωp	6080 GCTGGAGGATTCTACCAGGGAGACACAGTCACAGTTAGAAACAGAAGGCTCCCGATATCA 6139	Db 5159 CATCAAAATCAC
ò	466 nlyshrgValGlnAspLeuSerAlaGlyGlyGlyGerLeuThrAspSerGlyProGl 486	173
qq	6140 GAGGGAGATTGATAAACTC	5219
ò	ProGlyAlaGlnAlaProSerS	192
qa	6161 ACAGCGCCCATATGGGTCCCATCGAGAGACCCAGACTGA 6199	5279
È	506 ocys 507	200
da	6200 GTGT 6203	5339
RESULT US-09-	RESULT 22 US-09-542-615A-119	219
; Seg. ; Pate	; Sequence 119, Application US/09542615A ; Patent No. 6518256	::: Db
GENE APP	KAL INFOKWATION: LICANT: Wang, Tongtong	Oy 228 uCysArgGluLe
APE	LICANT: Fans, Michael D. LICANT: Banqur. Chaitanya S.	Db · 5459 CACAGAGAACCT
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AAAGTGTCAAAGAAGCTCACTTGAGGAATGAGCATTTCCAGAAGGGGAT 5398
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Nancy A.
Gary R.
COMPOUNDS AND METHODS FOR THERAPY
AND DIAGNOSIS OF LUNG CANCER
121.455C8
NUMBER: US/09/542,615A
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243	APPLICANT: Hosken, Nancy APPLICANT: Fanger, Gary R. APPLICANT: Li, Samuel X. APPLICANT: Nang, Adjun	; AFFLICANI: SKEIKY, IGSII A.M. ; TITLE OF INVENTION: COMPOSITII ; TITLE OF INVENTION: AND DIAG	CURRENT APPLICATION NUMBER: UCRRENT FILING DATE: 2000-06 NUMBER OF SEQ 1D NOS: 358	; SOFINARE: FASTSED TOT WINDOWS; SEQ ID NO 119 ; LENGTH: 8948 ; TYPE: DNA	OKGANISM: HOMO sapien 9-606-421B-119 nment Scores:	larity	arity:	US-10-023-523-8 (1-530) x US-09-	Qy 40 Gludiyaladinalaarg ::: Db 4895 GACGGAGACAATAAACAA	Qy 60 SerArgGlnLeuGluAsp	Db 4955 CTA	Oy 80 GlyGluAspGlyAla	Qy 99 ThrTyrValAlaArgAsn	Db 5033 GCT	Oy 119 ProSerLysGlyAspPro	134	Db 5108 GAAGCTGGAGGAAGACT	Qy 154 LysGlu-IleThrLeuLe	DD 5159 CATCAAAATCACCAACCT	Qy 173 uAlaAlaLeuCysLy	Db 5219 TGAGGATGACCTCCGGCA	Qy 192 sGlnMetLysLeuLeuGl	Db 5279 GACCCAGGAAGAGCTGAG	Qy 205 lGlnGluLysAsp	Db 5339 CCAGGAACAGGAAGTGT	219 lLeuAlaArgSer	5399	l Qy 228 ucysargGlubeuGlube
	243GlyValGlnArgAlaArgGluGluGluGluLysArgLys 255 5519 GGAGTACGATGAGAGGAGGAGCGAAGCGGACGATGATAAAATGCAACCAT 557	256Gluvalintserhistnedinvalint	265 -LeuasnaspileginLeuginMetGluGinHisasnGluargasnSerlysLeuargGl 284 ::: ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::: ::::::	284 nGluAsnMetGluLeuAlaGluArgLeuLysLysLeuIleGluGlnTyrGluLeuAr 303	303 gGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAl 323 :::	323 aLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLy 343	5813 AAGGCTGCAGAGGTGGAGGATGAGCTGAATCGTGCA		363 nGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAs ::::: 5868 -GAAACCAGGGTGAAACAGCGCCTGGAGTGTGAGAAACAGCAAATTCAGAA	383 nThrheuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMetTh	5918 TGACCTGAATCAGTGGAAGACTCAATATTCCCGCAAGGA	403 rLyslysllebyslysleuGlulysGluThrThrMetTyrArgSerArgTrpGluSerSe ::: ::: :::	423 rAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLys	5985AGAĠAĀĀĀĀĀĀGĀGĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀĀ	440GluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArg 456	45741aLeuGlnThrGluArgAsnAspLeuAs 466	6080 GCTGGAGGATTCTACCAGGGAGACACAGTCACAGTTAGAAACAGAAGGCTCCCGATATCA 613	466 nLysArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuThrAspSerGlyProGl	6140 GAGGGAGATTGATAAACTCAG 616	486 uArgArgProGluGlyProGlyAlaGlnAlaProSerFroArgValThrGluAlaPr	6161 ACAGCGCCCATATGGG	506 oCys	6200 GTGT	ESULT 23 S-60-606-4218-119	Squence 119, Application US/09606421B		APPLICANT: Fan, Liqun APPLICANT: Kalos, Michael D.	Bangur, Chaitanya

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5399 AGAAGATAAAAGCAGAAGCTTAAATGAAAGCAAAATAGAAATTGAGAGGCTGCAGTCTCT 5458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyPro
AT A.W.
POSITIONS AND METHODS FOR THE THERAPY
THO DIAGNOSIS OF LUNG CANCER
455C9
FIBER: US/09/606,421B.
                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                   JS-09-606-421B-119 (1-8948)
                                                                                                                 indows Version 3.0
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; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER; CURRENT APPLICATION NUMBER: US/09/221,107; CURRENT APPLICATION NUMBER: US/09/221,107; CURRENT FILING DATE: 1998-12-22; NUMBER OF SEQ ID NOS: 161; SOTTWARE: Patentin Ver. 2.0; SOTTWARE: Patentin Ver. 2.0; SOTTWARE: Patentin Ver. 2.0; TYPE: DNA; ORGANISM: Human US-09-221-107-119 Alignment Scores: 3.62e-13 Length: 8948 Fred. No.: 268.00 Marches: 128 Score: 268.00 Marches: 145 Percent Similarity: 23.62* Mismatches: 179 Opery Match: 25	-023-523-8 (1-530) x US-09-221-107-119 (1-8948) 40 GluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuA :::	A 504; P 133 A 510° A 510° A 510° A 510° A 510° A 510° A 510° A 515° A 51° A	Db 5219 TGAGGATGACCTCCGGCAGCAGGAGGATGGCTGGATGGCCACCTGAGGGAAAAGCAGAG 5278 Qy 192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuVa 205	228 2459 243 5519
Db 5459 CACAGAGAACCTGACGAGGAGCACTTGATAGAGAAGAAGAACTGCGGAACCTGAGGT 5518 Qy 243GlyValGlnArgAlaArgGluGluGluGluGluGluLyBArgLy8 255 Db 5519 GGAGTACGATGACCTGAGGAGCGAACGGAACGGACAGTGATAAAAATGCAACCAT 5578 Qy 256GluValThrSerHisPheGlnValThr	Oy 303 gGluGluHisTleAspLysValPheLysHisLysAspLeuGlnGlnLeuValAspAl 323 :::	383 5918 403 5957 423 5985 6020	Oy 457	Db 6200 GTGT 6203 RESULT 24 US-09-221-107-119 ; Sequence 119, Application US/09221107 ; Pathor No. 6660338 ; APPLICANT: Wang, Tongtong

1—4 H—H	GluvalThrSerHisPheGlnValThr
	nGluAsnMetGluLeuAlaGluArgLeuLysLysLeulleGluGlnTyrGluLeuAr 303 :::: ::: GCAGGCTTTAGAGGCATCTAATAGGATTCAGGAATCAAAGAATCAAGAGTGTACTCAGGTGGT 5758 GGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAl 323 ::: :::
30 0	lnArgGluLy etLysGlnGl
i ⊒	
01 - E	nThrLeuSerLysSerSerGluvalPheThrThrPheLysGlnGluMetGluLysMetTh 403
4 1 1 A	
GA JVa JVa	
rgPr 	oGludlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaPr
t io	SULT 25 1-08-875-435B-5 Sequence 5, Application US/08875435B Patent No. 6593304 APPLICANT: Hascawa Kazuhide

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TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM. ISOFORM PROTEIN INSERTED INTO
TITLE OF INVENTION: VECTOR DNA, MICRORGANSIM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCIEROSIS COMPRISING THE
FILLE OF INVENTION: RECOMBINANT DNA
FILLE REFERENCE: 07898-013001
CURRENT APPLICATION NUMBER: US/08/875,435B
PRIOR RAPLICATION NUMBER: PCT/JP96/00134
PRIOR FILING DATE: 1996-01-25
PRIOR FILING DATE: 1996-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3912 GCGGGCCCGGGGCGCGCGACGACGACGACCACAAGCTGCAGAATGAAGTGGAGGCGT 3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3972 CACGGCATGCTCAGCGAGGCCGAGGGCAAGGCCATCAAGCTGGCCAAGGAGGTGGCGTC 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4032 CCTCGGGTCCCCAGCATCCCAGGATACCCAGGAGCT-----GCTCCAAGAAGAAACCCGGCA 4085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 gGlmLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4086 GAAGCTCAACGTGTCCACCAAGCTGCGGCAGCTGGAGGAACAGGAACAGCCTGCAGGA
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4398 AGACTIGGATAACCAGCGGCAACTGGTGCCAACCTGGAAAGAAGCAGAAGAAGTTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 uAspGlyAlaGlnGlyGluProAlaGluPro------
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208
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Oryctolagus cuniculus
)8-875-435B-5
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261.50
37.54%
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t Local Similarit;
ry Match:
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LENGTH: 6644
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-----ThrProGluGluLysLeuAlaAlaLeuCysLysLysLysAlaGl 182

168

Arakawa, Emi Oda, Shoji Matsuda, Yuzuru Takahashi, Katsuhito Sugahara, Michihiro Ishiyama, Haruo

APPLICANT: Hasegawa, Kazuhide APPLICANT: Arakawa, Emi APPLICANT: Oda, Shoji APPLICANT: Marsuda, Yuzuru APPLICANT: Takahashi, Karsuhite APPLICANT: Ishiyama, Michihiro APPLICANT: Ishiyama, Haruo

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5583 GGTTGAGCAGGAGGCCAGAGAGAAGCAGGCGGCCGCCAAGGCGCTGAAGCAGAGGGACAA 5642
                                                                                                                                                                               5761
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                                                                                                                                                                            5702 AGGAGCAGGCAGAAAAGGAAACGCCAAGGTCAAGCAGCTCAAGAGGCAGCTGGAGGAG
                                                                                   5643 GAAGCTGAAGGAGATGCTGCTGCAGGTGGAAGACGAGCGCAAGATGGCTGA-GCAGTACA
                                                                                                                                 n-----ThrGluArgAsnAspLeuAsnLysArgValGlnAspLeuSerAlaGlyGl
                                           sGluLeuGluGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                          yGlnGlySerLeuThrAspSerGlyProGluArgArgProGlu----
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                                                                                                                                                                                                                                                                                                                  491 -----GlyProGlyAlaGlnAlaProSerSerProArg 501
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CITY: BOSTON
STATE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Policy
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FILING DATE:
ATTORNEY DATE:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-(
TELECHONE: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08195487 Patent No. 5783403
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PRIMARY STRUCTURE OF
PROTEIN THAT DEFINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1.6306
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HUR
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EDNESS: singl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5283 TGAGAAGCGCCGCCTGGAGGCCCGGATCGCACAGCTGGAGGAGGAGCTGGÀGGAGGAACA 5342
                     4518 CGAGGCTGAAGCAAAGGAAAAGGAAAACCAAGGCCTTGTCCCTGGCTCGGGCCCTCGAGGA 4577
                                                                                                                                                                                                    1638 AGACCTCGTCAGCTCCAAGGACGACGTGGGCAAGAACGTCCATGAGCTGGAGAAGTCCAA 4697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 uLysaAspPheleuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGl 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SerSerGluValPheThr-------ThrPheLysGlnGl 398
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                                                                   uLeuLeuGluGluHisArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSe 202
                                                                                                                                                         rGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaAr
                                                                                                                                                                                                                                                  222 gSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGl
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. PAGES: 1395-1408 DATE: MAR-1992 US-08-195-487-3	t Scoi Simila al Sir tch:	10-023-523-8 (1-530) x US-08-195-487-3 (1-6306) 3 SerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAla 2	CGCCAGGGTCCTGGAGAAGGAGGGGGAGAGAGAGAGAGAG	43	Oy 57 GluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln 76	Oy 77 GlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLys 96	Oy 97 SerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGlu 116	Oy 117 LysGluProSerLysGlyAspPro-AsnThr	127	134 uValGlyAspArgAspHisArgArgProGlnGluLysLysLysAlaLysGlyLe 15	Oy 152 uGlyLysGluIleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLy 172	172	Oy 192 sGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuAr 212	Oy 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232	Oy 232 uGlnargHisAsnargSerLeuLysGluGluGlyValGlnArgAlaargGluGluGl 251	Qy 251 uGluLysArgLysGluValThrSerHisPheGluValThrLeuAsnAspIleGlnLeuGl 271

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PRIMARY STRUCTURE OF OF NUMA, AN INTRANUCLEAR
PROTEIN THAT DEFINES A NOVEL PAITWAY FOR
SEGREGATION OF PROTEINS AT MITOSIS
STOURNAL OF CELL BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3798 GGAGAGCTGCGCTGCTGCAGGCAGAAGAACAGCAACAGTGCC
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| GAACGCAGCTCTGCGGGAGGAGGTGCAGAGCCTC----
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
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ATTORNEY/AGENT INFORMATION:
NAME: FITCHER ESQ, EDMUD R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPRONE: 617/248-700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPTON, DUANE A SZILAK, ILLYA
                                                                                                                                                                                                                                                                                                                                  LENGTH: 6306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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38.42%
23.16%
9.40%
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PUBLICATION INFORMATION:
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Best Local Similari
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AUTHORS:
AUTHORS:
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Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: DB: Match: US-10-023-523-8 (1-530) x US-08-46 Qy 3 SerProGlyGluble Db 3714 TCGCCAGGTCCTGGAGAAG	23	3798	Oy 57 GluGluLeuSerArgGlnLe	Qy 77 ClyGlyProGlyGluAspGl Db 3897 GGAGGCTGAGAACAGCGG	Oy 97 SerArgThrTyrValAlah Db 3951ACAGGCTGAGCGTC	Oy 117 LysGluProSerLysGlyAse Db 4005 GTTCTTCAGAAAGAGCAGG	Qy 127	4065 134 4125	Qy 152 uGlyLysGlulleThrLeuI 	Qy 172 sLeualaalaLeuCysLysI ::: ::: 4245 GGTGGCAGGAGCGAAGCGAA	Qy 192 sGlnMetLysLeuLeuGlnI :: :: ::: bb 4305 GCAGCTGAGCATGAAGA	Qy 212 gGlyGluHisSerLysAla\ [Qy 232 uGinargHisAsnargs	251	Qy 271 nMetGluGlnHisAsnGluA
Db 4965 TGAACAGACCTGCCGCCACCTTACTGCCCAGGTGCCCTGGAGGCACAGGTTGCCCA 5024 Qy 470GlnAspLeuSerAlaGlyGlnGlySerLeuThrAspSerGlyProGl 486	Qy 518 yGlnThrGlyProGlnGluProThrSer 527 ::: bb 5202 CACCAGGGGCCCTGGAGAACCAGCCTCA 5229	RESULT 28 US-08-466-390-3 ; Sequence 3, Application US/08466390 ; Patent No. 568562	SENERAL INFORMATION: APPLICANT: LIDGARD, GRAHAM P TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE	ITZ & THIBEAU	STREAT: 125 HIGH STREET ; CITY: BOSTON ; STATE: MA ; COUNTRY: USA	; ZIP: 02110 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	; APPLICATION NOWBER: US/08/466,330 ; FILING DATE: 06-UNN-1995 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INCRMATION: ; NAME: FITCHER ESO. EDWUND R.	REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: MTP-013 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000	_ U = -	; TYPE: MUCLEUC acld ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: cDNA	; FEATURE: ; NATURE: CDS ; LOCATION: 16306 ; PUBLICATION INFORMATION:	AUTHORS: COMPTON, DUANE A JATHORS: SZILAK, ILVA AUTHORS: CLEVELAND, DON W JITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR	; TITLE: PROTEIN THAT DEFINES A NOVEL PAIHWAI FOK ; TITLE: SEGREGATION OF PROTEINS AT MITOSIS ; JOURNAL: J. Cell Biol. ; VOLUME: 116 ; PAGES: 1395-1408	DATE: 1992 US-08-466-390-3

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GlyaladlnGlyGluProAlaGluProGluAspAlaGluLys 96
                                                                                                                                                                                                                                                                                                                                    PAACCTIGGCCGGCAGTTTCTGGAAGTG------GAGTT 4406
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|CGTGAGGAGCTGGAGCAGAGCAGCCGCTGGGGGACT 4184
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3AAGGCGCATGGCCTGCTGGCAGAGAAC------CG 4355
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gecentreacetigeageticaacaeacaeacaeacaea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192
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                                                                                                                                                                                                                                                                                                                                                                                LeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln 76
                                                                                                                                                              AlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAla 22
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Length:
Matches:
Conservative:
Mismatches:
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MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                        331 tLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLeuLeuLysGluAlaVa 351
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                                                                                                                                311 eLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluMe 331
                                                                                                                                                                                                                                                                                                              351 IGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnLe 371
                                                                                                                                                                                                                                                                                                                                                                                                 371 uAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSerGluVa 391
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APPLICANT: TOURATLY, GARY
APPLICANT: TOURATLY, GARAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                     1584 AGAGAGGCAGAAACTCACTGCCCAGGTGGAA-----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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3951 -----ACAGGCTGAGCGTGCGCAGGAGCTGGGCCAAGAATTGAAGGCGTGGCAGGAA 4004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: COMPTON, DUANE A
AUTHORS: SZILAK, ILYA
AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SEGREGATION OF PROTEINS AT MITOSIS
JOURNAL: J. Cell Biol
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: OS-JUN-1995
CLASSIPICATION: 536
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Mismatches:
Indels:
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Matches:
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE FOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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38.42%
23.16%
9.36%
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PAGE
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LOCATION: 1..6306
PUBLICATION INFORMATION:
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APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS (
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
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SOFTWARE: Patental
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 27, 829
REFERENCE/DOCKET NUMBER: MTP-OT
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
INFORMATION FOR SEG ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08467781 Patent No. 5780596 GENERAL INFORMATION:
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LOCATION: 1..6306
PUBLICATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: SZILAK, ILYA
AUTHORS: CLEVELAND, DOI
TITLE: PROTEIN THAT DEI
TITLE: SEGRECATION OF I
JOURNAL: J. CELL Biol.
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MOLECULE TYPE:
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|GCAGCTGAGCATGCTGAAGAGGGGCATGGCCTGCTGGCAGGAGGAGGAAC-----CG 4355
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1005 GITCTICCAGAAAGAGCAGGCCCTCTCCACCTGCAGCTCGAGCACACCAGCACACAGGC 4064
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Alignment Scores: 4.52e-12 Length: 6306 Score: 253.00 Matches: 132 Percent Similarity: 38.42% Conservative: 87 Best Local Similarity: 23.16% Mismatches: 242 Query Match: 1.36% Indels: 109 DB: 20	US-10-023-523-8 (1-530) x US-08-467-781-3 (1-6306) QY 3 SerProGlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAla 22 Db 3714 TCGCCAGGTCCTGGAGAGGGGGGAAG	3.7 £ 4. 4. 6. 7.6 £	57 GludluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsnGln	,	Db 3951AcAGGCTGAGGTGCGGAGGCTGGGCCAAGAATTGAAGGCGTGGCAGGAGA 4004	QY 127	Oy 134 uValGlyAspArgAspHisArgArgProGlnGluLySLySLySAlaLySGlyLe 152	Db 4185 GCGGGCAGAGCTGCGGGCCCCAGCGGGAGCTTGGGGAGGTTCCTCTGCGGGAGAA 4244 Qy 172 SLeualaalaleuCysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLy 192 ph 4246 GCGGGCAGAGGGAGAGGGAGAGGGGGGGGGGGGGGGGG	192 4305	Qy 212 gGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLe 232	Qy 232 uGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGl 251	Qy 251 uGluLysArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeuG1 271	Qy 271 nMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGl 291 :::::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SEGRECATION OF PROTEINS AT MITOSIS
                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Gaps:
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TILLING LALL: 0.1-0004 13.5

ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELEPHONE: (617) 248-7000
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TELEPHONE: (617) 248-7100
OPERATING SYSTEM: PC-DOS/MS-DOS
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38.42%
23.16%
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                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUA
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1395-1408
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Query Match:
                                                                             FILING DATE:
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Qy 103 gAsnGlyGluProGluProThrProValValTyrGlyGluLy 117 : : : : : : : :	117 sGluproserLysClyAspProAsnThrGluglulleArgGlnSerAspGluValGlyAs ::: ::: ::: 1018 AGCCACTGCTGCCAGGACA-CGGCAGGATGAAGGTGCTGCAGGCA	137 pArgAspHisArgArgProG1	157 rLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCy	177 sLystyrkladluLeuLeuGludluHisAr 	r	217 SA : 1229 GC	237	257	1335		Qy 316 uGlnGlnCeuValAspAlaLysLeuGlnGlnAlaGlnGlu330 :::	331		1625	Db 1676 TGGGGAGAGCTCAGAGCTGCAGAGCTGGAGCAGCAGCAGCAGCAGCAGAGCTGAGGAGCTGCAGAGCTGCAGAGCTGCAGAGCTGCAGAGCTGCAGAGCTGCAGAGCTGCAGAGCTGAGCTGCAGAGAGCTGCAGAGCAGAGAGCAGAGAGAG	nLeublaLeuTyrThrGluLysPheGluGluPheGlasnThrLeusertysSersergi 	Oy 390 uValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIJeLysLysLysLeu 409 1796 CGAGGGTGGGGCCCGGGCCCAGGTGGTGGTGGTGGTGGTGTGTGT	Qy 410 -GluLysGluThrThrMetTyrArgSerArgTrpGluSerSerAsnLysAlaLeuGl
470GlnAspLeuSerAlaGlyGlyGlyGlyGerLeuThrAspSerGlyProGl 486	486 uArgArgProGluGlyProGlyAlaGlnAlaProSerSerProArgValThrGluAlaPr 506 5085 cGGGGGTGGAGTTGAGAGCCTGGATTGACAGCCTGGATGTGAG 5141	506 oCysTyrProGlyAla	518 yGlnThrGlyProGlnGluProThrSer 527	IBSULT 32 15-09-976-594-640 : Sequence 640, Application US/09976594 Parent No. 6673549	O. 907.517. NT: Furness, Michael NT: Buchbinder, Jennes Ryperske IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS		PRIOR FILLION MODILE: 20/00-12 NUMBER OF SEQ ID NOS: 1143 SOFTWARE: PERL Program	O ID NO 040 LENGTH: 5185 TYPE: DNA ORGANISM: Homo sapiens	FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. 6673549 346209.3 -08-976-594-640	5.62e-12 Length: 250.50 Matches:	Partent Similarity: 22.80% Mismatches: 232 Query Match: 9.27% Indels: 24 OB:	US-10-023-523-8 (1-530) x US-09-976-594-640 (1-5185)	5 GlyGlnProGluAlaGlyProGluGlyAlaGlnGluArgProSerGlnAlaAlaProAla 24	25 ValGlubla 27 671 GCGATACGAGATCCTGACACCCAATGCCATCCCCAAGGCTTCATGGATGG		AlaargThrala-GinSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLe	uGluaspileLeuSerThrTyrCysValaspasnAsnGlnGlyGlyFroGlyGluAspGl	oGluAspAlaGluLysSerArgThrTyrValAlaAr

65 AspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 80	.81 GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArg 98	ThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGlu	596 ACAAGAGCATCAGATCCACCACCCCAAGTATCTCGTCACAAATCA 646 119 ProSerLysGlyAspProAsnThrGluGlulleArgGlnSerAspGluValGlyAspArg 138 :::	647 CACTATCGTAATCGAGAACACTTTGCTACTÁTÁCGGACAGCATCACTGGTT 697 139 AspHisArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLySGlulleThr 157	698ACGAĞGCAAATGCAAĞAACATGAGGACTCTGAĞCTTAGAGAACAAATGTCTGGC 754 158LeuleuMetGlnThrleuAsnThrleuSerThrProGluGluLysleuAla 174		815 GCTGAGATGAAGATCACCTCAGATTAGACAAGATCTTGAAACTCAGCGTAACAAT 874 190SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu 207 110SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu 207 110	208		238 SerLeutysGluGlyValGlnArgAlaArgGluGluGluGlu 252	253LysargLysGluValThrSerHisPheGlnValThrLeuAsnAspIle 268 1109 CTTTCAAAGCAGAAGAAATATACAGCATTTCCAAGCAGAAGAAGAAGCACTTCTT 1168	269 GlnLeuGlnMetGlu 273 ::: ::: 1189 CGACGTCAAAGAAATACCTAGAAATGCCGTCGCTTCAAGAGAAGAATGTTACTT 1228	274GlnHisAsnGluArgAsnSerLysLeuArgGln 284	285 GluasnMetGluLeualaGluargLeuLysLeuIleGluGlnTyrGluLeuargGlu 304	GluHislleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLys	LeuGlnGlnAlaGlnCluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAsp 	PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGluGluGluGluAlaVallGluAlaVallGluAlaVallGluAlaVallGluAlaVallGluAlaVallGluGluAlaVall	1454 CTAAGACGAAAGCATGTCTGGAAGTTCGACAACAGCCTAAGAGTTTGAAGTCTAAAGAA 1513
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Qy 429 uMetAlaGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLy 447 Db 1895 GACCAAGGGGAGAAAGCAGGGGGGGGCGGGGGGGGGGG	GCTGGAGGACACGCTGGACTCCACCAACGCACAGGAGCTCCGGTCCAAGAGGGAACA	Oy 449 nArgLeuGlülysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgVa 469	Qy 469 lGlnAspLeuSerAla	Oy 483 rGlyProGluArgArg	Oy 497 OSerSerProArgValThrGluAlaProCysTyrProGlyAla 511	Oy 512ProSerThrGlualaSerGlyGlnThrGlyPro 522	RESULT 33 US-09-688-188B-20 ; Sequence 20, Application US/09688188B ; Patent No. 6656716	GENBEAL INFORMATION: APPLICANT: PLOWMAN, GREGORY APPLICANT: MARTINEZ, RICARDO APPLICANT: WHYTE, DAVID	TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES FILE REPERENCE: 038602/038602/038602/038602/03868/188B CURRENT APPLICATION NUMBER: US/09/688,188B CURRENT FILING DATE: 2000-10-16	999- 999- MBER 998-	NUMBER OF SEQ 1D NOS: 155 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 20 LENGTH: 3824	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-688-188B-20	Alignment Scores: Pred. No.: 5.38e-12 Length: 3824 Score: 248.50 Matches: 139 Percent Similarity: 39.75% Conservative: 117	21.58% Mismatches: 9.20% Indels: 4 Gaps:	US-10-023-523-8 (1-530) x US-09-688-188B-20 (1-3824) QY 23 ProAlaValGluAlaGlu28	326 CCAGCAGTAGAAGCACAGGAAGAAGAAGAACAAGATCATGGTGTTGGCCGGACAGGA 385 29GlyProGlySerSerGlnAlaProArgLysProGluGlyAlaGlnAla 44	386 ACAGTTAATAGTGTTGGAAGTAATCAATCCATTCCCAGCATGTCCATCAGCAGCAGC 445 45 ArgThraladinserdivalalenaroasovalserginglulenserargginfengin 64	

Percent Similarity: 39.75% Conservative: 117 Best Local Similarity: 21.58% Mismatches: 197 Ouery Match: 9.20% Indels: 29 DB: 29	(0) x US-09-291-417D-20 (1-3824)	Oy 23 ProalaValGluAlaGlu	Oy 29GlyProGlySerSerGlnAlaProArgLySProGluGlyAlaGlnAla 44	Qy 45 ArgThralaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 64 ::::::::: ::::	65 AspIleLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly 8	Db 503 ATGATGGAGGAGACCACACAGTGATGTCTAACAGTTCTGTTATCCATTTAAAACCAGAG 562 Ov 81 GluaspGlyAlaGlnGlyGluProAlaGluAspAlaGluLysSerArg 98	263	64	Oy 119 ProserLysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArg 138	Oy 139 AspHisArgArgProGlnGluLySLySLySAlaLySGlyLeGlyLySGlulleThr 157	158 -	Db 755 TATAAGCGAATTGAGGCGACATCAAAAGCAACTTGATGACTCTGGAAAAAAAA		Qy 190SerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu 207 ::: :::	Oy 208	66	Qy 218 AlavalLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnArg 237	238 SerLeuLysGl	Db 1049 CAGCTTAAAGAGGAGCTAAATGAAAACCAGAGTACCCCCAAAAAAAA		09 CTTTCAAAGCAGAAGAGAATATACAGCATTTCCAAGCAGAAGAAGAAGCIAACCIICII	Cy 269 GlnLeuGlnMetGlu	Qy 274GluhisAsn	
2y 365 ThrHisLeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380.		401 LysMetThriysLysIleLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrp 420		Db 1673 GAGCAGTATGATCACAGCATTAATGAAATGCTCTCCACACAAGCCCTGCGTTTGGATGAA 1732 Qy 437	Db 1733 GCACAGGAAGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGGAACTGGAAGTGTTG 1792		Oy 443 GlyLeuGlnValLysIle	455	470 GlnAspLeuSerAlaGlyGlnGlySer	Db 1973 AGAGAGATTGAAGCTTTTGACTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCCTT 2032 Qy 481 ThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro 500	2033 TCTAATCTCTCCCTGAG	Oy 501 ArgValThrGluAlaFroCyGTyFrOGlyAlaProSerThrGluAlaSerCtly 518 Db 2051GCATTCAGCCACAGCTACCCGGGAGCTTCTGGTTGGTCACACACCCTACTGGG 2104	519 GlnThrGlyPro	DD	Sequence 20, Application US/09291417D ; Patent No. 6680170	GENERAL	APPLICANT: MAKTUEL, KILCAKUO APPLICANT: WHYTE, DAVID TITLE OF INVENTION: STEZO RELATED PROTEIN KINASES	FILE REFERENCE: 03860Z/032 CURRENT APPLICATION NUMBER CURRENT FILING DATE: 1999		; NUMBER OF SEQ ID NOS: 155 ; SOFTWARE: Patentin Ver. 2.1 : SEO ID NO 20	LENGT	11FE: ORGANI S-09-291-	Alignment Scores: 5.38e-12 Length: 3824 Pred. No.: 248.50 Matches: 139	*

APPL	TITLE TITLE NUMBE	ADI STE	CII	COMPI	, MEI	SOO	, CURRI	; FII ; CLP ; PRIOR	, API	, ATTOR	NAM	TELEC	TET ; TEI	EDOES :	TYP	TOP ;	TEMPT !	; US-09-023-	Alignment	Score:	Best Local	Query Maco DB:	US-10-023-	ζō	Db 4	ŏ	Db 4	ò	Db 4	ò	Db 4	Š
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1229 GGGCGTCATAACTTAGAGCAGGACCTTGTCAGGGAGGTTAAACAAAAGACAGAC	285 GluasnMetGluLeuAlaGluargLeuLysLysLeuIleGluGlnTyrGluLeuArgGlu 304 :::::::: 1289 AAGGACTTAGAQCATGCTACTCCGACARGAATCTATGCAAGAACTGAAGTTC 1348	305 GluḤişIleAspLysValPhelysHisLysAspLeuGlnGlnLeuValAspAlaLys 324	1349 CGCCACCTCAACACTTCAGAAGATGCGCTGTGAGTTGATCAGA 1393	LeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArgGluLysAsp	1394 TTACAGCATCAAACTGAGCTCACTAACCAGCTGGAATATAATAAGCGAAGAGAAGAAAA 1453	PheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGlu 3	CTAAGACGAAAGCATGTCATGGAAGTTCGACAACAGCCTAAGAGTTTGAAGTCTAAAGAA	365 ThrHisLeulysGinGlnLeuAlaLeuTyrThrGluLysPheGluGlu 380 1514 CTCCAAATAAAAAGAGTTTCAGGATACCTGCAAAATCCAAACCAGAACAAAGA 1573	381 PheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGlu 400	1574 TTAAGAAATCACCTGCTGGAGACTACACCAAAGAGTGAGCACAAA 1618	ystysteugluty	1619 GCTGTTCTGAAACGGCTCAAGGAGGAACAGACCCGGAAATTAGCTATCTTGGCT 1672	421 GluSerSerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArg 437	1673 GAGCAGTATGATCACAGCATTAATGAAATGCTCTCCACACAGCCCTGCGTTTGGATGAA 1732	437	1733 GCACAGGAAGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAGGAACTGGAGCTGTTG 1792	438AspLysGluLeuGlu 442	1793 AATGCGTATCAGAGCAAAATCAAGATGCAAGCTGAGGCACAACATGATGGAGGCTTCGC 1852	443 GlybeuGlnValLysIleGlnArgLeuGluLysLeu 454	1853 GAGCTTGAACAGAGGGTCTCCCTCCGGAGGGCACTCTTAGAACAAAAGATTGAAGAAGAG 1912	455 CysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgVal 469	1913 ATGTTGGCTTTGCAGAATGAGCGCACAGAACGAATACGAAGCCTGTTGGAACGTCAAGCC 1972	470 GlnAspLeuSerAlaGlyGlyGlnGlySer	1973 AGAGAGATTGAAGCTTTTGACTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCCTT 2032	481 ThrhspSerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro 500	2033 TCTAATCTCTCCCCTGAG 2050	501 ArgValThrGluAlaProCysTyrProGlyAlaProSerThrGluAlaSerGly 518	2051GCATTCAGCCACAGCTACCGGGAGCTTCTGGTTGGTCACACAACCCTACTGGG 2104	519 GlnThrGlyPro 522	2105 GGTCCAGGACCT 2116	RESULT 35	i-UV-UV3-655-1463 Semience 1463 Innlication IIR/Association
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Sequence 1463, Application US/09023655 Patent No. 6607879 GENERAL INFORMATION: APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4414 --------CTTGGAAGAAGAAGCAGAAGTTTGACCAGCTGTTAGCAGAAGA 4458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 GlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyrValAla 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LeuGluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAsp 82
LICANT: Jeffrey J. Seilhamer
LE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
LE OF INVENTION: EXPRESSION
BER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GinGluArgProSerGinAlaAlaProAlaValGlu
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                                                                                                                                                                                                          MORPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
UNRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/023,655
APPLICATION NUMBER: US/09/023,655
APPLICATION NUMBER:
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Matches:
Conservative:
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Gaps:
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                                                                            RESPONDENCE ADDRESS:
DDRESSEE: INCYTE PHARMACEUTICALS, INC.
FREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASIPICATION:
DRNEY/AGENT INFORMATION:
GWE: Zeller, Karen J.
SAUSTRATION WUMBER: 37,071
SFERENCE/DOCKET WUMBER: PA-0001 US
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TELEPAX: (650) 845-4166
RMATION FOR SEQ ID NO: 1463
QUENCE CHRRACTERISTICS:
LENGTH: 7596 base pairs
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23.80%
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TE: CALIFORNIA
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LERARY: GENBANK
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10-SD	LOCATION: 1213123 -060-410-1	<u>ک</u> ک	271 GlnMetGluGln 274 ::: 1939 AAAAGGGAAAAAAGGGAAGAAAGAAAGAAAGAAAGAAGGGG
Alignment S Pred. No.: Score:	5.89e-12 Length: 247.00 Matches:	3 & £	HisAsnGluArgAsnSerLysLeuArgGlnGluAsn
Best Lo Query 1 DB:	Conservation Mismatches: Indels: Gaps:	λο Λο	MetGlubeuAlaGluArgbeuLysbysbeulleGluGlnTyrGlubeuArgGluGluHis
-10	09-060-410-1 (1-3312)	윰 6	2059 TTAGAACATGCAATGTTACTGCGACAGCATGAATCCATGCAAGAACTGGAGTTTCGCCAC 2118
& qq	23 ProhlavalGlualaGlu	qa	CICAACACIAITCAGAAGAIGCGCIGIGAGIIGAICAGACIGCAA
& £	ıa	ç d	327 GlnalagluGluMetLeuLysGlualagluGluArgHisGlnArgGluLysAspPheLeu 346
3	ArgThralaGlnSerGlyAlaLeuArgAspValSerGluGluLeuSerArgGlnLeuGlu 64 ::::::::::::::::::::::::::::::::::::	ov da	347 LeuLysGluAlaValGluSerGlnArgMetCysGluLeuMetLysGlnGlnGluThrHis 366
3 & i	Asp1leLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly	8 G	367 LeulysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGln 382 ::: ::: 2284 ATAAAAAAGCAGTTTCAGGATACCTGCAAATTCAAACCAGACAGTACAAGGATATAAGG 2343
9 & A	ATGATGGAGGGAGACCATACAGTGATGTCTAACAGTTCTGTCATCCACTTAAAACCTGAG GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 	& ଶ	383 ASDThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMet 402
g &	1327 GAGGAAAATTACCAAGAAGAAGAGTCCTAGA	ර් සි	403 ThrLysLysLieLysLysLeuGluLysGluThrThrMetTyrArgSerArgTrpGluSer 422 ::::: 2389 CTGAAAAGACTCAAGGAGGAACAGACTGGGAAGTTAGCCATCTTGGCTGAGCAG 2442
원 상 원	1360ACAÁGAGCATCAGCTČCÁCAGTCTCCAĞCTCTCGTCACAĀTCACATTAT 1416 121 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 111 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 111 LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140 111 LysGlyAspArgAspHis 111 LysGlyAspArgAspHis 140	& 8	SerAsnLysAlaLeuLeuGl
?;	ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThr	යි දි	437 GAAGCAGAATGCCAGGTTTTGAAGATGCAGCTACAGCAGGAACTGGAGCTGTTGAATGCA 2562
දු දු	AGACAGATGCAAGAACATGAGCAGGACTCTGAACTTAGAGAACAGATGTCTGGTTATAAGLeuleumetGlnThrleuasnThrleuserThrProGluGluLysleualaAlaleu :::	\text{\text{6}}	438
d y	CGGATGAGGCGACAGCATCAGAAGCAGCTGATGACTCTGGAAAATAAACTGAAGGCAGAA CysLysLysTyralaGluLeuLeuGluGluHisArgAsnSer :::	රු සි	445 GlnValLysTle
දුරු පු	ATGGACGAACATCGGCTCAGATTAGACAAAGATCTTGAAACTCAGCGCAACAATTTCGCT GlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu ::: :::::	જે તુ	457 AlaleuGlnThrGluArgAsnAsp
do ob	GCAGAAATGGAGAAACTTATTAAGAAACACCAAGCTTCTATGGAAAAAGGGGTAAAGTG	Oy Dp	472 Leuseralaglyglyglnglyser
d y	1705 ATGGCCAACGAGGAGAAAAATTCCAACAACACATTCAGGCTCAACAGAAGAAAGA	ko a	483 SerGlyProGluArgArgProGluGlyProGlyAlaGluAlaProSerSerPro 500
os pe	1765AATAGCTTTTTGGAGTCTCAAAAAAGAAATATAAACTTCGAAAAGAGCAGCTT 1818 240 LysGluGluGlyValGlnArgAlaArgGluGluGluGlu 252	<i>&</i> 8	501 ArgValThrGluAlaBroCysTyrProGlyAlaProSerThrGluAlaSerGly 518 2863 ACTGGGGGTTCAGGACTCACTGGGGTCATCCGTGGGTAGGCACCACCAAGGTTGGGGT 2922
q	1819 AAGGAGGTGAATGAAAACCAGAGCACACCTAAAAAAAAAA	ò	
qq	::	DD RESULT	2923 CATCCGATGCAAGGCGGACCCCAA 2946 37

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1267 ATGATGGAGGGAGCCATACAGTGATGTCTAACAGTTCTGTCATCCACTTAAAACCTGAG 1326
                                                                                                                                                                               LysGlyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHis 140
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                                    GluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGluLysSerArgThrTyr 100
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                                                                                                         ValAlaArgAsnGlyGluProGluProThrProValValTyrGlyGluLysGluProSer
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                                                                                                                                                                                                                                                      141 ArgArgProGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThr-
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                                                                        1327 GAGGAAAATTACCAA---GAAGAAGGAGATCCTAGA
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                                                                                                                    LITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3312
142
118
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/723,458
FILING DATE: 27-No. 6586242-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/060,410
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 121..3123
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                        Cobb, Melanie
Hutchinson, Michele
Chen, Zhu
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3312 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   Sequence 1, Application US/09723458
Patent No. 6586242
GENERAL INFORMATION:
APPLICANT: CODD, Melanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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247.00
40.12%
21.91%
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Best Local Similarity:
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     US-09-723-458-1
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DB:
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13 The properties of the p		Query Match: 9.10% Indels: 118
11	Oy 383 AsnThrLeuSerIysSerSerGluValPheThrThrPheLysGlnGluMetGluLysMet 402	4 Gabs:
13 A STATE CONTRICTOR C	2344 AATCACCTACTGGAGACTACACCAAAGAGTGAGCACAAAGCTGTT	0-023-523-8 (1-530) x US-09-220-132-79 (1-58
13 12 13 13 13 13 13 13	403 ThrLysLyslleLysleugluLysgluThrThrMetTyrArgSerArgTrpGluSer	117 LysgluProSerLysglyAspProAsnThrGluGluIleArgGlnSerAspGluValGly 136
13 PRODUCTOR CONTINUES 15 PRODUCTOR CONT	423 SerAsnLysAlaLeuLeuGluMetAlaGluGluLysThrValArg	137 AspargAspHisArgArgProGlnGluLysLysLysLysGly 15
15 The first content conte	2443 TATGATCATAGCATTAATGAAATGCTCTCCACACAAGCTCTGCGTTTGGATGAAGCACAG	2500 GAGAAALAGATITAAACATITAGAGATITGAAAAGAAHTGCTGAAAAGTAGCAAGGCTAGCCTAGCCT
15 The Control Con	437	152 DeuGlyLySGLU
13	438	165 ThrLeuSerThrProGluGluLysLeuAlaAlaLeuCysLysLysTyr 1::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
19 Januari	445 GlnValLysIle	181 AladluLeuLeuGluGlu
### 3 = ### 1	457 AlaLeuGlnThrGluArgAsnAspheuAsnLysArgValGlnAsp	197 LeuGlnLysLysGlnSerGlnLeu
483 SerGIVEPROSILAR-SPECTAL CONTRACTOR	472 Leuseralaglyglyglnglyser	205
State Accordance Accordan	483 SerGlyProGluArgArgProGluGlyProGlyAlaGlnAlaProSerSerPro	217 LysalaValLeualaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArg 2 ::: :::
244 ValGinargalacdicululysarglyValThrEsHisePhiceChnale 297 Chacacantachaccconnal 246	501 ArgValThrGluAlaProCysTyxProGlyAlaProSerThrGluAlaSerGly	235HisasnargSer
192-79 192-79 193-194	519GlnThrGlyProGln 2923 CATCCGATGCAAGGCGGACCCCAA	244 ValGinargalaargGluGluGluGluLysargLysGluValThrSerHisPheGlnVal
	132-79 144 1572-11 Length: 5857 158-70 158-70 158-70 158-70 158-70 158-70 158-70 168-70 178-7	264 ThrLeudsnaspileGlnLeuGlnMetGluGlnHishsnGludrgAsnSerLysLeu 28 3031 AGTATTGAGGACATGACAAGGTGAACAGAGCCAGCAAGAAGCAGCTAAAAAGCAT 30 283 ArgGlnGluAsnMetGluLeualaGluArgLeuLysLysLeuIleGluGlnTyrGluLeu 30 283 ArgGlnGluAsnMetGluLeualaGluArgLeuLysLysLeuIleGluGlnTyrGluLeu 30 3031 GAGAAGAAAGAAAGAAATGGAGAATTGCGGACTGGAAAAGAAAAAAAA

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41		ProAsnThrdluGlulleArgGlnSerAspGluValGlyAspArgAspHisArgArgPro		199 LystysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLysAla 218	1581 CTACGTGAACAGGAGGAGAGGCTGTGTGAACAGAGGAGGAGGAGAGGTACGTGAA 1631 259 SerHisPheGlnValThrLeuAsnAsp1leGlnLeuGlnMetGluGlnHisAsnGluArg 278 [337GluarghisGlnargGluLysAspPheLeuLeuLysGlualavalGluSer 353
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		<u>.</u>	STEROIDS				
Oy 368 LysGlnGlnLeuAlaLeuTyrThrGluLysPheGluGluPheGlnAsnThrLeu 385	GGGAGAAGCAGGACGAAGTC ValargaspiysGluLeuGlu Valarsi GTGCTCAATAATCAGTTG ArgalaLeuGlnThrGluArg :::	Qy 467 LysargValGlnAspLeuSerAla 474	; PATENT NO. 66-53-94 ; PATENT NO. 16-51-51-94 ; APPLICANT: Furness, Michael ; APPLICANT: Furness, Michael ; APPLICANT: Buchbinder, Jenny ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH ; FILE REFERENCE: PA-0041 US ; CURRENT APPLICATION NUMBER: US/09/976,594 ; CURRENT PILING DATE: 2001-110-12 ; PRIOR APPLICATION NUMBER: 60/240,409	03	US-09-976-b94-268 Alignment Scores: 2.71e-11 Length: 6617 Pred. No.: 244.50 Matches: 143 Score: 40.78\$ Conservative: 107 Best Local Similarity: 23.33\$ Mismatches: 177 Query Match: 4 Gaps: 30		Db 867 CAAGCAGGGTGCACTCCCCAGGAGCTCTGAGTGAGAAGCTGTTGGTACAGGA 926 Qy 26 GlualaGluGlyProGlySerSerGlnalaProargLysProGluGly 41

SEQ ID NO 248 LENGTH: 7453 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAMFKEY: CDS LOCATION: (1)(4362)	620-312D-248 nent Scores: 5.94e-11 Length: No.: 241.50 Matches: it Similarity: 38.45% Conservati	Accal Similarity: 22.94\$ Mismatches: Match: 8.94\$ Indels: 4 Gaps: -023-523-8 (1-530) x US-09-620-312D-248 (1-7453)	1 LysserSerProGlydlnProGluAlaGlyPro	12Gluglyalagin 15	16 GluargProSerGlnalaalaProAlaValGlualaGluGlyProGlySerSerGlnala 35	36 ProArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspVal 55	56 SerGluGluLeuSerArgGln62 ::::: 4297 ACGGTGGACCTGCAGGTCGCCTCCCAACTTGGAGAAGAAGAAGAAGAA 4356	63	76 GlnGlyGlyProGlyGluAspGlyAlaGlnGlyGluProAlaGluProGluAspAlaGlu 95 :::	96 LysSerArgThrTyrValAlaArgAsnGlyGluProGluProThrProValValTyrGly 115	116 GluLysGluProSerLysGlyAspProAsnThrGluGlulleArgGlnSerAspGlu 134	135 ValGlyAspArgAspHisArgArgProGlnGlu-LysLysLysAlaLysGlyLeuGlyLu 154	154 sGlulleThrLeuLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAl 174	174 aAlaLeuCysLysLysTyrAlaGluLeuLeuGluGluHisArgAsnSerGlnLysGlnMe 194 	t.psteuvalgl 	206 nGluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaArgSerLysLeuGl 226	
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354 GlnArgMetCysGlu	SerGluValPheThrThrPheLysGlnGluMetGluLysMetThrLysLysIl :::::::::::::::::::::::::::::::::	CTGTGGCAGCAGGAGACTCTGGluMetalaGluGluLysThrValArgAs	GlnArgLeuGluLysLeuCysArgAlaLeuGln	- Thrgl	LeuSeraladlyGlyGlnGlySerLeuThrAspSerGlyProGlubrgArgEr 	ProGlyAlaGlnAlaProSerSerProArg	CCGAGICIGCAGCAGCAGAGCAGTAGCIGGA ProserThrGluAlaSerGlyGlnThrGlyProGlnGlu ProserThrGrowth	4	Sequence 248, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION: APPLICANT: Tang, Y. Tom	: Liu, Chenghua Asundi, Vinod : Zhang, Jie Ren, Feiyan		Yang, Yonghong Wang, Jian-Rui Zhou, Ping Ma, Yunging		No. 6569662 Polypeptid IP2B NUMBER: US/	TFILING DATE: 2000-07-19 APPLICATION NUMBER: 09/552,317 FILING DATE: 2000-04-25 APPLICATION NUMBER: 09/488,725	TLING DATE: 2000-01-21 OF SEQ ID NOS: 1105 RE: pt_FL_genes Version 1.0	

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Wang, zniwei
John Tillinghast
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                                                                                             gAlaArgGluGluGluGluLysArgLysGluValThrSerHisPheGlnValThrLeuAs 266
                                                                                                                                                               nAspileGlnLeuGlnMetGluGlnHisAsnGluArgAsnSerLysLeuArgGlnGluAs 286
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                               uSerLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnAr
                                                                                                                                                                                                                                                                                             306 sIleAspLysValPhe-----LysHisLysAspLeuGlnGlnLeuValAspAl
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                                                                 -GCGGAGCTGGAGGATGAGAGGAAACAGCG
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744 AACCAGGGATGAG---CAGAATGAAGAGAAGAAGAGCGGCTGCTGATCAAACAG--
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5760 AGGTCAG---CACCCTGAAGAACCGGCTGAGGCG 5790
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4241 ::: :::||| 1345 ACGGTGGACCTGGACCACCAGGCCCAGGTCGCCTCCAACTTGGAGAAGAAGCAAGAA 4404 --AGAACCGCCTGCAGCAG-GAGCTGGACGACCTC 4344 16 GluArgProSerGlnAlaAlaProAlaValGluAlaGluGlyProGlySerSerGlnAla 35 4122 CAGGAAGAACCTGGAGAAGCAAGTGCTGGCCCTGCAGTCCCAGTTGGCTGATACCAAGAA 1182 GAAAGTAGATGACGACCTGGGAACAATTGAAAGTCTGGAAGAAGCCAAGAAGAAGCTTCT 1242 GAAGGACGCGGAGGCCCTGAGCCAGCGCCTGGAGAAGAAGACACTGGCGTATGACAAACT 36 ProArgLysProGluGlyAlaGlnAlaArgThrAlaGlnSerGlyAlaLeuArgAspVal HITLE OF INVENTION: No. 6569662el Nucleic Acids and HILLE OF INVENTION: Polypeptides Matches: Conservative: Mismatches: Indels: US-10-023-523-8 (1-530) x US-09-620-312D-249 (1-7501) 1 LysSerSerProGlyGlnProGluAlaGlyPro CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/520,3 PRIOR APPLICATION NUMBER: 09/525,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 NUMBER OF SEQ ID NOS: 1105 SEQ ID NO 249 LENGTH: 7501 Application US/09620312D SerGluGluLeuSerArgGln-

		RESULT 4. RESULT 4. RESULT 4. RESULT 4. Sequence 30, Application US/09595684B Fatent No. 6544766 Retent No. 6544766 REAPLICANT: Debahi, Cara APPLICANT: Obabhi, Cara APPLICANT: Wood, Kenneth APPLICANT: Wood, Kenneth APPLICANT: Wood, Kenneth TITLE OF INVENTION: Human Kinesins and methods of producing TITLE OF INVENTION: Human Kinesins and methods of producing TITLE OF INVENTION: and purifying human Kinesins FILE REFERENCE: cytopo36 CURRENT APPLICATION NUMBER: US/09/595,684B PRIOR APPLICATION NUMBER: 09/295,612 PRIOR APPLICATION NUMBER: 09/295,612 PRIOR APPLICATION NUMBER: 09/295,612 RIGH APPLICATION NUMBER: 09/295,612 RIGH APPLICATION NUMBER: 09/295,612 RIGH APPLICATION NUMBER: 09/295,612 RIGH APPLICATION NUMBER: 09/295,612 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 30	LENGTH: 8257
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63 4405 GTTTGACCAG 76 GINGIVGIVP 4456 AGAGCGGAGA 96 LysSerArgT 4492 116 GluLysGluP	135 ValGlyAspA 4570 GCAGCTCCGA 154 SGlulleTht 4624 AAACGTTCAC 174 aAlaLeuCye 4682 194 tLysLeu 194 tLysLeu 4732 CAAGCTTCGT 206 nGluLySAsg	226 uSerLeucys 841GTC 246 GALAARGGL 885 GGGGCTTGGC 266 nASDIleGlr 1830 GACCTCGAA 286 nMetGluLe 1990 CGGCAAGCTC 306 SILEASDLY 306 SILEASDLY 306 CAGAGATGA 307 CAGAGATGA 308 CAGAGATGA 308 CAGAGATGA	323 alysLeuGlt
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3049 ATTTCTGAGGAAG 3088 AATACAGGAAAA 3088 AATACAGGAAAA 3188 GATTTGGAAGCTA 103	ATGGAGGAA 3087	Db 4153 AAAACGATAAAAAAAAAAA 3147	0y 	103		3327 Qy 340		4450		3495 173	Db 4570 AAGAAGAGATGAGAAA 3555 OV 398	Db 4630 TIAGAAGCAATCAATGATAAATTACAAAGAACAAAGTCCA	Action A	3675 Qy 431	4	208 LysaspHisLeuArgGly	SAGGATATATAAGAAGAAATTGAAGCTACAAGGCCTACAAGAA 3795 Qy 450 ArgLeuGluLysLeuCysArgalaLeuGluThrGluArgAsnAspLeu	GATGAACTAAGA 3855	Oy 470 GInAspleuserala 474 222 ArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsn 236 :::::::	256 U	3972, ; Patent NG ; GENERAL I 274 ; APPLICAN	4032 ; APPLICANT: ASUND ; APPLICANT: Zhand	LysLeuargGlnGluasnMetGluLeuala 290; APPLICANT: Ren, Feiy ; APPLICANT: CTGGCAAGAATAGAAATGGAAAGGCTCAGGTTGAAT 4092; APPLICANT: Zhao, Qin	euArgGluGluHisIleAspLysVal 310
	3049 ATTTCTGAGGAAGTTTCCAGGAATTTGCAT	75 AsnglnglyGlyProGlyGluAspGlyAlaGlnGly	ProGluAspAlaGluLysSerArgThrTyrValA :	103	111 ProValValTyrGlyGluLysGluProSerLysG	3268 GAGAGTGTTATAGCAGAAAAAGGAACAATTGAAGA(124ProAsnThrGluGluIleArgGlnS	3328 ACCATTGAAACCAGGAAGAATTAAGACTTCTTG	141 ArgArgProGlnGluLysLysLysAga=LysG: 	160 MetGlnThrLeuAsnThrLeuSerThrProGluG	3436 TCTAGGACCTGTGACAGACTGGCAGAAGTTGAAG	CTCCAAGAAAAACAGCAACAACTTCTTAATGTAC		3556 ARGALITARICARATIAGAGARITIARAGARICARAT. 174AlaAlaLeuCysLysLy	3616 CATATGGAAACAGAGAGGCTTGAGTTGGCTCAGA	188 ArgAsnSerGlnLysGlnMetLysLeuLeuGlnL::::::::::::::::::::::::::::::::::::	208 LysAspHisLeuArgGly:::	3736 AGAGACCACCTTAGAGGATATATAAGAGAAATTG	3796 GAACTAAAATTGCTCATATTCACCTAAAAGAAC	222 ArgSerLysLeuGluSerLeuCys	237 ArgSerbeuLysGluGluGlyValGlnArgAlaA. ::: :::	3916 ACCAAATTACAAGAAGAGATCCCAGTGCTTC 257 ValThrSerHisPheGlnValThrLeuA	3973 GIGAAAAAGTCAGIGAGACTCAGGAAACAAIGA	275 HisAsnGluArgAsnSerLysLu	291 GluArgLeuLysLysLeulleGluGlnTyrGluL

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AAGAGGAAACTATT 4569
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|GCTGCAAGAAGTT 4449
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TTAAGGAAAAAGAG 4869
InGlnLeuValAsp 322
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AACATATTAGAGAA 4212
                                                                 FAAATATGAAAGAA 4272
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|TAGCTAAACACCTG 4509
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3973 GTGAAAAAGTCAGTGAGACTCAGGAAAGAATGAACTGGAGTTATTAACAGAACAG 4032
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                                                                                       3616 CATATGGAAACAGAGGCTTGAGTTGGCTCAGAAACTTAATGAAAATTATGAGGAAGTG
                          3556 AAGATTAATGAAATAGAGAATTTAAAGAATGAATTAAAGAACAAAGAATTGACATTGGAA
                                                                                                                        188 ArgAsnSerGlnLysGlnMetLysLeuLeuGlnLysLysGlnSerGlnLeuValGlnGlu
                                                                                                                                                                                                                                                                                                                      ArgSerLysLeuGluSerLeuCys------ArgGluLeuGlnArgHisAsn
                                                           ---AlaAlaLeuCysLysTyrAlaGluLeuLeuGluGluHis
                                                                                                                                                                                                                                                        ------GluHisSerLysAlaVal-----LeuAla
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TCTAGGACCTGTGACAGACGTTGAAGAAAACTAAAGGAAAAGGCCAGCAA 3495
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                                                                         APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TILE REPRENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
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Matches:
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PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL-Genes Version 1.0
SEQ ID NO 130
LENGTH: 8503
                               Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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20.16%
Zhou, Ping
Ma, Yunging
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ORGANISM: Homo sapiens
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US-09-620-312D-130
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Best Local Similarity:
Query Match:
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LOCATION: (91)
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DD 4030 TAGGARGCAATCAATCATAAATTACAGAACAAGATCCAAGAGATTTATGAGAAAGAA	4690 CAACTTAATATATAAAAATTAGTGAGGTTCAGGAAAAGTGAATGAA	AlaGluGluLysThrValArgAspLysGluLeuGluGlyLeuGlnValLysIle		Qy 449GIn 449	Db 4810 TTGACCAACAGACTTCAAGAAAGTCAAGAAAATACAAATTATGATTAAGGAAAAAGAG 4869	Qy 450 ArgLeuGluLysLeuCysArgAlaLeuGlnThrGluArgAsnAspLeuAsnLysArgVal 469	аавстасьсев в в в в в в в в в в в в в в в в в в	Qy 470 GlnAspLeuSerAla 474	Db 4930 AAAGAAATTGTAGCT 4944	RESULT 44	US-09-620-312D-1065 ; Sequence 1065, Application US/09620312D	D. 6569	, APPLICANT: Tang, Y. Tom	CANT:	CANT:	: Chen, Rui : Zhao, Qin	CANT: Wehrma CANT: Xue, A	CANT: Yang,	PLICANT:	; APPLICANT: Wang, bunrus ; APPLICANT: Wang, Zhiwei ; APPLICANT: Wang, Zhiwei	JANT: Domanac, Radoje T.		CURRENT APPLICATION NUMBER: US/09/620,312D	CONTENT FILLING DAILS: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317	; FRIOR APPLICATION NUMBER: 09/488,725 . DETOR FILLING DARF: 2006-01-21	; NUMBER OF SEC IN SEC. OF SEC	1065 1065 1083	NA W. Homo gandan	FEATURE: FEATURE:	; NAME/KEY: CUS ; LOCATION: (634)(4275) TIS-09-620-3120-1065	1 jonnent Goves.	7.18e-11 Length: 237 50 Matches:	t Similarity: 40.34% Conservative: ocal Similarity: 24.89% Mismatches:	8.79% Indels:	US-10-023-523-8 (1-530) x US-09-620-312D-1065 (1-4892)

54 pValSerGluGluLeuSerArgGlnLeuGl 3092 GGCCAATGAGGCGCTGAAGAAATGAATGAA 74 nAsnGlnGlyGlyProGlyGluAspGlyAl 3129 - CAGCAAGA-GGCCGGGAAGGCCA	03 03 03 03 03 03 03 03	122 lyAspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAsp 3298 CGGACGCGGAGCTGGCCCAGGCCCAGGGTGGCAGCAGCAGCAGCTGGCTC 140HisArgArgProGlnGluLySLySLySlyLeuGlyLeuGlyLySGluIleThrL				Oy 227 erLeuCysArgGluLeuGlnArgHisAsnArgSerLeuLysGluGlyUal- 244 ::	Db 3718 TGCAGGCAAAGAAGAAGGAGGATCGCCAGATGAAGCATCTTGTCCAGGCCCTGCAGGCCT 3777 Qy 264 hrLeu	3838 TGGAAGCCGGGCATTCAAGGCGGCCTCCTTGGACTGACTGACTGACTGACTGACTGACT	OP 311 heLysHisLysAspLeuGlnGlnLeuValAspAlaLysLeuGlnGlnAlaGlnGluM 331 Db 3933	Oy 351 alGluserGlnArgMetCysGluLeuMetLysGlnGlnGluThrHisLeuLysGlnGlnL 371
373 LeuTyrThrGluLysPheGluGluPheGlnAsnThrLeuSerLysSerSer 389 1642 GGCTTAACCCAAAGAATCGAGGAGCTAGAAGACCAACAAAAATCTGCAGAAAGGCAGAG 1701 390 GluValPheThrThrPheLysClnGluMetGluLysMetThrLysLysIleLysLysleu 409	GAATGTGGAAACTCTAGCCTCATGGCAGAAGTGGAAAATCTTCGAAAGGTGTGCTTGAA MELAlaGluGluLySTh.valargaspLysGluLeuGluGlyLeuGlnVal	447 LYSITEGINARGLEGGULLYSLeuCygargalaLeuGinThrCluargasnaspleuasn 466	ULT 45 09-976-594-735 equence 735, Application US/09976594 FARDAY TAMODAM TAM	APPLICANT: Furness, Michael APPLICANT: Furness, Michael APPLICANT: Buchbinder, Jenny TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REPERBOCE: PA-0041 US CURRENT APPLICATION NUMBER: US/09/976,594	PRIORENT FILING DAIE: 2001-10-12 PRIOR FILING DAIE: 60/240,409 PRIOR FILING DAIE: 2000-10-12 NUMBER OF SEQ ID NOS: 1143 SOFTWARE: PERL Program LENGTH: 5467	TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. 6673549 3151579CB1	Alignment Scores: Pred. No.: Score: Score: Score: Percent Similarity: 23.7.00 Matches: Conservative: Mismatches: Mismatches: A Gaps: A A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A Gaps: A A Gaps: A Gaps: A A A Gaps: A A A A A A A A A A A A A A A A A A A	US-10-023-523-8 (1-530) x US-09-976-594-735 (1-5467) QY 6 GlnProGluAlaGlyProGluGlyAlaGluGlu	17	

Percent Similarity: 39.87% Conservative: 106 Best Local Similarity: 22.97% Mismatches: 219 Query Match: 4.0% Indels: 27 BB: 27 IIS-10-023-523-8 (1-530) x IIS-09-252-991A-15560 (1-3402)	3 SerProGlyGlnProGludlaGlyProGluGlyAlaGl ::: :::	22 AlaProAlaValGluAlaGluGlyProGlySerSerGlnAlaProArgLysProGluGly::::	42 AlaGinAlaArgThrAlaGinSerGlyAlaLeuArgAspValSerGluGluLeuSerArg	62 GlnLeudluAspileLeuSerThrTyrCysValAspAsnAsnGlnGlyGlyProGly:	Oy 81 GluAspGlyAlaGln-GlyGluBroAlaGluProGluAs 93	Qy 93 pAlaGlubysSerArgThrTyrValAlaArgAsnGlyGluBroGluBroThrProVa 112	Oy 112 lvaltyrdlygluLysGluProSerLysGly	Qy 123 -AspProAsnThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgAr 142	Qy 142 gProGlnGluLysLysLysalaLysGlyLeuGlyLysGluIleThrLe 158	Qy 158 uLeuMetGlnThrLeuAsnThrLeuSerThrProGluGluLysLeuAlaAlaLeuCys 177	Qy 178 LysLysTyrAlaGl 182 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 182 uleuleuGludluHisArgAsnSerGlnLysGlnMetLys	197 uGlnLysLysGlnSerGlnLeuValGlnGluLysAspHisLeuArgGlyGluHisSerLy	Db 2416 CTGGCGGCGACCTGAACGGGCGGGTCGGTCAGCGCGAGCGGGGTCATCGGCGACCAGGAGGT 2357 Ov 217 sAlaValieuAlaArgSerLvsbeuGluSerLeuCysArgGluzeuGluArgHisAsnAr 237	2356 CGCCTTCGAGGCCCTGGTGGCCCAAGCAGCGCGGT	Qy 237 gSerLeuLysGluGluGlyValGlnArgAlaArgGluGluGluGluGluJy 253 ::	253 sArgLysGluValThrSerHisPheGlnValThrLeuAspAspIleGlnLeuGl 271	DB 2269 CITCAACCAGGIGCAGGCTTCTATTCGGICGGGGGACAICGCCCGGGIGAGA 2210 Qy 271 nMetGluGlnHigAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaG1 291
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Alignment Scores:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1568
LENGTH: 3606
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235.00
39.87%
22.97%
8.70%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-15688
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61

350

93

142

524

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Page 55

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Conservative:
Mismatches:
Indels:
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Matches:
                                                                                Sequence 1, Application US/08875435B Patent No. 6593304 GENERAL INFORMATION:
1803 CGGCTTCGGCAAGGCG 1819
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233.50
38.13%
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Emi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                                                                                                                              APPLICANT: Hasegawa,
APPLICANT: Arakawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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LENGTH: 6175
                                                                  US-08-875-435B-1
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217 sAlaValLeuAlaArgSerLysLeuGluSerLeuCysArgGluLeuGlnArgHisAsnAr 237
                                                                237 gSerLeuLysGluGluGlyValGlnArgAlaArg------GluGluGluGluLy 253
                                                                                            919 -----GCCGATGCCGGCATCGAACGCTGCGCGACGGCCATCACGAGTTGTCCGAACG 971
                                                                                                                                                                                              271 nMetGluGlnHisAsnGluArgAsnSerLýsLeuArgGlnGluAsnMetGluLeuAlaGl 291
                                                                                                                                                                                                                                                             291 uArgLeuLysLysLeuIleGluGlnTyr-----------GluLe 302
                                                                                                                                                                                                                                                                                                                            uArgGluGluHisIleAspLysValPheLysHisLysAspLeuGlnGlnGlnLeuValAs 322
                                                                                                                                                                                                                                                                                                                                                                                           322 pAlaLysLeuGlnGlnAlaGlnGluMetLeuLysGluAlaGlu------GluArgHi 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 sGlnArgGluLysAspPheLeuLeuLysGluAlaValGluSerGlnArgMetCysGluLe 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 uGluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGluMe 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 tGluLysMetThrLysLysLysLysLeuGluLysGluThrThrMetTyrArgSerAr 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 sGluLeuGluGlyLeuGlnValLysIleGln------ArgLeuGluLysLeuCy 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 ySer-----LeuThrAspSerGlyProGluArgArgProGlu-GlyProGlyAla- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 -----glnAlaProSerSerFroArgValThrGluA 505
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                                 -----cadececriegreeceage---cadececer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 uMetLysGlnGlnGluThrHisLeuLysGlnGlnLeuAlaLeuTyrThrGluLysPheGl
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                                                                                                                               sArgLysGluValThrSerHisPheGlnValThrLeuAsnAspIleGlnLeu-----Gl
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APPLICANT: Matsuda, Yuzuru
APPLICANT: Takahashi, Katsuhito
APPLICANT: Takahashi, Katsuhito
APPLICANT: Takahashi, Katsuhito
APPLICANT: Sugahara, Michihiro
APPLICANT: Sugahara, Michihiro
APPLICANT: Ishiyama, Haru
APPLICANT: Ishiyama, Haru
APPLICANT: Ishiyama, Haru
TITLE OF INVENTION: PEC MYOSIN HEAY CHAIN SMI ISOFORM PROTEIN INSERTED INTO
TITLE OF INVENTION: VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: WECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: WORDEN: US/08/975,435B
TITLE OF INVENTION: NUMBER: US/08/75,435B
CURRENT APPLICATION NUMBER: PCT/JP96/00134
PRIOR APPLICATION NUMBER: PCT/JP96/00134
PRIOR APPLICATION NUMBER: PCT/JP96/00134
NUMBER OF SEQ ID NOS: 5
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23 954 GGAAAC	GTACGCAAGGCCACACTGCAGCAACTGAGCAATGAGCTGGCCACAGAACGCAGCAGCAGCAGCAGAACGAAC	qq
23	399 MetGluLysMetThrLysLysIleLysLysLeuGluLysGluThrThrMetTvrArgSer 418	ŝ
ח	5340 GAGGAAGAGCAACATGGAGGCCATGAGTGATAGA 5378	qa
m (379 GluGluPheGlnAsnThrLeuSerLysSerSerGluValPheThrThrPheLysGlnGlu 398	δδ
-10-023-523-	ACACTGCAGGATGAGAGAGCGCCGCCTGGAGGGATCGCCCAACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	qq
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Percent Similarity: Best Local Similarit Ouery Match:	GCTGACCTGGAGAAGAAGAAGCTGGCCGAGGAGCTAGCTA	Z 43
Score:	בובס בייים ביים ביים בייים בייים בייים בייים בייים בייים בייים בייים בייים ביי	è
Alignment Scores:	325LeuGlnGlnAlaGlnGluMetLeuLysGluAlaGluGluArgHisGlnArg 341	S da
ORGANISM: Pseudo	5100 GCCTCCAGGGATGAGATCTTTGCCACCTCAAAAGAGAAAGAA	අ ධ .
SEQ ID NO 6666 LENGTH: 3702	324 324	ζ
PRIOR FILING DATI NUMBER OF SEQ ID	5040 CAGCTTCGAAAACTGCAGGCTCAGATGAAGGACTTCCAAAGAGAGGCTGGATGATGATGTGCCCGT 5099	qq
PRIOR FILING DATE PRIOR APPLICATION	324	ò
CURRENT FILING DA	CAGGCTGACTCAGCCATCAAAGGGAGGAAGCCATCAAG 5039	qa
FILE REFERENCE:	000	ò
APPLICANT: Marc TITLE OF INVENTIO	289 298 289 298 289 298 289	
Sequence 6666, App Patent No. 655179	4860 CAGAATGAGGAGAAGGAGGAGCTACCTGCAGCAGCTGCACGAGTATGAGACTG 4919	qq
RESULT 49 US-09-252-991A-6666	288 US	ò
5858 CCGTG	Argcaggccctcaaggccagttrgaaccgatctccaggctrggar	qq
522	SerHisPheGlnValThrLeuAsnAsnJleGlnLeuGlnWetGlu	ò
5798 CAACC	TCGGAGGATGACGTGCAGGCCACTGAGGATGCCAGGATGCGGGATAGAGTTCAA	. AG
y 511 Alapr	LenivsGhGhGhGvValGhabrahabraGhghghghghughughrannan	ò
b 5738 GGTCA		다. 같
y 491 GlyPr	Vallenk] a ArdSeviveleng in Sevient and representations.	ò
b 5678 GGAGG	4650 CTGGTCAGCTCCAAGGATGATGTAGGCCAAGAACGTGCATGAACTTGAAGAAAGGTCCAAGAGTTCCAAGAAGGATCCAAGGGT	' ପ୍ର
y 477 GlnGl	LeuValGluLysAspHisLeuArgGlyGluHisSerLysAla	ò
b 5619 GCGGC	4590 CIGGAAGCCAAAGAAGCACTGCAAGAAGAACAACAACAAGAAGAAGAACAACAAACA	: A
y 460 ThrGl	184 LeuGluGluHisArcAsnSerGlnLvsGlnMerlvsfeuleuGluGluHisArcAsnSerGln	ò
:: 555,9 CTGGA	4530 GCAGAGGCCAGGGAAAAGGACCAAAGGCTTTGACTCTAAGCCCTGGAGGAAGCC	i d
444 Le	168ThrProGluGuille all a blaten of the form of t	ò
b 5499 AGCAA	:::	୍ ପୁ
y 438 Asply	158 LeuLeuWetGlnThrLeuAsnThrLeuSer	ò
b 5439 ACGGC	4410 TTGGACAACCAGGGCAACTGGTATCCAATCTGGAAAAGAAGAAGAAGAAATTTGACCAG	ą a
Y 419 ArgTı	138	ò

2088	Qy 311 eLysHisLysAspLeuGlnGlnGlnLeuValAspAlaLysLeuGlnGlnAlaG;	Oy 331 tLeuLysGluAlaGluGluArgHisGlnArgGluLysAspPheLe	348	2238	Qy 368 sGinGinLewAlaLeuTyrThrGluLysPheGluGluFheGlnAsnThrLeuSe 	388	DD 2344TIGCAGCAGCAGGICGAGGAGGACGACCCAGCAATI.	2385 ATTGCT	Qy 424 nLysAlaLeuLeuGluMetAlaGluGluLysThrValArgAspLysGluLeuGl ::	444	2499 CGAACAGCGTCT		2555 AG	OY 480LeuThrAspSerGlyProGluArgArgProGluGlyProGlyAlaGlnA.	498SerSerProArdValThrG	2672 ATTGGCAACTATCGCT	Cy 509 oGlyalaProSerThrGluAlaSerGlyGlnThrGlyProG	2732 AGGCGCCCTGGATTCG	Oy 525 oThrSerAlaArgAla 530	SULT SO	US-09-010-147B-17; Sequence 17, Application US/09010147B; Parent No. 6651445	GENERAL INFORMATION: , GENERAL INFORMATION: , APPLICANT: Ni et al.	TITLE OF INVENTION: Human Proteins NOMBER OF SEQUENCES: 24 NOMBER OF SEQUENCES: 24	CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue	kville o	٠ ـ	/ MEDIUM TYPE: Floppy disk // COMPUTER: IBM PC : Commatible	
	56 SerGluGluLeuSerArgGlnLeuGluAspIleLeuSerThrTyrCysValAspAsnAsn	1071 76) 1131 GCGCCAĠĠĊĊCĀĠĠĊCGACAACCATCAGGCCCAGGGCGCCGTIĠĊĠĊGAĠĠĊTTT 1190	1191 CCAGCTGGAGAGCGAGGCCTGGAGGAAACGCTGGCCGAGCAAA-CCC	107 oGluproThrPro	125 YGluLysGluProSerLysGlyAspproAs	1310 AGCAGCAGCGCCATGTCGCGGAACAGGCGCAACTGCAGGCGGCATTGCGCGACAGCCAGG 1369	125 nThrGluGluIleArgGlnSerAspGluValGlyAspArgAspHisArgArgPr 143	143 OGlnGluLysLysLysAlaLysGlyLeuGlyLysGluIleThrLeuLeuMetGlnThrLe	1429 -CAACGTGGCGGGGGGGCTCGAAAGCCAGGGGGGGCAGCTCCCGGAGTGGAAAAATCCCT 1487	163 uAsnThrLeuSerThrProGluGluIysLeuAlaAla	1488	1548 CGAGCCGGACGACCAGCGCACGCTGGACGAATTGCGCCGGCAGACGATAGCCTGGA		1608 ACGACAACAAGCGCTCCACAAGGAATGGCÁÁCAGGCCCTCGACCÁCGCCACGGCCTGGC 1667	207GluLysAspHisLeuArgGlyGluHisSerLysAlaValLeuAlaAr		1728 GAAACGACAAGCCAATGCGCCGAGGAGGTGAAGGCGGCGGAGCAGGCCCTGCAGGT	230ArgGluLeuGlnArgHisAsnArgSerLeuLysGluGluGlyValGlnArgAlaAr 248	1788 CACCCGCGAGTTGCTCCAGCGCCCAACGTCTGGCCCGCCAGCGGCGAGCAACTGCG	248 G	249Gludludludlurshr	1908 CCATTCCGAGCAACTGCTCGCCCCTCGGTGAACACGACGACGACGAGGAGGTCCGGGC		1968 CAAGCAGTCCCTCGAGCGGCTGCGACACCTGGGTCGGTCTGCGCGAGGGCTATTCCAG 2027	274 nHisAsnGluArgAsnSerLysLeuArgGlnGluAsnMetGluLeuAlaGluArgLeuLy 294 2028 CCAGCGGGAAAGACTCAACCAGAGTGCCAGGAGCAGCAGGAACTGACTG		
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----SerAs 424 ::: GCGGACTTT 2438 -LeuLeuLy 348 |||::: GCTGATCGC 2237 uGluGlyLe 444 |::: :: TCAGCAAAT 2498 GGAACACC 2791 ----- 2343 :: -GCAACTGA 2554 GCACAACG 2177 ATTGCGTCC 2384 AGGCGGAAC 2614 SCGCCCAGG 2671 AGACGCTCC 2731 SerLysSe 388 IleLysLy 408 Alapro-- 497 GlnGluMe 331 Argasnas 464 479 ---TyrPr 509 GlnGluPr 525

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1653 GCAGCAGACTCGC-----CTCAAGGAGCTGGAGTCCCAGGTGTCGGAGAAGGA 1706
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:067 CACACTGCAGGCCGAGTGTGACCAGCAGAGCGAGACGGAGGCATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 rThrTyrCysValAspAsnAsnGlnGlyGlyProGlyGluAspGlyAjaGlnGlyGluPr 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         786 GGCGATTCTGAAACGCCAGCTGGAAGAAAAAAAAACTGCTGGCCACAGAAAAAAA
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               PatentIn Release #1.0, Version #1.30
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136
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Matches:
Conservative:
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                                                                                                           APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: JOACHAN L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF353
TELECOMMUNICATION INFORMATION:
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,1478
TLING DATE: 12-No. 6653445-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1.2931
; SEQUENCE DESCRIPTION: SEQ ID
US-09-010-1478-17
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2934 base pairs
                                                                                                                                                                                                                                                                TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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INFORMATION FOR SEQ ID NO: 17:
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STRANDEDNESS: single
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                                                                              462 gAsnAspLeuAsnLys---ArgValGlnAspLeuSerAlaGlyGlyGlnGlySerLeuTh 481
                                 442 uGlyLeuGlnValLysIleGlnArgLeuGluLysLeuCysArgAlaLeuGlnThrGluAr 462
                                                                                                                           481 rAspSerGlyProGluArgArg---ProGlu-------GlyProGlyAlaGlnAlaPr 497
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